

## PHENOTYPIC AND GENOTYPIC VARIATION IN TROPICAL MAIZE INBRED LINES FOR RESISTANCE TO THE MAIZE WEEVIL AND LARGER GRAIN BORER

MWOLOLO JK<sup>1</sup>, OKORI P<sup>1</sup>, MUGO S<sup>3</sup>, TEFERA T<sup>3</sup>, YOSEPH B<sup>3</sup>, OTIM M<sup>4</sup> & MUNYIRI SW<sup>1,5</sup>

<sup>1</sup>Makerere University, P. O. Box 7062, Kampala, Uganda

<sup>2</sup>Pwani University College, P.O. Box 195, 80108 Kilifi, Kenya

<sup>3</sup>International Maize and Wheat Improvement Center (CIMMYT), P. O. Box 1041-00621, Village Market, Nairobi, Kenya

<sup>4</sup>National Crops Resources Research Institute, Namulonge, P.O. Box 7084 Kampala, Uganda

<sup>5</sup>Chuka University College, P.O. Box 109, Chuka 60400, Kenya.

### ABSTRACT

The maize weevil (*Sitophilus zeamais*) and larger grain borer (*Prostephanus truncatus*) are economically-important postharvest insect pests that cause severe losses in stored grain. The use of host-plant resistance is the most effective and benign way of overcoming storage-pest damage. The objectives of this study were to estimate heritability and to identify maize inbred lines with dual resistance to weevil and larger grain borer (LGB). One hundred and twenty (120) inbred lines were evaluated in the field for adaptation and tested in the laboratory for resistance to the LGB and weevil. Insect-damage parameters namely grain damage, weight loss, flour weight and number of insects, were measured. Heritability, genotypic and phenotypic variances for the damage traits were determined. Genotype stability for insect pest resistance was determined based on genotypic variance and coefficient of variation (CVi) for each genotype. There were significant differences ( $P < 0.001$ ) among the lines for all the traits measured. Heritability values were high (ranging from 0.7-0.9) in all the traits, and the genotypic variance was higher (ranging from 0.012-0.04) than the environmental variances (0.007-0.033) for all the traits. Dual resistance and stability were observed in CKSPL10028, CKSPL10035, CKSPL10088, CKSPL10021, CKSPL10042, CKSPL10295 and CKSPL10112.

**KEYWORDS:** Postharvest Insect Pests, *Prostephanus Truncatus*, *Sitophilus Zeamais*, Host-Plant Resistance

### INTRODUCTION

Maize is an important crop in Kenya, serving both as staple and as a source of income. Maize grain needs proper storage after harvesting in order to maintain its constant supply as source of food (Adetunji, 2007). Despite the importance of maize, postharvest insect pests cause serious losses in both quality and quantity, particularly in the tropics and sub-tropics. The *Sitophilus zeamais* (Motschulsky) (Coleoptera: Curculionidae) causes annual postharvest losses in maize of 20-30 % on average by making tunnels in the maize grains (Rees, 2004). The larger grain borer (LGB) (*Prostephanus truncatus* (Horn) (Coleoptera: Bostrichidae)) is an exotic postharvest insect pest responsible for losses of maize worldwide, and the pest has now spread to more than 18 African countries (Omondi et al., 2009; Tefera et al., 2010). The LGB causes qualitative and quantitative grain losses by feeding on the kernels and burrowing into them for oviposition. Losses due to the LGB are estimated to range from 9-45% depending on the duration of storage (Gueye et al., 2008; Kumar, 2002). The damage caused by the maize weevil and LGB is irreversible and leads to huge losses, thus aggravating food insecurity. The two pests are of economic importance in the tropics, hence breeding for resistance to them is crucial. The use of resistant varieties is the cheapest, most effective and ecologically safest method of protecting grain against insect pests, since it does

not require any special technology to be adopted by the farmer: a factor which would influence favorably the adoption rate of improved maize varieties.

Maize inbred lines represent a fundamental resource for studies in genetics and for plant breeding towards crop improvement. Though mainly used in hybrid development, they are also critical for genetic diversity studies including the development of linkage maps, and for conducting phenotype-genotype association analyses in plant species in relation to traits of interest (Burr et al., 1998; Thornsberry et al., 2001).

Quantitative inheritance for postharvest insect-pest resistance has been confirmed in maize (Derera et al., 2001; Dhliwayo and Pixley, 2003). Quantitative resistance in general can be affected by genotype x environment interaction (G x E) leading to plasticity of expression across different environments (Pinnschmidt and Hovmøller, 2002). An adequate understanding of the G x E component is essential in order to maximize the use of host-plant resistance for the management of crop pests or diseases. Different concepts of stability have been identified (Lin et al., 1986). Stability of a genotype is denoted if its variance in different environments is small and is accordingly referred to as static stability (Becker and Léon, 1988). This concept is useful for traits such as resistance to diseases or other biotic stress factors, and the parameters used to describe this type of stability are the co-efficient of variability for each genotype and the genotypic variances across environments (Francis and Kannenberg, 1978; Letta and Tilahun, 2007). In order to deploy genotypes effectively across wide environmental conditions, it is imperative that G x E interactions are clearly understood.

Genetic variability is important for progress in breeding programs and new sources of resistance are needed for effective breeding for resistance to postharvest insect pests (Tefera et al., 2011a). Understanding the genetic variability is the starting point for gaining better knowledge of the biochemical, biophysical and genetic basis of host-plant resistance; this is essential in ensuring that traits being selected meet consumer demands. The exploitation of maize inbred lines for the generation of hybrids resistant to postharvest insect pests requires a detailed knowledge of the genetics among the inbred lines and an understanding of their genetic diversity. Provision of the genetic information among diverse inbred lines in response to maize weevil and larger grain borer attack would form a basis for a stable breeding program towards addressing postharvest losses. The different genotypic components of variance and heritability are important in determining selection efficiency (Omoigui et al., 2006). The objective of this study was, therefore, to estimate genetic variability and to identify inbred lines with dual and stable resistance to the maize weevil and LGB.

## **MATERIALS AND METHODS**

### **Germplasm**

One hundred and twenty (120) maize inbred lines including resistant and susceptible checks were used in the study. These included lines which had been developed for storage pest resistance, drought tolerance, stem borer resistance and yield in the CIMMYT breeding programs

### **Experimental sites and design**

Field trials were established at the Kiboko and Embu centers of the Kenya Agricultural Research Institute (KARI). Kiboko is a dry, mid-altitude agro-ecological zone, situated at about 975 m above sea level, while Embu is a moist, mid-altitude zone at 1350 m above sea level. The test lines were planted in an alpha lattice design (20 x 6) with two rows of 5 m replicated three times at each location for two seasons in 2010 and 2011. Two seeds were planted per hill and later thinned to one, giving a density of 53,333 plants per hectare. In order to ensure a healthy crop, agronomic practices including weeding, fertilizer application, stem-borer control and supplemental irrigation were done when necessary. At

harvest the maize ears were sun dried to a moisture content of 12-13% and shelled to obtain grains for insect-resistance bioassays.

### Evaluation of Maize germplasm for Resistance to the Maize Weevil and LGB

The insects used in the experiment were obtained from the KARI/CIMMYT Kiboko Maize Entomology Laboratory where they were reared on the grains of maize cultivar PH3253 under controlled conditions (28°C and 75% relative humidity (R.H.)). The maize grains were disinfested by fumigating with phostoxin tablets for seven days to eliminate field infestation. Samples of 100 grams of grain were taken from each plot of the three replications. The kernels were placed in two separate 250 ml jars, infested with 50 unsexed 7-10 day old maize weevils and LGB separately, and stored for three months at 26-28°C and 70-75% R.H. in the Entomology laboratory at KARI/CIMMYT Kiboko. The experimental design in the laboratory was a completely randomized design replicated three times for each of the two insect pests.

### Data Collection

After 90 days, the contents in each jar were sieved to separate grains, insects and flour. The grain weight loss and flour produced were measured and the number of adult progeny counted. The percentage grain-weight loss was determined by subtracting the final weight from the initial weight and expressing it as a percentage (Tefera *et al.* 2011b). The weight of the flour produced was measured with an electronic balance and expressed as a percentage of the initial weight. Data on flour produced (%) and weight loss (%) was arcsine transformed, while progeny data was log transformed before statistical analyses.

### Statistical Analysis

The data for individual and combined locations was subjected to analysis of variance complemented with Tukey's honestly significant difference (HSD) multiple range test for the individual traits using the GLM procedure of SAS. The genetic variability was computed based on the grand mean, mean squares and error variances of the traits evaluated. The phenotypic and genotypic variations were estimated according to Uguru (2005):

$$V_p = MSg/rl \quad (1)$$

$$V_g = (MSg - MSe)/rl \quad (2)$$

$$V_e = MSe \quad (3)$$

where  $V_p$ ,  $V_g$  and  $V_e$  are phenotypic, genotypic and environmental variances, respectively;  $r$  = number of replications;  $l$  = number of locations;  $MSg$  = mean square;  $MSe$  = mean square error.

Phenotypic coefficient of variation ( $P_{cv}$ ), genotypic coefficient of variation ( $G_{cv}$ ) and environmental coefficient of variation ( $E_{cv}$ ) for comparing the variations among traits were computed according to the method suggested by Allard (1960):

$$P_{cv} = (\sqrt{V_p}/X) * 100 \quad (4)$$

$$G_{cv} = (\sqrt{V_g}/X) * 100 \quad (5)$$

$$E_{cv} = (\sqrt{V_e}/X) * 100 \quad (6)$$

where  $X$  is the grand mean for each trait.

The broad sense heritability was calculated as the ratio of the genotypic variance ( $V_g$ ) to the phenotypic variance ( $V_p$ ) (Allard, 1960). Stability was determined using the genotypic variance ( $S_i^2$ ) and the genotypic co-efficient of variation (CVi) which have been suggested as appropriate measures of stability of static traits based on the percentage weight loss (Letta and Tilahun 2007; Xie and Mosjids 1996). The two statistics were computed as shown:

$$S_i^2 = \sum_{j=1}^q (X_{ij} - \bar{\sigma}_i)^2 / q - 1 \quad (7)$$

$$CV_i = S_i / \bar{\sigma}_i * 100 \quad (8)$$

where  $X_{ij}$  = the observed weight loss mean value of genotype  $i$  in environment  $j$ ;  $X_{ij} - \bar{\sigma}_i$  = the deviation from grand mean of weight loss;  $q$  = number of environments and  $\bar{\sigma}_i$  is mean of genotype  $i$  over all the environments.

Genetic correlations ( $r_G$ ) of the damage traits between the two insects to establish if either of the insects can be used for screening for resistance were calculated using the modified formula of Falconer and Mackay (1996):

$$r_G = r_p / \sqrt{(H^2 B^x \times H^2 B^y)} \quad (9)$$

where  $r_G$  = genetic correlation;  $r_p$  = phenotypic correlation between  $x$  and  $y$ ;  $H^2 B^x$  = heritability of the trait in question under maize weevil attack;  $H^2 B^y$  = heritability of the trait in question under LGB attack. The different seasons in each location were considered as separate environments, therefore, thus giving a total of four environments.

## RESULTS

### Resistance to the Maize Weevil

The analysis of variance showed significant differences ( $P < 0.05$ ) among the inbred lines in maize weevil progeny emergence, grain weight loss and flour weight. The genotype  $\times$  environment interaction for all the traits was also significant. The mean weight loss for the most resistant and susceptible lines was 3.26 and 24.23%, respectively (Table 1). Using percentage weight loss, the genotypes were categorized as resistant (1-5%), moderately resistant (5.1-8%), moderately susceptible (8.1-10%), susceptible (10.1-13%) and highly susceptible (>13.1%) (Tefera *et al.*, 2011c). Based on this categorization, the inbred lines were found to be moderately resistant (47%), resistant (10%) and moderately to highly susceptible (43%) (Fig.1). The spread of the genotypes across the five categories followed a fairly normal distribution as expected from a random selection.

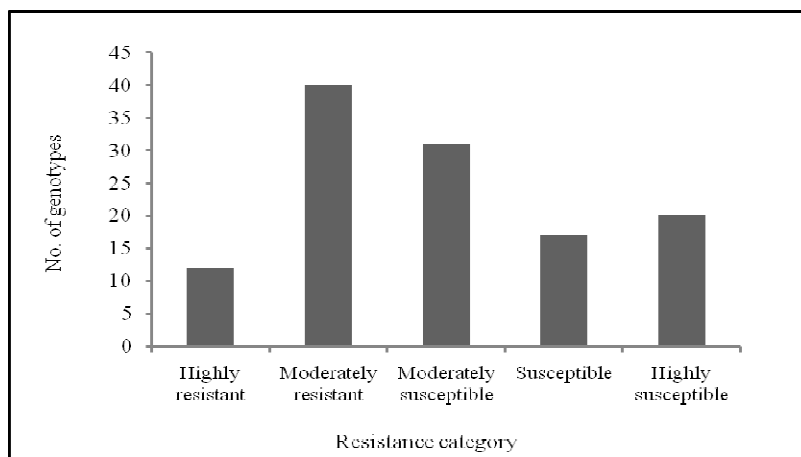


Figure 1: Frequencies of Maize Found from a Screen of 120 Maize Inbred Lines for Resistance to Weevil.

\*The material was classified into 5 categories based on the kernel weight loss classification method of Tefera *et al.* (2011).

The number of emerged adult insects was highest among the susceptible inbred lines (Table 1). Most of the resistant lines originated from “CubaGuard” a Caribbean germplasm accession at CIMMYT which showed significant levels of resistance to storage pests, though with poor agronomic traits (Kumar, 2002). Inbred lines which had been developed for stem-borer resistance (CKSB series) were categorized as moderately resistant to susceptible hence there was insufficient evidence to conclude that there was an association between resistance to the stem-borer and resistance postharvest insect-pest (Table 1).

**Table 1: Resistance Parameters and Stability Co-Efficients of the 20 Most Resistant and 20 Most Susceptible Inbred Lines Evaluated for Maize Weevil Resistance**

Entry	Name	No.of insects	Flour weight (%)	Weight loss (%)	Grain damage (%)	Genotypic variance (Si <sup>2</sup> )	Genotypic coefficient of variation	Remarks
70	CKSPL10028	27.92	0.11	3.26	5.42	0.09	57.43	Resistant
71	CKSPL10035	30.42	0.21	3.30	9.89	0.07	42.25	Resistant
66	CKSPL10309	28.92	0.72	3.90	9.94	0.08	39.81	Resistant
69	CKSPL10021	20.58	0.20	3.94	5.57	0.07	39.17	Resistant
73	CKSPL10042	26.77	0.19	4.13	8.17	0.08	40.23	Resistant
86	CKSPL10112	28.46	0.24	4.53	9.34	0.06	30.42	Resistant
27	CML204	24.33	0.19	4.56	6.41	0.08	40.91	Resistant
67	CKSPL10295	49.17	0.44	4.64	14.91	0.08	36.95	Resistant
97	CKSPL10218	41.75	0.29	4.67	12.24	0.08	37.95	Resistant
93	CKSPL10186	33.26	0.24	4.80	6.50	0.08	39.94	Resistant
78	CKSPL10081	24.75	0.24	4.86	10.31	0.07	34.92	Resistant
82	CKSPL10088	34.00	0.30	4.92	14.82	0.06	29.68	Resistant
87	CKSPL10113	82.08	0.75	5.10	23.77	0.06	27.47	Resistant
83	CKSPL10089	31.61	0.30	5.11	12.24	0.07	33.72	Resistant
75	CKSPL10074	35.75	0.25	5.24	11.03	0.11	54.03	Resistant
92	CKSPL10170	35.67	0.20	5.33	10.86	0.10	44.83	Resistant
2	CKSPL10177	49.17	0.43	5.45	14.44	0.14	67.38	Resistant
4	CKSBL10028	58.75	0.57	5.46	20.67	0.04	22.89	Resistant
14	CKSPL10035	66.67	0.44	5.59	15.36	0.13	58.78	Resistant
<b>Mean</b>		<b>38.42</b>	<b>0.33</b>	<b>4.67</b>	<b>11.68</b>	<b>0.08</b>	<b>40.99</b>	
<b>R check</b>	<b>CKSPL10229</b>	<b>58.33</b>	<b>0.22</b>	<b>3.90</b>	<b>7.60</b>	<b>0.06</b>	<b>30.66</b>	<b>Resistant</b>
16	CML264	121.83	0.90	12.92	41.94	0.07	20.25	Susceptible
105	CKSBL10028	49.75	0.36	13.15	20.20	0.07	27.78	Susceptible
53	DTPWC9-F16....	115.25	0.80	13.22	34.95	0.09	24.27	Susceptible
61	CML489	133.33	0.91	13.35	38.00	0.04	11.38	Susceptible
28	CKSBL10034	160.00	1.10	13.44	33.14	0.03	9.08	Susceptible
33	CKSBL10025	122.67	0.78	13.72	28.58	0.11	30.85	Susceptible
60	CML441	157.42	1.34	13.77	40.78	0.08	22.08	Susceptible
11	CKSBL10015	110.42	1.30	13.88	32.17	0.09	24.65	Susceptible
6	CKSBL10045	179.42	1.50	14.62	52.91	0.02	6.29	Susceptible
59	CZL03007	145.58	1.18	14.84	39.94	0.10	24.89	Susceptible
120	CKSBL10045	177.42	1.33	16.51	44.39	0.10	23.07	Susceptible
62	CZL01005	183.08	1.70	16.67	45.21	0.10	24.03	Susceptible
24	CML334	167.83	1.72	16.69	49.19	0.10	24.87	Susceptible
58	CZL00003	191.83	1.78	16.92	55.24	0.05	12.34	Susceptible
41	CML159	224.83	3.26	17.46	41.74	0.09	27.97	Susceptible
42	CML197	223.17	3.33	18.84	47.08	0.04	8.69	Susceptible
56	CML443	168.08	2.09	19.76	48.69	0.09	19.64	Susceptible
46	CZL03014	229.08	1.86	20.69	50.66	0.01	2.96	Susceptible

Entry	Name	No.of insects	Flour weight (%)	Weight loss (%)	Grain damage (%)	Genotypic variance (Si <sup>2</sup> )	Genotypic coefficient of variation	Remarks
10	CML312	153.17	1.40	22.26	48.36	0.08	15.55	Susceptible
7	CKSPL10344	186.00	1.91	23.88	46.05	0.14	28.67	Susceptible
<b>Mean</b>		<b>160.01</b>	<b>1.53</b>	<b>16.33</b>	<b>41.96</b>	<b>0.08</b>	<b>19.47</b>	
S check	CML395 (SC	247.33	2.71	24.23	62.90	0.11	21.22	Susceptible
CV		23.65	34.51	32.90	33.20			
P Value		P<0.001	P<0.001	P<0.001	P<0.001			

\*R check-Resistant check; S check-susceptible check; CV-coefficient of variation; P Value-probability value at 5%

The stability coefficients showed that lines CKSPL10229, CKSPL10088, CKSPL10113 and CKSPL10042 were the most stable in their resistance to maize weevil attack (Table 1). They had low weight loss (<5.5) and smaller Si<sup>2</sup> (0.06) and relatively low CVI (<31). They all originated from “CubaGuad” and “Kilima” that had been identified as a source of resistance to postharvest insect-pests in CIMMYT maize breeding programs. The phenotypic variance was slightly higher than the genotypic variance for all the traits. However, the genotypic variances for all the traits were higher than the environmental variances (Table 2). The phenotypic and genotypic coefficients of variation were high for number of insects and grain damage.

**Table 2: Estimation of Variance Components and Heritability Among the 120 Inbred Lines Evaluated**

Trait	Mean	MS	Mse (Ve)	Vp	Vg	PCV	GCV	ECV	H <sup>2</sup> B	H <sup>2</sup> B (%)
No.Insects	2.16	0.14	0.033	0.05	0.040	21.60	18.89	1.53	0.76	76.43
Flour weight	0.40	0.04	0.007	0.014	0.012	12.01	10.92	1.89	0.83	82.68
Weight loss	0.52	0.07	0.009	0.022	0.020	14.83	13.76	1.77	0.86	86.06
Grain damage	0.65	0.09	0.022	0.031	0.023	17.45	15.19	3.39	0.76	75.74

Key: MS=mean square; MSe=mean square error; Vp=phenotypic variance; Vg=genotypic variance;

Ve=environmental variance; Pcv=phenotypic coefficient of variation; G cv=genotypic coefficient of variation;

Ecv=Environmental coefficient of variation; H2B=Broad sense heritability

### Resistance to the Larger Grain Borer

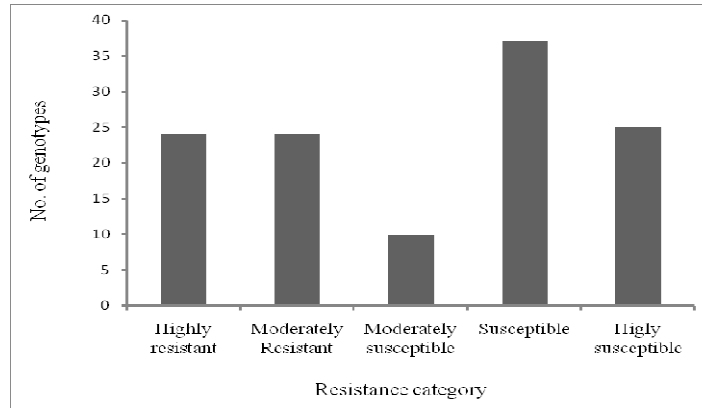
There were significant differences ( $P < 0.05$ ) among the inbred lines in larger grain borer progeny emergence, percentage grain weight loss, flour weight and grain damage. The inbred lines were categorized as resistant (<15%); moderately resistant (15.1-20%), moderately susceptible (20.1-25%), and highly susceptible (>25%) based on the percentage weight loss (Tefera *et al.*, 2011c). The mean weight loss for the most resistant and susceptible lines was 13% and 50 % respectively

**Table 3: Resistance Parameters and Stability Coefficients of the 20 Most Resistant and 20 Most Susceptible Inbred Lines Among the 120 Evaluated for Larger Grain Borer Resistance**

Entry	Name	No. of insects	Flour weight (%)	Grain damage (%)	Weight loss (%)	Genotypic variance (S <sup>2</sup> )	Genotypic coefficient of variation	Remarks
70	CKSPL10028	92.1	8.9	20.7	13.2	0.01	20.54	Resistant
14	CKSPL10035	90.2	8.5	28.4	15.3	0.02	33.18	Resistant
84	CKSPL10090	108.3	10.0	24.9	16.1	0.01	25.59	Resistant
98	CKSPL10224	106.7	8.5	23.5	16.3	0.00	17.11	Resistant
69	CKSPL10021	122.9	10.3	31.3	16.5	0.02	33.01	Resistant
71	CKSPL10035	124.6	11.4	29.2	16.5	0.02	37.81	Resistant
82	CKSPL10088	112.5	10.7	27.4	16.8	0.01	25.61	Resistant
110	CKSBL10041	108.0	11.6	32.1	16.9	0.01	19.23	Resistant
96	CKSPL10212	136.4	10.5	30.7	16.9	0.00	13.68	Resistant
74	CKSPL10070	111.4	10.7	30.3	17.1	0.02	30.83	Resistant
83	CKSPL10089	126.5	9.1	24.9	17.4	0.02	28.09	Resistant
73	CKSPL10042	119.0	11.7	30.1	17.5	0.02	34.71	Resistant
86	CKSPL10112	127.6	10.9	28.3	17.8	0.03	35.72	Resistant
67	CKSPL10295	118.6	12.4	32.4	18.2	0.03	43.42	Resistant
78	CKSPL10081	121.3	10.6	28.3	18.4	0.03	37.64	Resistant
40	CML144	133.5	12.2	23.6	18.6	0.03	40.45	Resistant
75	CKSPL10074	142.5	11.6	36.5	18.8	0.01	20.81	Resistant
79	CKSPL10085	119.7	11.5	29.4	19.3	0.01	25.25	Resistant
81	CKSPL10087	131.0	12.7	28.5	19.6	0.01	20.39	Resistant
91	CKSPL10164	127.1	12.8	38.5	19.6	0.01	23.42	Resistant
<b>Mean</b>		<b>119.0</b>	<b>10.8</b>	<b>28.9</b>	<b>17.3</b>	<b>0.0</b>	<b>28.3</b>	
<b>R check</b>	<b>CKSPL10229</b>	<b>127.4</b>	<b>11.0</b>	<b>29.9</b>	<b>19.7</b>	<b>0.00</b>	<b>8.23</b>	<b>Resistant</b>
20	CKSBL10014	224.2	20.6	41.9	32.8	0.03	30.19	Susceptible
113	CKSBL10025	230.8	19.6	38.3	33.2	0.02	22.97	Susceptible
109	CKSBL10023	232.5	21.3	44.8	33.3	0.01	15.51	Susceptible
10	CML312	174.4	20.1	58.3	33.6	0.02	22.02	Susceptible
111	CKSBL10039	218.5	19.9	47.9	34.4	0.03	24.44	Susceptible
6	CKSBL10045	206.5	22.4	46.0	34.6	0.02	21.82	Susceptible
42	CML197	89.7	6.8	24.4	34.6	0.02	21.76	Susceptible
60	CML441	208.9	22.8	42.1	34.7	0.16	62.23	Susceptible
104	CKSBL10013	199.9	20.5	50.5	34.8	0.02	22.69	Susceptible
54	P100C6-200-1...	198.8	22.0	40.7	35.0	0.01	16.84	Susceptible
53	DTPWC9-F16....	239.6	23.8	43.4	35.5	0.02	22.28	Susceptible
34	CML442	215.0	22.2	54.9	35.7	0.00	10.64	Susceptible
46	CZL03014	256.2	22.6	58.6	35.8	0.01	11.56	Susceptible
118	CKSBL10046	240.2	25.6	45.4	36.9	0.01	10.45	Susceptible
62	CZL01005	213.2	24.6	46.3	37.0	0.02	20.19	Susceptible
120	CKSBL10045	241.0	24.0	49.2	37.0	0.01	15.70	Susceptible
11	CKSBL10015	262.4	25.8	42.9	38.5	0.02	23.87	Susceptible
58	CZL00003	257.3	27.7	53.7	40.5	0.02	20.37	Susceptible
56	CML443	249.7	25.5	50.8	42.8	0.01	11.14	Susceptible
<b>Mean</b>		<b>218.9</b>	<b>22.0</b>	<b>46.3</b>	<b>35.8</b>	<b>0.02</b>	<b>21.4</b>	
<b>S check</b>	<b>CML395</b>	<b>309.8</b>	<b>32.3</b>	<b>58.6</b>	<b>50.0</b>	<b>0.01</b>	<b>10.88</b>	<b>Susceptible</b>
	CV	9.7	34.7	33.8	37.2			
P value	Entry	<0.001	<0.001	<0.001	<0.001			

\*R check-Resistant check; S check-susceptible check; CV-coefficient of variation; P Value-probability value at 5%

Among the lines evaluated for LGB resistance, 40% were resistant to moderately resistant, 8% were moderately susceptible and 52% were susceptible to highly susceptible (Figure 2). The distribution of the lines in the different classes in response to the larger grain borer is evidence of inherent genetic variability among them with respect to resistance. This would form a basis for breeding for resistance as part of an integrated pest management strategy.



**Figure 2: Frequencies of Maize Found from a Screen of 120 Maize Inbred Lines for Resistance to LGB.**

\*The material was classified into 5 categories based on the kernel weight loss classification method of Tefera et al. (2011).

Stability for resistance to the larger grain borer across environments was observed in lines CKSPL10028, CKPL10070, CKSPL10088, CKSPL10089, CKAPLOO90, CKSPL10212 and CKSPL10224 (Table 3). They had low weight loss (< 20) and smaller values for the  $Si^2$  (<0.03) and relatively low CVI (<30) than the other inbred lines, an indication that their reaction to the larger grain borer in different environments was not variable; this would imply that screening the material for resistance to LGB at one location is adequate. Most of the highly susceptible genotypes also showed high stability in their response to attack by the larger grain borer.

Dual resistance to the two postharvest insect pests was observed among the most resistant lines (Tables 1 and 3). Those susceptible to maize weevil were also susceptible to the LGB. Those showing resistance to both postharvest insect pests were CKSPL10028, CKSPL10035, CKSPL10088, CKSPL10021, CKSPL10042, CKSPL10295 and CKSPL10112. Phenotypic and genotypic correlations between the traits in respect to the two insects were significant. The genetic correlations between traits in response to maize weevil and larger grain borer attack were 0.88, 0.84, 0.67 and 0.60 for percentage weight loss, grain damage, flour weight and number of insects respectively.

## DISCUSSIONS

There were significant differences among the inbred lines in maize weevil and LGB progeny emergence, grain weight loss and flour weight. The results of this study showed that genetic diversity for resistance to the maize weevil and LGB resistance exists among tropical maize inbred lines, thus offering the opportunity to exploit the variability with the aim of reducing post-harvest insect-pest losses through genetic improvement. Genetic diversity is normally exploited for the incorporation of important traits lacking in improved crop varieties by using conventional and genetic engineering approaches (Dhliwayo and Pixley, 2003). The phenotypic and genotypic coefficients of variation were high for number of insects and grain damage. The high genotypic variance in comparison with the environmental variance is an indication that the traits are under genetic control.



This implies that most of the variation among the genotypes is due to their genetic make-up with little influence from the environment. This also suggests that maize improvement for resistance to storage pests is possible through selection (Oyiga and Uguru 2011). The broad sense heritability was high (76-86%) for all the traits. Heritability and genetic variance estimates are useful in predicting the outcome of selection of the best genotypes from a population (Ubi et al., 2001). The high values of heritability would mean that it is possible to pass the traits of interest from the parents to the offspring following selection (Rashwan, 2010).

Stability for maize weevil and LGB resistance across environments was observed, suggesting that it is possible to breed for improved varieties which are resistant to storage pests in different ecological zones. The existence of stability in both categories can be exploited with the aim of developing molecular markers for marker-assisted recurrent selection. This would be in accordance with the advances in molecular breeding where molecular markers have been recognized as a tool in supporting conventional breeding (Edwards and Singh, 2006; Ranjekar et al., 2003). In addition, this would shorten the period needed to identify resistant germplasm, since post-harvest screening for three months would be suppressed.

Dual resistance to the two postharvest insect pests was observed among the most resistant lines. The results suggest the possibility of a breeding program to address resistance to multiple storage pests. Moreover, it's possible that the mechanisms of resistance to storage pests are similar and are conditioned by the same genes. Earlier studies have shown that it is possible to transfer resistance genes through conventional breeding (Dhliwayo et al., 2005). Currently progress has been achieved in genetic improvements to maize hybrids in respect of resistance to storage pests through with the efforts made by the CIMMYT breeding program (Tefera et al., 2011c).

Phenotypic and genotypic correlations between the traits in respect to the two insects were high and significant. The percentage weight loss is the most important trait for discriminating between genotypes and placing them into resistant and susceptible categories (Mwololo et al., 2012). The high genetic correlation for weight loss implies that the genetic influence on resistance to the two postharvest insect pests among the genotypes is similar; this is an indication that genotypes selected for their resistance to one insect would also be resistant to the other insect.

## **CONCLUSIONS**

Genetic variation exists among maize inbred lines and forms the foundation for a successful breeding program to address postharvest losses due to insect pests. Genotypic variances were high (0.012-0.04) compared to environmental variances (0.007-0.033) for insect-damage parameters. The broad sense heritability was also high (76-86 %), therefore it is possible to breed for resistance through selection. The dual-resistant lines identified (CKSPL10028, CKSPL10035, CKSPL10088, CKSPL10021, CKSPL10042, CKSPL10295 and CKSPL10112 ), can be used as donor lines to introgress postharvest insect-pest resistance genes into adapted but susceptible genotypes, or as parents for new breeding ventures. The most resistant and susceptible inbred lines identified can be deployed in quantitative trait loci-mapping and association-mapping projects for the identification of molecular markers for use in marker-assisted selection.

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