

**GENETIC RESISTANCE TO BEAN STEM MAGGOT (*O.SPENCERELLA*) IN  
UGANDAN BEAN GENOTYPES**

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## **DECLARATION**

I declare that my thesis is an original dissertation which has not been submitted to any institution.

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## **DEDICATION**

To my parents Mr and Mrs. Murenju for their love, guidance and provision throughout the years. To my sisters and brothers for the untiring support and encouragement. Lastly, to my husband Odutu Alfred for the love and encouragement without which I would not have come this far.

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## ABSTRACT

Common bean (*Phaseolus vulgaris*.L) production has been greatly affected by the bean stem maggot (BSM), an insect pest which exists in 3 species namely *O.spencerella*, *O.phaseoli* and *O.centrocematis*. Among the 3 species, *O.spencerella* and *O.phaseoli* are of major economic importance and cause up to 100% yield loss. In Uganda, the breeding program seeks to avert this problem by developing resistant varieties for the Ugandan farmers. To achieve this, the breeders require information to guide breeding decisions. The objectives of this study were to determine the level of resistance to the bean stem maggot (*O.spencerella*) in the exotic and local Ugandan bean genotypes, determine the nature of inheritance of BSM (*O.spencerella*) and heritability of resistance to BSM (*O.spencerella*). Genetic variability for resistance to the BSM was determined under natural infestation where the 32 genotypes which included 4 Ugandan varieties and 28 introductions from Malawi that were reported to be resistant to the pest were evaluated for percent plant mortality, number of ovipunctures, number of pupae and stem damage scored on a scale of 1-9. Significant effects were obtained for number of ovipunctures ( $P \leq 0.05$ ), stem damage ( $P \leq 0.01$ ) and number of pupae in the stem ( $P \leq 0.001$ ) suggesting that the genotypes had varying levels of resistance to the BSM under Uganda environments. Several of the screened parents were resistant and moderately resistant with very few being susceptible. Some of the resistant sources that can be utilized include Line 19, 51, 12, 136, 6 and G 21212.

Based on the results of the screening study, 16 Malawi genotypes were crossed to NABE 4, NABE 15, NABE 16 and NABE 17 using a NCD II without reciprocals to generate information about the inheritance of resistance to BSM. The F1 seed were advanced to F2 and the resultant progeny used for the inheritance evaluation. The analysis of variance showed that the general combining ability (GCA) for the male and female parents was not significant for all resistance parameters. Similarly, the specific combining ability (SCA) was also not significant. Both the narrow sense and broad sense coefficient of genetic determination values were low for all resistance parameters which included percent mortality, number of ovipunctures, number of pupae in stem and stem damage. The NS-CGD was in the range of 0.00 to 0.11 and BS-CGD in the range of 0.00 to 0.42. Such estimates suggest that non-additive gene action is more important

compared to the additive gene action in transmitting the genes that confer resistance to the BSM (*O. spencerella*).

The results of the general predictability ratio (Bakers ratio) for the resistance parameters showed that the SCA effects were much higher compared to the GCA effects in conferring resistance to the F2 progeny as the ratio was in the range of 0.00 to 0.37. The NS-CGD and BS-CGD for yield were 0.475 and 0.577 respectively which indicated moderate heritability with GCA effect estimates being higher than the SCA estimates as shown from the general predictability ratio of 83% supporting the predominance of additive gene action in conditioning yield potential.

The evaluation of heritability was also conducted under natural bean fly infestation. The F2 seed derived from the hybridization of the local and Malawi genotypes were advanced to F3 and used for BSM resistance evaluation. The heritability estimates for resistance to BSM were obtained using mid- parent offspring regression. Both the F2 and F3 progeny data which were regressed to the mid parent scores revealed that the F2 and F3 had heritability estimates in the range of 1% - 97% and 4% -37% for the different resistance parameters. This suggests that for some parameters with high heritability estimates, selection should be done early unlike those with low heritability where selection is recommended in later generations.

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# CHAPTER ONE

## INTRODUCTION

### 1.0 Background

#### 1.1 Origin and Evolution

Common bean (*Phaseolus vulgaris*.L) originated from the Americas, where it evolved from a wild growing vine in Middle America and Andes (Gepts & Debouck, 1993) as supported by molecular, morphological and archeological analysis (Singh et al., 1991) and later was domesticated in South America (Chaco'n S et al., 2005) .

The interspecific dispersal of the wild bean populations resulted in the formation of the two broad categories of the Andean and Mesoamerican gene pools (Knüpffer & Ochsmann, 2001). These gene pools were then selected for crop improvement resulting in the different agronomic groups, races and the use differences of the common bean (Knüpffer & Ochsmann, 2001). The gene pools are divided into 6 races; 3 of Middle American origin (Jalisco, Durango, Mesoamerica) and 3 of Andean South American origin (Peru, Nueva Granada, Chile) (Knüpffer & Ochsmann, 2001). The Jalisco climbing bean is from the moist central Mexican highlands while the Durango medium size seeded bean is from the dry highland of Mexico, On the other hand, Mesoamerica small seeded bean is from the low lands of Central America and Mexico (Singh et al., 1991) . The races in the Andean gene pool differ by virtue of their growth habit (Singh et al., 1991).

In Africa where both gene pools are cultivated (Singh et al., 1991), beans of both gene pools were introduced by the Portuguese in the coastal areas (Purseglove, 1976) and have since then spread inland and become a food crop with varying levels of importance and acquired different cultivars with local names (Leakey, 1970).

## **1.2 Importance of common beans**

Worldwide, common bean is the most important grain legume for direct consumption (Broughton et al., 2003). It is the second most important source of calories after maize in most parts of Sub Saharan Africa (SSA) (IBP, 2014) where they account for 4% of the calories (Akibode & Maredia, 2011). The high consumption of the crop is attributed to its nutritional attributes of protein, vitamins, micronutrients (Fe, Zn), minerals (Broughton et al., 2003) and fiber (Dursun, 2007). In Uganda where the bean is consumed both as a vegetable and grain (Hillocks et al., 2006), its calorific contribution is close to 6% (Haggblade & Dewina, 2010) which is slightly higher than that reported for the SSA region. Uganda ranks 3<sup>rd</sup> in the countries where pulses provide 10% of per capita protein intake (Akibode & Maredia, 2011) with an estimate of over 15 million people who regularly consume beans (Anon., 2003) .

As a grain, it is an important cash crop which is marketed in rural and urban areas (Broughton et al., 2003). Uganda consumes nearly 80% of its bean production and the rest is exported to South Sudan, Kenya, Congo, Sudan and Rwanda through informal border trade routes or for relief supply by the world Food Program 9 (WFP) (Anon., 2005). In 2011, Uganda earned approximately USD 20 million from export of 35920 MTs of beans (MAAIF, 2012).

In addition to the roles beans play in nutrition and income generation, they serve a purpose of improving soil fertility through nitrogen fixation (Broughton et al., 2003). For this reason, common beans like other pulses are included in most cropping systems.

## **1.3 Bean production and constraints**

The great lakes countries of Africa, Uganda, Burundi, Rwanda and Congo (Eastern) have high bean production that is mainly based in rural communities (Wortmann & Allen, 1994). These rural communities utilize limited inputs for bean cultivation (Broughton et al., 2003) as a monocrop, in rotations or in associations where it is usually intercropped with cereals, bananas and root crops (Broughton et al., 2003) . According to a report by UBOS (2010), 35.3% of the plots under bean cultivation are of pure stands and mixed stands comprise the other 64.7%.

The country's production is wide spread with high production in the western, northern and central regions (World Bank, 1993). The estimated Ugandan production and yields from 2004 to 2013 as shown in table 1.

**Table 1: Ugandan bean production trend (2004-2013)**

<b>Year</b>	<b>Area harvested ( ha)</b>	<b>Yield (Hg/ha)</b>	<b>Production (tonnes)</b>
2004	812000	5603	455000
2005	828000	5773	478000
2006	849000	4994	424000
2007	870000	5000	435000
2008	896000	4911	440000
2009	925000	4886	452000
2010	952000	4863	463000
2011	983460	4550	447430
2012	1060000	4013	425400
2013	1100000	4191	461000

Source: FAO (2014) FAOSTAT | © FAO Statistics Division 2014 | 20 August 2014

The estimates show that the area under production has increased over the years but the yield and production have not followed the same trend as expected due in part to unimproved cultivars and other production constraints including abiotic and biotic constraints like diseases, insect pests, drought, low soil fertility (Broughton et al., 2003) and nutrient toxicities (World Bank, 1993). A complex of viral, bacterial and fungal diseases attack beans (World Bank, 1993) such as angular leaf spot, rust, anthracnose, Ascochyta blight, floury leaf spot, web blight, scab, root rots and

common bacterial blight (Wortmann et al., 1998). Considerable damage and loss is caused by insect pests before and after harvest. The bean stem maggot (BSM) *Ophiomyia spp* (Diptera: Agromyzidae) is considered the most important bean field pest in eastern and southern Africa (Hillocks et al., 2006) and bruchids are important storage. Some of the other insect pests include aphids, pod borers, foliage beetles, thrips and pod bugs (Wortmann et al., 1998) to which several of the cultivated preferred varieties are prone undermining the farmers' yields.

The bean stem maggot (BSM) exists in 3 species; *Ophiomyia spencerella* (Greathead), *O.phaseoli* (Tyron) and *O. centrosematis* (De Meijere) (Greathead, 1968). Among the 3 species, *O. phaseoli* and *O. spencerella* are more important than *O.centrosematis* with *O. spencerella* causing more damage in some instances. *Ophiomyia centrosematis* is of less economic importance because it normally exists in low numbers (Abate & Ampofo, 1996) since it is a poor competitor compared to the other species (Letourneau, 1994) and also because it has a preference for soybean compared to common bean (Talekar et al., 1988). The species prevalence is dependent on altitude, with *O.phaseoli* and *O.spencerella* being dominant in the lower and higher altitudes respectively (Songa, 1999). The species composition and pattern of infestation vary with location (Abate & Ampofo, 1996) time of sowing (Songa, 1999) and temperature (Oree et al., 1990).

The adults of *O.phaseoli* deposit their slender white eggs on leaves and *O.spencerella* on the hypocotyl of the bean plants though oviposition is not limited to these parts (Karel, 1985). After an incubation period of 2-4 days, the hatched larvae mine through the leaf and petiole then descend to the stem and root and later return to the stem base where pupation occurs and after 7 days, the adult flies emerge (Greathead, 1968).

The stem damage at the stem root junction of the plant caused by the larvae interferes with the vascular system resulting to yellowing and wilting of bean seedlings. Edwards & Singh (2006) reported that when early infestation occurs, even low pest densities cause economic loss. BSM damage is aggravated by late planting and high temperatures which favor the increase in the bean

fly population (Songa, 1999) . Poor soil fertility and drought conditions also increase plant damage by the bean fly (Greathead, 1968).

Several approaches have been recommended for management of BSM which include use of resistant varieties (Miklas et al., 2006), intercropping, insecticide application (Kyamanywa, 1997), use of deep straw mulching (Letourneau, 1994) and seed dressing (Byabagambi & Kyamanywa, 1997). Natural enemies to the BSM like the parasitoid wasp, *Opius phaseoli* (Hymenoptera; Braconidae) can control the pest levels especially of *O. phaseoli* as compared to *O. Spencerella* (Letourneau, 1994).

#### **1.4 Problem statement**

In Uganda, the bean stem maggot (BSM) is the main field insect pest which causes losses of up to 100% (Abate & Ampofo, 1996) especially if early infestation occurs (Nderitu, 1993). The control of the BSM in Africa has mainly dwelt on traditional pest management practices and rarely on the use of pesticides (Abate et al., 2000). The use of chemicals to control the pest poses health risks and kills natural enemies (Clement et al., 1998) since the available chemicals are persistent in the environment (Abate, 1991). The use of natural enemies like the parasitoid *Opius phaseoli* can be opted for to keep the pest population in check, however, they do not reduce the pest population to levels that minimize economic loss (Letourneau, 1994). Intercropping as a method of controlling bean damage by the BSM requires that beans should have a lower population than the other crop in the field. For example for the intercrop control method to be effective, Peter et al (2009) reported that when intercropped with maize, beans should comprise one third of the crop in the field which does not favour the bean farmer. In spite of the extent of bean production devastation due to BSM, no resistant lines have been identified in Uganda. Also literature that exists about the genetic mode of inheritance of resistance has mainly dwelt on *O.phaseoli* Tyron yet the most prevalent species in central Uganda is *O.Spencerella* (Mulumbaa et al., 2012).

## **1.5 Justification**

Uganda has an ever increasing population which must be supplied with food of which beans comprise a major part of the daily diet. The country's bean production is, however, not as high as expected due to numerous production constraints like the bean stem maggot (BSM) which can destroy entire fields causing up to 100% yield losses (Abate & Ampofo, 1996). The use of resistant cultivars has been recorded elsewhere to reduce the dependence on pesticides and ensure stable yields in varied environmental conditions (Miklas et al., 2006).

Several sources of resistance to BSM have been reported but have not yet been utilized in Uganda as most of the research has been done on *O.phaseoli* (Ojwang et al., 2010) .

Research on BSM resistance has shown predominance of additive to non additive gene action (Ojwang et al., 2011). However, most of the work on gene action has been done on *O.phaseoli* so there is no information regarding the nature of inheritance of resistance to *O.spencerella*. In soybean the inheritance to bean fly (*Melanagromyza sojae* Zehner) resistance fits the one major gene together with polygenes where resistance is completely dominant (Wang & Gai, 2001) . The resistance to *O.Spencerella* species in the existing bean germplasm in Uganda is not well documented. According to Ojwang et al (2011), the heritability of resistance to *O.phaseoli* varied between 22% - 45% indicating low to moderate estimates. Heritability estimates for *O.spencerella* have not been documented so there is a need to bridge this gap to enable the Ugandan bean breeding program make informed breeding decisions.

## **1.6 General objective**

The main objective of the study was to establish the natural level of BSM resistance and the nature of inheritance of resistance in the Ugandan genotypes.

## **1.7 Specific objectives**

1. To determine the level of resistance to the bean stem maggot (*O.spencerella*) in the Malawi and local bean genotypes.
2. To determine the nature of inheritance of BSM resistance in the bean genotypes.
3. To determine the heritability of resistance to BSM.

## **1.8 Hypothesis**

1. Malawi and local bean genotypes have different levels of resistance to BSM.
2. The inheritance of resistance to BSM is predominantly additive in nature.
3. The heritability estimates for resistance in Malawi and local bean genotypes to BSM is low.

## CHAPTER TWO

### LITERATURE REVIEW

#### 2.0 Resistance to the bean stem maggot

The ultimate degree of damage done by the BSM is determined by the resistance posed by the host plant exhibited through resistance mechanisms (Rogers, 1979). This resistance is governed by three basic components or mechanisms which include non-preference, antibiosis and tolerance (Maxwell et al., 1972). The non-preference may be for oviposition, shelter or food, primarily due to the presence or absence of some chemical or physical factors (Maxwell et al., 1972).

The resistance to BSM achieved through tolerance has been reported to be available in bean cultivars with tannin like substances in the epidermis and with thickened hypocotyls (Greathead, 1968). Also, high leaf pubescence, thin stems and long internodes have been associated with tolerance of beans to *O.phaseoli* species (Maerere & Karel, 1984). Some local land races in Uganda and Tanzania were found to be resistant to the BSM and this was attributed to their ability to develop adventitious roots and thickened hypocotyles (Greathead, 1968). In the case of *O. spencerella*, Narayan & Wen Jin (1993) reported pigmentation and degree of lignification as the factors that were attributed to plant tolerance. Similar studies have been done for other legumes like soybean and cowpea. For soybean plants, small pubescent unifoliate leaves, small cotyledons and hypocotyls have been associated with resistance (Narayan & Wedanimbi, 1993). Dharmasena & Fernando (1988) reported that in cowpea the resistance to the bean fly was associated to morphological features and the susceptible varieties had high stem moisture, large leaf area and large stem thickness.

Resistance or tolerance levels evaluated during screening experiments rely on several damage and incidence parameters. However, some authors have recommended the use of some parameters at specific stages of plant growth as they provide accurate resistance scores and are consistent. Nderitu (1993) reported that accurate identification of resistant varieties to BSM

should be done early in the crop cycle when the ovipositing female population is high due to their behavioral adaptation to ensure survival of the offspring to maturity by feeding on the most nutritive crop. Scoring for seedling mortality and damage as compared to the bean fly counts and infestation has been recommended by Abate (1990). Maerere & Karel (1984) reported that larval-pupae counts, ovipuncture counts and stem damage recorded at 14 - 42 DAP at 1 week intervals could be used as the criteria for BSM resistance evaluation. The number of larval mines can be used as an indicator for number of oviposition sites since the *O.phaseoli* mine in the leaf lamina remains unbranched for at least 1mm (Rogers, 1979).

In soybean, number of insects in stem and number of insects in the petiole are both indicators of resistance to the bean fly but number of insects in stem is a better parameter as compared to number of insects in the petiole (Wang & Gai, 2001).

Based on these parameters, several sources of resistance have been reported in common bean (Ojwang et al., 2010), haricot bean (Abate, 1990) and soybean (Narayan & Wedanambi, 1993). For most of the crops, varying levels of resistance have been obtained among the screened germplasm since cultivars can differ significantly in their level of non-preference or egg antibiosis status (Rogers, 1979) .

In the screening for resistance to *O.phaseoli*, Ojwang et al., (2010) used geometric mean (GM) selection index and genotype X environment (GE) component analysis to identify resistant genotypes. Genotypes GBK 047821, GBK 047858, CC 888 (G15430) and Macho (G22501) were found to be resistant to bean fly (*O.phaseoli*) basing on their low to moderate values for the resistance parameters (Ojwang et al., 2011).

Sariah & Makundib (2007) reported the Tanzanian bean variety ZPV 292 as tolerant to BSM infestation based on the number of pupae in the bean stems and number of cracked stems. CIAT –Tanzania screened for BSM resistance under natural infestation and found Mlama 49, Mlama 127, G222501 to be resistant to the bean fly (Hillocks et al., 2006).

Mushi & Slumpa (1998) reported that from the screening done in Selian Agricultural Research Institute, 38 lines out of the 214 lines from VEF 90 showed moderate to high resistance to BSM basing on the number of pupae, number of dead plants and plant survival at physiological maturity. Ogecha et al., (2000) recommended 9 out of 21 varieties basing on low percent mortality for release since they were resistant to BSM in western Kenya. Maerere & Karel (1984) based on the damage and incidence parameters to select cultivars A 489, A429, BAT 1570, TMO 118, BAT 1500, A476 and TMO 101 which showed low levels of resistance to the BSM. Other sources of resistance have been found in haricot beans where 4 accessions out of the 1510 screened accessions showed resistance to the agromyzidae bean fly (Abate, 1990). These documented sources of resistance can therefore be utilized by breeding programs to introgress resistance to the market class varieties. Also, the pursuit of potentially useful sources of resistance should begin with cultivars grown or previously grown in the areas of interest before exotics, land races and wild types are screened (Kennedy & Barbour, 1992).

## **2.1 Inheritance of resistance to the bean stem maggot**

Breeders need information regarding the heritability of the traits they intend to improve since it directly influences the decisions about the selection methods for the populations (Fehr et al., 1987). To ascertain the inheritance of trait, information regarding combining ability is important. Breeders use the general combining ability (GCA) values to identify the parents that have potential to combine with other parents and produce offspring with superior performance. According to Jatoi et al (2011) specific combining ability (SCA) is of importance during hybrid crop development while GCA is useful for hybridization and selection programs. Heritability estimates are based on the genetic constitution rather than the non- genetic factors and helps direct the breeders on the selection methods (Fehr et al., 1987).

According to Milkas et al., (2006) common bean insect resistance and tolerance is generally quantitative and controlled by many genes. The expression of the resistance to BSM is attributed more to additive gene effects as compared to non-additive gene effects as reflected from the GCA(59.6%) and SCA (24.3%) values for variation in crosses for plant survival (Mushi &

Slumpa, 1998). Some crosses in the same study indicated that non-additive gene effects were of more importance. The results indicated that BSM resistance was controlled by multiple genes thus the recommendation to use pedigree combined with single pod descent and recurrent methods as the breeding methods..

Ojwang et al (2011) reported general predictability ratios ranging from 0.63-0.9 indicating the predominance of additive gene effects to non-additive gene effects in controlling BSM based on the stem damage, plant mortality and pupae in stem. Dominance is also an important component in the inheritance of resistance to the BSM, however, additive gene effects are greater (Ojwang et al., 2011). The narrow sense heritability values for stem damage of 0.22 - 0.45 indicated low to moderate heritability of the resistance trait which makes it difficult to predict the performance of progeny since some of the resistance is not heritable (Ojwang et al., 2011). Similar findings in relation to the predominance of additive to non additive gene effects in the inheritance of resistance to the BSM were reported by Mushi & Slumpa (1998) but they also noted that for some parental combinations, non-additive gene effects were more important than the additive gene effects.

Distabanjong & Srinives (1985) reported that in mung bean the resistance to bean fly was polygenic and predominantly additive as evidenced from the 6 generations tested i.e. P1,P2, F1, F2, Back cross 1(BC1) and B2. In some trials, non-additive gene effects and dominance were important with dominance towards the resistant parents. Epistatic gene effects were sufficient to be considered as one of the factors affecting the gene action of resistance to BSM.

In soybean, the inheritance of resistance to BSM fitted the one major gene together with polygene model with greater major gene effects than the additive and dominance gene effects of the polygenes. The resistance to BSM was completely dominant and the heritability for the major gene was higher than that of the polygenes (Wang & Gai, 2001).

**CHAPTER THREE**  
**MATERIALS AND METHODS**

**3.0 Genetic plant material**

The genetic material used included twenty eight (28) recombinant inbred lines (RILs) introduced from the Malawi bean breeding program that were reported to be resistant to the BSM. In addition, use was made of four (4) Ugandan susceptible varieties that have both consumer and market demand (Table 2). All the genetic materials were screened for resistance to BMS under natural field infestation.

Table 2: Genetic materials used in the study

Designated line No	Accession name	Source
L 1	BH 21134-1-1-1-M-M-M-M	Malawi
L 88	BH 21134-88-1-1-M-M-M-M	Malawi
L 44	BH 21134- 44-1-1-M-M-M-M	Malawi
L 47	BH 21134- 47-1-1-M-M-M-M	Malawi
L 65	BH 21134-65 -1-1-M-M-M-M	Malawi
L 46	BH 21134-46-1-1-M-M-M-M	Malawi
L 14	BH 21134- 14-1-1-M-M-M-M	Malawi
L 130	BH 21134-130 -1-1-M-M-M-M	Malawi
L 43	BH 21134-43 -1-1-M-M-M-M	Malawi
L 12	BH 21134- 12-1-1-M-M-M-M	Malawi
L 48	BH 21134- 48-1-1-M-M-M-M	Malawi
L 38	BH 21134-38-1-1-M-M-M-M	Malawi

L 42	BH 21134- 42-1-1-M-M-M-M	Malawi
L 80	BH 21134-80-1-1-M-M-M-M	Malawi
G21212	G 21212	Malawi
L 6	BH 21134- 6-1-1-M-M-M-M	Malawi
L 37	BH 21134-37-1-1-M-M-M-M	Malawi
L 136	BH 21134-136-1-1-M-M-M-M	Malawi
L 30	BH 21134-30-1-1-M-M-M-M	Malawi
L 32	BH 21134- 32-1-1-M-M-M-M	Malawi
L 3	BH 21134- 3-1-1-M-M-M-M	Malawi
L 19	BH 21134- 19-1-1-M-M-M-M	Malawi
L 149	BH 21134-149-1-1-M-M-M-M	Malawi
L 139	BH 21134-139-1-1-M-M-M-M	Malawi
L 40	BH 21134- 40-1-1-M-M-M-M	Malawi
L 51	BH 21134-51-1-1-M-M-M-M	Malawi
L 9	BH 21134-9-1-1-M-M-M-M	Malawi
144	BH 21134- 144-1-1-M-M-M-M	Malawi
N 16	NABE 16	Uganda
N 15	NABE 15	Uganda
N 4	NABE 4	Uganda
N 17	NABE 17	Uganda

### **3.1 Description of the study area**

The study was conducted at the National Crops Resources Research Institute (NaCRRI) located in the central region of Uganda. NaCRRI is positioned at 0° 32'N / 32°37'E, at an altitude of 1160 msl. The annual bimodal rain fall received is 994 mm/year with minimum and maximum temperatures of 16.1° C and 29.1° C respectively. The screening experiment was carried out in the field under the natural infestation of the bean flies since *O.Spencerella* is the most prevalent species in central Uganda and Namulonge in particular (Mulumbaa et al., 2012).

### **3.2 Experiment I: Screening for resistance to the bean stem maggot in the Malawi and local genotypes**

#### **3.2.1 Experimental design**

The experiment was established close to a field where a susceptible bean variety (NABE 4) had been planted 3 weeks earlier to increase the bean fly infestation pressure to enable effective screening of the genetic materials. The field experiment was laid out in an alpha lattice design. The 32 genetic materials were planted in 4 lattice blocks with each block containing 8 genotypes and the experiment was replicated twice. The genotypes were planted in 2m rows at a spacing of 50 x 10 cm between and within rows respectively. Each of the 2m row plots had 20 plants from which data was collected.

#### **3.2.1 Data collection**

**Number of ovipunctures:** At 2 weeks after planting, an ovipuncture count on the two primary leaves was obtained from 5 randomly selected plants in accordance with Songa's (1999) method. To ensure that the correct ovipuncture count was obtained, the data collection was done in a knelling position on a bright day, as this eased the visibility of the oviposition sites. For each plant, the ovipunctures of each primary leaf were recorded separately and the average number obtained from the 5 plants calculated.

**Percent plant mortality:** The number of dead plants due to BSM per genotype was recorded from the first to the fourth week and in each week data was collected once. This was done by uprooting the dead plants and critically examining for the cause of stem damage. Confirmation for BSM cause of death was stem damage, presence of larvae or pupae within the dead plant's stem.

**Stem damage and number of pupae in the stem:** At 5 weeks after emergence (WAE) 5 plants from each genotype were randomly selected and carefully uprooted by loosening the soil around the roots with a knife to obtain the entire root system without damage. The plants were then placed in paper bags with the roots properly protected and transported to the laboratory for critical examination of the root surface. This was done by cleaning the root free of soil with the use of a tooth pick. After which the stem damage for each plant was properly scored.

Visual assessment was then done and damage scored on a scale of 1-9 where 1- represented no damage and 9- extreme damage in accordance with Kornegay & Cardona (1998) damage rating scale. The number of pupae were counted after carefully using a tooth pick to remove the sheath and expose the pupae as described by Ojwang et al (2011).

### **3.2.2 Data analysis**

The average for the data collected for number of ovipunctures, percent plant mortality, stem damage and number of pupae in stem were compiled in the excel sheet then imported to Genstat 14<sup>th</sup> edition and subjected to Residual maximum Likelihood (REML) analysis to obtain the variance components. The lattice linear model was used for analysis:

## Equation 1

Lattice linear model  $Y_{ijk} = Y_{...} + R_j + G_i + B/R_{jk} + e_{ijk}$

Where  $Y_{ijk}$  : Individual observation

$Y_{...}$  : Grand mean

$R_j$  : Replication effect

$G_i$  : Genotype effect

$B/R_{jk}$ : Blocks within replication

$e_{ijk}$  : Error

### 3.3 Experiment II: Determining the nature of inheritance of BSM resistance

#### 3.3.1 F1 Population development

In the Namulonge screen house, 16 genotypes that showed high to moderate resistance based on the results of the screening experiment were planted in large buckets measuring (36 x 31 x 14) cm which provided enough space for growing 4 plants per bucket. Staggered planting was done to ensure synchronized flowering between the male and female parents. At the flowering period, the North Carolina II (NCD II) mating design without reciprocals was used to cross the two groups of bean plants i.e. the Ugandan and Malawi genotypes. The Uganda varieties were used as the female parents and the Malawi genotypes used as the male parents since the Uganda preferred market varieties were to be improved.

A 16\*4 NCD II mating design without reciprocals was done to obtain F1 seed for the crosses as shown in table 3.

**Table 3: Parental lines and derived F1 from NCDII mating design**

♂ parents (Resistant lines)	♀ parents (susceptible local varieties)			
	N17	N16	N4	N15
L 47	N17× L47	N16 × L 47	N4 × L 47	-
L 19	N17× L 19	N16 × L 19	N4 × L 19	N15 × L 19
L 65	-	-	N4 × L 65	-
L 43	N17 × L 43	N16 × L 43	N4 × L 43	N15 × L 43
L 51	-	N16 × L 51	N4 × L 51	-
L 80	N17 × L 80	N16× L 80	-	-
L 12	N17 × L 12	N16 × L 12	N4 × L 12	N15 x L12
L 38	N17 × L 38	-	-	-
L 136	N17 × L 136	N16 × L 136	N4 × L 136	N15 × L 136
L 139	-	N16 × L 139	-	-
G21212	N17 × G21212	N16 × G21212	N4 × G21212	-
L 40	N17 × L 40	N16 × L 40	N4 × L 40	N15 × L 40
L 42	N17 × L 42	N16 × L 42	N4 × L 42	
L 32	N17 × L 32	N16 x L32	N4 × L 32	N15 × L 32
L 48	N17 × L 48	N16 × L 48	N 4× L 48	N15 × L 48
L 37	N17 × L 37	N16 × L 37	N4 × L 37	N15 × L 37

Six F1 seeds obtained from each successful cross were then advanced to F2 as a way of generating more seed to be used for evaluating the inheritance of BSM resistance.

### **3.3.2 Experiment for combining ability estimation**

Parental genotypes and the derived F2 progeny were used for the evaluation of combining ability estimates. The experiment was laid out in an already established bean field to ensure a high and fairly uniform pest pressure. In the field, a 10× 7 Alpha lattice design with 2 replications was used for BSM evaluation of the parents and F2 progenies. Each of the 10 blocks had 7 genotypes planted in 2m rows that contained 20 plants. The plants were planted at a spacing of 50 × 10 cm between rows and within rows respectively.

### **3.3.3 Data collection**

Data on number of ovipunctures, percent plant mortality, number of pupae in stem, stem damage was collected as described in 3.3.2. In addition, at maturity, plants were harvested from a 0.5m<sup>2</sup> area, threshed and seeds cleaned. Using a digital weighing scale, the weight of these seeds was obtained and then used to compute the yield per hectare.

### **3.3.4 Data analysis**

The data collected was analyzed using Lattice analysis and GenStat 14<sup>th</sup> edition. F2 progeny and parental data were used to estimate error variance, (Dobholkar, 1999). North Carolina Design II (NCD II) was used to estimate the general combining ability (GCA) and specific combining ability (SCA) for the F2 progenies using the model suggested by Singh & Chaudhary (1997). The general predictability ratio (Bakers ratio) was calculated based on Baker's (Baker, 1978) method.

The analysis of NCD II was based on the linear model suggested by (Lynch & Walsh, 1998)

$$Z_{ijk} = \mu + s_i + d_j + I_{ij} + e_{ijk}$$

Where  $\mu$ : mean phenotype of the population

$s_i$  and  $d_j$ : Additive effects of the  $i^{\text{th}}$  and  $j^{\text{th}}$  parents

$I_{ij}$  : Non additive gene effects due to  $i$  and  $j$  parents

$e_{ijk}$ : Deviation of the observed phenotype of the  $k^{\text{th}}$  offspring of  $i$  and  $j$  parents

The significance for both the GCA and SCA were determined using the student t-test. Variance components were calculated using error variance at an entry mean basis. Since the crosses were derived from parents considered as fixed, the heritability estimates were determined by broad and narrow sense coefficient of genetic determination (BS-CGD& NS-CGD) which were computed from variance components for the GCA, SCA and error estimates. The Baker's ratio was also computed from the same variance components

### **3.4 Experiment III: Determination of the heritability of resistance to BSM**

Parental genotypes together with the F3 progenies (Table 4) were evaluated for resistance under field conditions.

**Table 4: Parental lines and F 3 progenies evaluated for bean stem maggot resistance under field conditions.**

♀	♂	parents			
parents	N17	N16	N4	N15	
		<u>F3 progeny</u>			
L 47	N17*L 47	-	-	N15*L 47	
L 19	N17* L 19	-	-	N15* L 19	
L 43	N17* L 43	-	-	N15* L43	
L 51	N17* L 51	N16* L 51	N4* L 51	-	
L 80	N17* L 80	N16* L 80	-	-	
L 12	N17* L 12	N16* L 12	N4* L 12	-	
L 136	N17* L 136	-	N4* L136	N15* L 136	
L 139	N17* L 139	-	-	-	
G21212	N17* G21212	N16* G21212	N4* G21212	-	
L 40	N17* L 40	N16* L 40	-	N15* L 40	
L 42	-	N16* L 42	N4* L 42	-	
L 32	N17* L 32	N16* L 32	-	-	
L 48	-	-	-	N15* L 48	
L 37	N17* L 37	N16* L 37	-	-	

### **3.4.1 F3 Population development**

After the F2 evaluation of resistance, the remnant F2 seed was advanced to F3 in the screen house. These were planted in plastic troughs measuring 36 x 32 x 14cm and management was provided to ensure proper growth of the F2 plants.

### **3.4.2 Experimental design**

Prior to the establishment of the trail experiment, Nabe17 was planted in an open field to ensure BSM pressure and after 3 weeks the evaluation materials were planted. The F3 progenies together with the parental genotypes were planted in a completely randomized block design (CRBD) with 2 replications. Each of the replications had 31 entries with each having 10 plants at a spacing of 10 by 50 cm between plants and rows respectively.

### **3.4.3 Data collection**

The parameters measured, timing and data collected were the same as indicated in section 3.3.2.

### **3.4.4 Data analysis**

The F3 progeny data was analyzed using Genstat 14<sup>th</sup> edition to obtain a mid-parent-offspring regression and estimate heritability. The mean scores of the F3 progeny were regressed to the calculated mid-parent value (Falconer & Mackay, 1996). The slope of the fitted regression line was used to directly estimate the narrow sense heritability ( $h^2$ ) (Falconer, 1989). The heritability analysis followed the assumptions stated by Fehr (1993):

- i. The character of interest has diploid Mendelian inheritance
- ii. The population is randomly-mated
- iii. The population is either in a linkage equilibrium or has no linkage among loci controlling the trait
- iv. Parents used are non-inbreds

- v. There is no environmental correlation between the performance of the parents and the offspring.

The analysis was also based on the standard linear regression model by Fernandez & Miller (1985) ;

$$Y_i = \beta_0 + \beta_1 X_i + e_i \quad \text{Where;}$$

$Y_i$ : Mean of the progenies of the  $i^{\text{th}}$  family

$\beta_0$ : Intercept

$\beta_1$ : Linear regression coefficient

$X_i$ : mean of the Mid-parent of the  $i^{\text{th}}$  family and  $e_i$ : Random error

## CHAPTER FOUR

### RESULTS AND DISCUSSIONS

#### 4.0 Response of genotypes to the field infestation of the BSM

The results of the analysis of variance of genotypes indicated that the 32 genotypes responded differently for the 3 parameters of resistance (Table 5).

**Table 5: Mean squares for parental genotypes to field infestation of BSM**

SOV	Df	Mean squares			
		OVP	%PMT	SD	PU
Total	63				
Rep	1	102.52	0	0.526	0.49
Rep/block	6			2.973	0.28
Genotypes	31	31.71 *	0.71 ns	3.136 **	0.825***
Error	25	14.97	0.87	1.025	0.185
LEE	21			1.153	0.197
F-prob		0.02	0.714	0.007	0.001
F -value		2.12	0.81	2.72	4.19

Level of significance: \*\*\*  $P \leq 0.001$ , \*\*  $P \leq 0.01$ , \*  $P \leq 0.05$ , OVP = Number of ovipunctures on leaf at 17 DAP, % PMT = % Plant mortality from 1-4 weeks after emergency, SD = Stem damage at 31 DAP, PU =Number of pupae in the stem at 31 DAP

Significant effects were obtained for number of ovipunctures ( $P \leq 0.05$ ), stem damage ( $P \leq 0.01$ ) and number of pupae in the stem ( $P \leq 0.001$ ) suggesting that the genotypes had varying levels of resistance to the bean stem maggot which would allow for selection of resistant genotypes among the different genotypes. The genotypes that showed resistance if acceptable to the farmers and the market could either be used directly by farmers in their field or utilized by breeders to introgress BSM resistance genes into the Ugandan market class varieties.

The results of cultivar means (Table 6) revealed that number of ovipunctures were in the range of 2.65-18.45, with the resistant genotypes recording ovipuncture count on the leaves of less than a score of 3 while the highly susceptible recorded a score of above 14.

**Table 6: Mean reaction scores of the parental genotype under field infestation**

<b>Line</b>	<b>Stem damage</b>	<b>% Mortality</b>	<b>No of Pupae</b>	<b>No of ovipunctures</b>
32	1.698	2.5	0.12	18.45
42	2.315	5	0.492	3.4
51	2.465	2.5	0.319	6.5
6	3.239	2.5	0.628	4.5
12	3.303	12.5	0.589	6.8
19	3.365	2.5	0.418	2.65
G 21212	3.439	2.5	0.628	8.65
136	3.623	2.5	0.541	5.4
37	3.628	0	0.425	5.65
9	3.736	5	0.613	12.5
43	3.903	5	0.789	5.1
47	4.122	0	0.87	3.75
80	4.223	7.5	0.941	5.55

40	4.436	7.5	1.313	8
NABE 4	4.474	7.5	0.983	2.7
NABE15	4.577	0	1.321	7.7
30	4.828	0	1.325	5.9
46	4.838	0	1.258	5.4
NABE16	4.874	2.5	1.583	2.7
48	4.899	7.5	0.804	10.7
130	4.922	2.5	1.17	6.4
139	5.061	0	0.734	14.8
65	5.126	2.5	0.955	5.1
44	5.326	2.5	1.155	5.4
149	5.877	2.5	1.521	12.3
14	5.938	0	2.358	7.65
1	5.997	2.5	2.149	11.8
38	6.115	5	2.292	6.2
144	6.161	2.5	2.334	13.65
3	6.198	0	1.62	14.1
88	6.297	0	1.649	4.3
NABE17	6.299	5	2.304	7.5
Mean	4.54	3.13	1.13	7.54
Sed	1.07	4.66	0.44	3.87
Lsd	2.22	9.52	0.91	7.89
%CV	23.65	149.3	39.24	51.3

The least ovipuncture count was recorded on bean genotypes line 19 (2.65), NABE 16 (2.7) and NABE 4 (2.7) while the highest were recorded on line 32 (18.45), 139 (14.8) and 3 (14.1). The low ovipuncture numbers on the leaves of line 19, NABE 16 and NABE 4 suggested that these genotypes possessed resistance characteristics like high pubescence that limited leaf puncture and oviposition. Mushebezy and Karel (1985) reported that high pubescence density in bean plants is associated with low BSM ovipuncture counts.

The mean performance of most of the genotypes for number of ovipuncture, pupae in stem and stem damage followed a fairly similar trend. This trend was as expected, with genotypes having large number of ovipuncture having more pupae in stem and higher stem damage. The results, however, showed that this was not the case for Line 32 which had the highest number of ovipunctures (18.45) and the least stem damage (1.698) and numbers of pupae in stem (0.12) suggesting that this line had antibiosis resistance which prevented the growth of the mining larvae in the vascular system of the stem. Li et al., (2004) explained this antibiosis mechanism as resistance which was exhibited through reducing the fecundity, longevity and increasing the mortality of the pest such that it does not reach the pupae stage.

Similarly Line 139 had high number of ovipunctures (14.8) and low pupae number (0.734), line 48 had 10.7 ovipuncture count, 0.804 number of pupae and line 9 had 12.5 and 0.613 number of ovipuncture and pupae respectively.

The genotypic means for stem damage were in the range of 1.7 - 6.3 which showed that most of the genotypes had resistance genes with a few that showed moderate susceptibility for stem damage based on the scale of Kornegay & Cardona (1998). The least stem damage was shown by Line 32 (1.698), line 42 (2.315) and line 51 (2.465) which had means in the range of 1-2.5 suggesting that they were resistant while line 88 (6.297) and NABE 17(6.299) had the highest means therefore had more stem damage and were rendered susceptible (Kornegay & Cardona, 1998).

The results also showed that among the Ugandan preferred market class varieties NABE 4, NABE 15 and NABE 16 which had low scores for the stem damage, number of pupae in stem and number of ovipunctures were more resistant to the bean stem maggot than NABE 17. NABE 17 had a stem damage rating of 6.299 and 2.304 number of pupae therefore was considered susceptible to the pest (Kornegay & Cardona, 1998). Abate (1990) recommended the use of stem damage as the best indicator for BSM resistance.

This study focused on the *O.spencerella* species and genotype G21212 was found to be resistant owing to its low means for stem damage (3.439), number of pupae (0.628) and number of ovipunctures (8.65). In earlier screening work for resistance to *O.phaseoli* under natural infestation, same genotype was found to be resistant to the species (Ojwang et al., 2010).

The correlation analysis (Table 7) of all the parameters revealed that number of pupae in the stem was strongly and positively correlated to stem damage ( $p \leq 0.001$ ) which indicated that stem damage could be effectively used to predict the number of pupae in stem score and facilitate indirect selection for resistant genotypes (Hallauer et al., 1988).

**Table 7: Correlation analysis for the resistance parameters to the bean stem maggot**

	% Mortality	No ovipunctures	No Pupae	Stem damage
% Mortality	1			
No_of_ovipunctures	-0.094	1		
Pupae	-0.155	0.096	1	
Stem_damage	-0.222	0.116	0.883***	1

Level of significance: \*\*\*  $P \leq 0.001$

On the other hand, number of ovipunctures had a weak positive correlation to number of pupae in stem and stem damage. Due to this weak correlation, number of ovipunctures cannot be used reliably to indicate the level of resistance of the genotypes. Greathead (1968) and Songa (1999) reported that not all leaf punctures have eggs deposited in them and, therefore, number of ovipunctures is just an indication of the level of adult bean fly infestation on the bean plant but not resistance of a genotype.

Results from the North Carolina Design (NCD II) analysis of variance for percent plant mortality, number of ovipunctures, stem damage, number of pupae in stem and yield are presented in Table 8.

**Table 8: NCD II Analysis of variance for BSM resistance for the male and female parental groups in the F2 generation**

SOV	DF	Mean squares					
		% MT	OVP 2	OVP4	No pupae	SD	Yield(t/ha)
GCAf	3	4.692	21.080	7.9	0.070	0.199	127240
GCAm	15	9.563	21.200	18.95	0.077	0.474	38666
SCA	29	8.213	33.380	25.33	0.069	0.525	133517
Error (lattice)	53		20.845	15.12	0.097	0.333	107768.5
Error (RCB)	71	6.140					
$\delta$ GCAf		-0.12067	0.020	-0.602	-0.002	-0.011	118259.3
$\delta$ GCAm		1.141	0.118	1.277	-0.007	0.047	2743.167
$\delta$ SCA		2.073	12.535	10.210	-0.028	0.192	25748.5
Baker's ratio		0.369	0.011	0.062	0	0.206	0.825
NS-CGD		0.111	0.004	0.026	0	0.064	0.475
BS-CGD		0.335	0.378	0.419	0	0.407	0.577

OVP 2 and OVP 4: Number of ovipuncture at week 2 and week 4 respectively

% MT: Percent mortality. SD: stem damage, GCAm and GCAf: General combining ability for male and female parents, SCA: Specific combining ability, NS-CGD: Narrow sense coefficient of genetic determination, BS-CGD: Broad sense coefficient of genetic determination.

The general combining ability for male (GCAm) and female (GCAf) parents were not significant for any of the parameters thus indicating that both the selected male and female parents did not contribute significantly to the bean genotype resistance for the bean stem maggot. Similarly, the specific combining ability was not significant for all parameters in the generalized NCD II ANOVA suggesting that the individual parental combinations were similar in terms of their difference from the predicted performance based on the means and the GCA values.

Both the narrow sense and broad sense coefficient of genetic determination values were low for all resistance parameters with the Narrow sense coefficient of genetic determination (NS-CGD) lying in the range of 0.00 to 0.11 and Broad sense coefficient of genetic determination (BS-CGD) in the range of 0.00 to 0.42. Low NS-CGD estimates especially for the pupae in stem (0.00) suggested the importance of non-additive gene action in the inheritance of resistance to the bean stem maggot. The performance of the progeny cannot, therefore, be predicted from the parental performance since inherited portion is very small. These results are in contrast to the reports of Ojwang et al (2011) who used a different set of genotypes and reported low to moderate narrow sense heritability estimates in the range of 0.22 to 0.45 and the predominance of additive to non-additive gene action in the study of *O. phaseoli* resistance. The low estimates of the narrow sense coefficient of genetic determination suggested that high selection pressure needs to be used during the breeding process (Gonzales et al., 2004).

The results of the general predictability ratio (Bakers ratio) for the resistance parameters showed that the SCA effects were much higher compared to the GCA effects in conferring resistance to the F2 progeny as the ratio was in the range of 0.00 to 0.37 (Table 8) implying that dominance and other forms of epistasis are important in controlling the resistance to BSM. Ojwang et al. (2011) reported general predictability ratios ranging from 0.63-0.9 indicating predominance of additive gene effects to non-additive gene effects but, Wang & Gai (2001) reported that in soybean, the inheritance of resistance to the bean fly (*Melanagromyza sojae* Zehntner) was completely dominant with the heritability for the major gene being higher than that of polygenes. Distabanjong and Srinives (1985) and Mushi and Slumpa (1998) reported the importance of

additive gene action but acknowledged that non-additive gene effects were also important and could not be ignored as was the case in the current study.

The NS-CGD and BS-CGD for yield were 0.475 and 0.577 respectively which indicated moderate heritability with GCA effect estimates being higher than the SCA estimates as shown from the general predictability ratio of 83%. Such a high percentage suggested the important role of additive gene action in conditioning yield potential. The predominance of additive gene effects suggested that yield could reliably be selected for in early generations using simple selection procedures like pure line selection and pedigree (Singh & Oswalt, 1991). Similar results of the predominance of additive gene action for yield inheritance were reported by Ojwang et al (2011).

#### 4.1 Combining ability effects for parents

Results of the female and male parent GCA effects for all the parameters are presented in Table 9.

**Table 9: Estimates of general combining ability of female and male parents**

Parents	%PMT	OVP 2	OVP4	SD	pupae	Yield
♀ parents						
N 16	0.760	1.887	0.326	0.096	-0.062	-5.708
N 17	-0.970	-0.663	0.146	-0.141	0.056	-142.708
N 4	-0.210	-0.143	-1.154	-0.014	0.004	85.292
N 15	0.590	-1.993	1.154	0.084	0.012	103.292
♂ parents						
L 19	-1.763	0.126	-4.151*	0.636*	0.183	-3.146
L 65	-0.263	-5.444	-2.071	0.872	0.455	-240.146
L 43	1.367	0.056	1.919	0.357	0.006	81.854
L 51	-1.993	-5.304	5.729*	-0.203	-0.014	180.854
L 80	-0.363	-1.004	0.319	-0.448	-0.163	-102.146
L 12	1.337	-0.134	1.969	-0.245	0.061	-74.146
L 38	2.997	2.706	-2.471	-0.234	0.113	183.854
L 136	-0.513	0.526	-2.631	-0.278	-0.006	122.854
L 139	-3.733	-3.604	-3.611	-1.04	-0.44	-20.146
G21212	-0.333	4.166	-1.461	-0.395	-0.11	183.854

L 40	0.117	-3.944	0.069	-0.388	-0.242	39.854
L 42	-1.163	-0.384	-1.711	0.462	0.258	52.854
L 32	3.867**	2.446	3.759	-0.145	-0.041	-88.146
L 48	1.367	-1.954	0.239	0.028	0.023	-73.146
L 37	-1.133	3.866	0.169	-0.019	0.099	-177.146
L 47	-1.763	0.876	0.549	0.374	-0.123	-45.146

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% PMT= percent plant mortality, SE= standard error, OVP 2=number of ovipunctures at week 2, OVP4= Number of ovipunctures at week 4, SD= Stem damage, N=NABE variety, L=Line number, \*\*\*, \*\*, \* = Significant levels at  $P \leq 0.001, 0.01, 0.05$  respectively

The female parents had non -significant GCA effects for all the resistance parameters and yield. For resistance of a genotype to a pest, significant negative GCA values are desired (Ajala et al., 2008) since such estimates are possessed by genotypes which confer resistance to the pest. Among the female parents, NABE 4 had negative GCA values for percent mortality (-0.210), stem damage (-0.014), number of ovipunctures at 2 weeks (-0.143) and at 4 weeks (-1.154). This indicates that this particular variety was the best general combiner as compared to the other female parents and can be utilized effectively in the breeding program. NABE 17 which had negative GCA values for percent mortality (-0.970), number of ovipunctures at week 2 (-0.663) and stem damage (-0.141) could also be utilized for hybridization.

For yield, positive GCA estimates are desired (Nsabiyera et al., 2013) and were obtained for NABE 4 (85.292) and NABE 15 (103.292). Among the female parents, NABE 17

(-142.708) and NABE 16 (-5.708) were the poor general combiners for yield since they had negative GCA values and therefore are not suitable for inclusion in the hybridization program.

Among the male parents, Line 139 was the best general combiner for resistance to the BSM since it had negative GCA effects (Ajala et al., 2008) for percent plant mortality (-3.733), number of ovipunctures at week 2 (-3.604) and week 4 (-3.611), stem damage (-1.04) and number of pupae in stem (-0.44). The results are evidence that line 139 strongly introgressed its resistance genes for BSM to the progeny. The same genotype was however a poor combiner for yield as shown by the negative GCA estimate

(-20.146). Line 51, Line 80, Line 136 and G21212 also had negative GCA values for most of the parameters indicating that they are good general combiners for resistance to the bean stem maggot. L 19 had a significant negative ( $p \leq 0.05$ ) GCA value estimate for number of ovipuncture at week 4 suggesting that it contributed to BSM resistance. Results further indicated that some of these genotypes like Line 51(180.854), Line 136 (122.854) and G21212 (183.854) are good general combiners for yield, so they can be utilized in breeding for both yield and bean stem maggot resistance. L 43, however, contributed negatively to resistance since it had all positive GCA effects for all parameters and was, therefore, the worst combiner among the male parent. Significant positive GCA effects were shown by Line 19 ( $P \leq 0.05$ ) for stem damage and Line 32 ( $P \leq 0.01$ ) for percent mortality indicating that they significantly contributed to susceptibility of the F2 progeny to the bean fly.

Line 38 (183.854) and G21212 (183.854) were the best general combiners for yield while Line 65 (-240.146) and Line 37 (-177.146) were the worst combiners for the character.

#### **4.2 Specific combining ability estimation**

The results of the estimates for specific combining ability effect are presented in Table 10

**Table 10: Estimates of specific combining ability for the crosses**

Female	Male	% MT	OVP 2	OVP 4	SD	No Pupae	Yield
N4	12	-4.097*	6.455	1.508	3.514	-0.166	-359.053
N4	19	-0.998	-7.206	0.242	-8.034	0.019	-216.032
N4	32	-1.623	-1.468	-7.627**	5.879	0.013	197.2181
N4	37	3.377	-1.103	-4.21	2.251	0.05	274.2181
N4	40	2.127	-0.108	-1.764	0.557	-0.047	484.9681
N4	42	0.903	0.832	2.959	-2.917	-0.08	-280.053
N4	43	-4.123*	-3.486	1.083	-5.748	0.098	571.2181
N4	47	-0.998	-5.416	-2.537	7.151	0.113	23.71808
N4	48	3.377	11.469	2.255	8.525	0.063	-644.032
N4	51	-0.765	1.545	7.053*	-6.772	0.062	170.247
N4	65	0	0	0	0	0	0
N4	136	0.252	1.872	-1.757	3.21	-0.11	231.9681
N4	G21212	2.57	-3.385	2.796	-7.616	-0.013	-454.386
N15	12	0.078	-8.574	-0.682	-8.674**	-0.563	113.1875
N15	19	0.703	5.174	0.752	2.994	0.437	270.9375
N15	32	0.078	-5.409	9.500***	-17.218	-0.056	-138.813
N15	40	-3.672	6.731	-3.924	9.419	-0.091	-237.063
N15	43	2.578	-0.206	-5.908*	5.022	0.083	-405.813
N15	37	0.703	3.224	-4.333	16.224	0.293	292.6875

N15	48	-2.422	-0.991	1.792	-4.774	-0.207	218.9375
N15	136	1.953	0.051	2.803	-2.993	0.105	-114.063
N16	12	-0.067	-4.576	1.916	-4.34	0.468	-217.547
N16	19	-1.968	6.553	-0.959	9.569**	-0.384	-75.5258
N16	32	2.407	6.631	1.817	8.319	0.031	42.72417
N16	37	-2.593	3.446	-4.661	10.88	0.385	8.724167
N16	40	-1.343	-6.699	7.219**	-10.854	0.117	87.47417
N16	42	-0.067	0.581	-3.378	6.589	-0.112	-276.547
N16	43	4.907**	5.383	6.323*	1.729	-0.05	133.7242
N16	47	-1.968	5.373	-1.334	-	0.025	-313.776
					21.989**		
N16	48	2.407	-7.822	-1.122	-3.283*	-0.238	395.4742
N16	51	0.765	-1.545	-7.053*	6.772	-0.062	-170.247
N16	80	1.635	0.322	1.939	0.079*	-0.255	-164.073
N16	136	-3.218	-1.809	0.964	-0.965	0.032	153.4742
N16	139	0	0	0	0	0	0
N16	G21212	-0.9	-5.836	-1.671	-2.505	0.044	396.12
N17	12	-0.862	6.232	9.553***	-4.457**	0.129	-396.13
N17	19	2.263	-4.521	-0.035	-4.529	-0.072	20.62025
N17	32	-0.862	0.247	-3.69	3.02	0.012	-101.13
N17	37	4.164*	-1.88	-3.424	0.827	-0.302	576.5994

N17	38	0	0	0	0	0	0
N17	40	2.888	0.077	-1.531	0.878	0.022	-335.38
N17	42	-0.836	-1.413	0.419	-3.672	0.192	556.5994
N17	43	-3.362	-1.691	-1.498	-1.003	-0.13	-299.13
N17	47	2.263	-3.181	8.205**	-1.386**	-0.431	-2.62975
N17	48	-3.362	-2.656	-2.925	-0.468	0.383	29.62025
N17	80	-1.635	-0.322	-1.939	-0.079*	0.255	164.073
N17	136	1.013	-0.113	-2.009	0.748	-0.026	-271.38
N17	G21212	-1.67	9.22	-1.125	10.122	-0.031	58.26609

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SE	1.752	0.649	2.750	0.408	0.22	232.130
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% MT= percent plant mortality, OVP 2=number of ovipunctures at week 2, OVP4= Number of ovipunctures at week 4, SD= Stem damage, \*\*\*, \*\*, \* = Significant levels at  $P \leq 0.001$ , 0.01, 0.05 respectively

Parental combinations which have negative SCA for pest (BSM) resistance traits are desired (Ajala et al., 2008) for breeding purposes. For percent mortality, crosses N4 x L 12 and N4 x L 43 had negative significant ( $p \leq 0.05$ ) SCA estimates therefore possess BSM resistance genes and should be included in the breeding program for further advance. The SCA effects for N16 x L 43 and N 17x L 37 were positive and significant at 0.01 and 0.05 respectively therefore should not be utilized for the resistance breeding since they confer susceptibility.

Number of ovipunctures at week 4 had significant ( $p \leq 0.001$ ) and positive SCA estimates for crosses N15 x L 32 and N17 x L 12. Crosses N16 x L 43 and N 4 x L 51 had positive SCA values that were significant at  $p \leq 0.05$ . Similarly, crosses of N16 x L40 and N17 x L47 had positive and significant ( $p \leq 0.01$ ) SCA effects. These single cross combinations have the

undesired susceptible genes therefore cannot be included for further hybridization. On the contrary, crosses N15 x L 43 and N16 x L 51 which had negative and significant ( $p \leq 0.05$ ) SCA estimates for number of ovipunctures can be included for further hybridization since they have BSM resistance genes.

For stem damage, crosses of N15 x L12, N 16 x L47, N17 x L 12 and N17 x L47 had significant ( $p \leq 0.01$ ) and negative SCA values. The SCA effects for stem damage for crosses N16 x L 48, N17 x L80 were negative and significant at  $p \leq 0.05$ . For the same trait, cross N16 x L80 had a significant negative SCA value at  $p \leq 0.05$ . This implies that the parents of these crosses introgressed their resistance genes to the progeny and these specific combinations can be used in the breeding program in the development of BSM resistant bean varieties. On the other hand, cross of N16 x L19 had a significant positive SCA value at  $p \leq 0.01$  therefore should not be included for advance in the breeding program.

The crosses that had NABE 17 as the female parent performed better for resistance as evidenced from the negative SCA values for most parameters per cross which was expected owing to the fact that it was a good general combiner (Table 10) for resistance to the bean stem maggot.

Crosses for NABE 4 with line 40 and 43 gave high SCA estimates for yield and also had negative SCA effects for resistance traits suggesting that progenies from these crosses could give better yields a breeding program and also confer resistance to the pest. Number of pupae in stem, number of ovipunctures and yield did not have any significant positive or negative SCA effects implying that the resistance performance of the specific combinations from the hybridization did not differ.

### **4.3 Parent-offspring regression analysis**

The results of the parent-offspring regression analysis of F2 and F3 progeny data for the resistance parameters are presented in table 11.

**Table 11: Analysis of variance for regression of F2 and F3 means on the mid parent means**

Mean squares										
Source	Df	F2					F3			
		% PMt	OVP2	OVP4	PU	SD	% PMt	OVP2	OVP4	SD
Regression	1	0.695	0.26	10.06	0.237	0.771	0.65	83.25	0.52	5.389**
Residual	29	6.914	26	20.78	0.07	0.461	13.29	23.43	24.34	0.483
Total	30	6.707	25.14	20.42	0.075	0.472	12.87	25.42	23.51	0.472
b		0.01	0.02	0.16	0.49	0.97	0.109	0.37	0.04	0.366
R <sup>2</sup>		0.0035	0.0003	0.0164	0.105	0.2778	0.002	0.109	0.0007	0.055

Df= degrees of freedom, % PMT= percent plant mortality, OVP 2=number of ovipunctures at week 2, OVP4= Number of ovipunctures at week 4, PU= Number of pupae, SD= Stem damage, b = regression coefficient, R<sup>2</sup> = coefficient of determination, \*\*, \* = Significant levels at P≤ 0.01, 0.05 respectively.

The analysis of F2 progeny data showed that the variance for all parameters were not significant suggesting that the response of genotypes did not vary for resistance to the bean stem maggot and therefore could not allow for selection.

The regression coefficient “b” which is a direct estimate of narrow sense heritability ( $h^2$ ) (Poehlman & Sleper, 1995) was in the range of 0.01 - 0.97 (Table 11). Resistance parameters like percent plant mortality (1%), number of ovipunctures at week 2 (2%) and week 4 (16%) had low estimates of heritability which implies that these traits are conditioned by non-additive gene effect and, therefore, selection for resistance based on these parameters should be done in later generations (Poehlman & Sleper, 1995). A high heritability estimate was obtained for stem damage (97%) and a moderate heritability for pupae in stem (49%) indicating the predominance of additive gene action in conditioning the resistance of the bean plants to the BSM based on

these traits. The selection method used by the breeding program for these traits should be those implemented in early generations which will save the resources and obtain quick genetic advance (Poehlman & Sleper, 1995). The regression coefficient of determination showed that only about 27% ( $R^2$ ) variation of the F2 progeny means can be explained by their parental means, therefore phenotypic selection of progeny based on their parental means cannot be reliably used by the breeding program.

The F3 parent offspring regression analysis of results showed significance of the variance for stem damage at  $p \leq 0.01$  respectively. Results showed non-significance for percent plant mortality, number of ovipunctures at week 2 and week 4. The regression coefficient ( $b$ ) which gives an indication of the narrow sense coefficient of genetic determination for percent plant mortality (10.9%), number of ovipunctures at week 2 (37%) and week 4 (4%), stem damage (36.6) were low. Low estimates for the narrow sense heritability implied that the inheritance of these traits is predominantly controlled by non-additive gene action, therefore, the selection based on these characters should be done in later generations (Singh & Oswalt, 1991) and high selection pressure should be used (Gonzales et al., 2004). The F3 progeny mean scores could only be explained by their parental values up to a percentage of 10% based on the coefficient of determination ( $R^2$ ) values making prediction of progeny performance based on parental scores difficult and unreliable.

## CHAPTER FIVE

### CONCLUSION AND RECOMMENDATIONS

#### 5.0 Conclusion

The study revealed that there was genetic variability among the Malawi and local bean genotypes utilized in the study. Several of the screened parents were resistant or moderately resistant with very few being susceptible. Sources of resistance identified included Line 19, 51, 12, 136, 6 and G 21212. The Ugandan varieties whose resistance levels were earlier unknown were found to possess considerable amount of resistance.

The inheritance study revealed that non-additive gene action was more important compared to the additive gene action in transmitting the genes that confer resistance to the BSM (*O. spencerella*). The results also showed that it was not possible to predict the performance of the progeny based on the parental performance. The yield predictability ratios, however, indicated the predominance of additive gene action for yield.

The heritability study based on mid- parent offspring regression revealed that both non-additive and additive gene action is responsible for conditioning resistance to *O. spencerella*. The heritability estimates for other resistance parameters were low but some parameters like pupae in stem and stem damage had high narrow sense heritability estimates.

#### 5.1 Recommendations

The following have been recommended:

- The genotypes Line 19, 51, 12, 136, 6, G 21212 and Line 139 should be used for introgression as they showed considerable resistance to *O. spencerella*. For yield, line 38 and G21212 were the best general combiners and so should be utilized for hybridization.

- An in-depth study should be conducted to ascertain the morphological and chemical characteristics possessed by the resistant genotypes. This will ease the selection of resistant genotypes to be used in the breeding program.

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