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Response to S1 recurrent selection for resistance to two stem borers, *Busseola fusca* and *Chilo partellus*, in two tropical maize populations

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Abstract Stem borers, *Busseola fusca* and *Chilo partellus*, are among the key devastating lepidopteran insect pests of maize causing grain yield losses. Recurrent selection studies for stem borer resistance in maize are limited. However, maize populations carrying resistance genes to these stem borers have not been exploited fully in breeding programmes. The objective of the study was to separately improve resistance to *B. fusca* and *C. partellus* stem borers for two maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc and therefore grain yield after two cycles of S1 progeny recurrent selection. Cycle 0 and the advanced generations (cycle 1-susceptible, cycle 1-resistant and cycle 2-resistant) were evaluated at three locations in Kenya using a 35×12 α-lattice design with 2 replications. The net reductions in cumulative tunneling, number of exit holes and leaf feeding damage scores ranged from 0 to 69 % for both populations after two cycles of selection. In the two populations, each cycle of selection for borer resistance improved grain yield by 0.5–0.8 t ha^{-1}. Actual net gains in grain yield with reference to cycle 0 were 43 % for population CML395/MBRC5 Bc under *B. fusca* infestation and 70 % under *C. partellus* infestation. For population CML444/MBR/MDR C3Bc, the actual net gains in grain yield were 25 % under *B. fusca* infestation and 36 % under *C. partellus* infestation. The reductions in the injurious effects attributable to leaf feeding damage, cumulative stem tunneling and number of exit holes contributed towards the 43 and 70 % net genetic gain in grain yield under *B. fusca* and *C. partellus* infestation respectively, for both populations. Broad sense heritability (H^2) for grain yield ranged from 2 to 98 % in both maize populations. The study showed that two cycles of S1 progeny recurrent selection was effective in accumulating favourable alleles for *B. fusca* and *C. partellus* stem borer resistance.

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Introduction

There are limited studies on recurrent selection for stem borer resistance in tropical maize. Although

many maize varieties with high yield potential are available on the market, some limitations have precluded some farmers in Kenya from access to these modern varieties because of the high cost of hybrid seed. In addition, hybrid seed may impose other limitations namely fertilization, pesticides, mechanized equipment and efficient management required to exploit the full genetic potential of these high yielding maize varieties in many parts of Kenya and in the tropics (Acquaah 2009; Ana Paula et al. 2013).

Plant breeding has led to the development of new maize varieties with better resistance and agronomic traits to biotic and abiotic stresses. Among these biotic stresses, the African stem borer, *Busseola fusca* and the spotted stem borer *Chilo partellus* are serious insect pests of maize in tropical environments. Breeding for stem borer resistance in maize is challenging because the trait is quantitative and involves polygenes with low heritability (Sharma et al. 2007; Sandoya et al. 2010; Oloyede-Kamiyo et al. 2011). Cartea et al. (1999) suggested that recurrent selection approaches would be the most suitable for the improvement of stem borer resistance. This breeding scheme is effective in increasing favourable alleles of agronomic and economic traits of importance in maize populations. The S1 progeny recurrent selection scheme is characterized by the additive genetic effects that are more important than the non-additive gene effects in stem borer resistance in maize populations (Sandoya 2008; Schnable and Springer 2013).

The S1 progeny recurrent selection scheme is widely used in maize breeding. Various successful examples of its application in various crops against pests and diseases were reported (Ordás et al. 2009). A greater amount of breeding efforts have been dedicated towards improvement of resistance to maize stem borers in Africa, Europe and Asia (Kumar 1997; Andre 2003; Mugo et al. 2005; Sharma et al. 2007; Butrón et al. 2009; Sandoya et al. 2010; Barros et al. 2011; Khalifa 2013). Several cycles of recurrent selection have been used to improve maize for resistance against various stem borers species (Ana Paula et al. 2013; Dhillon and Gujar 2013; Oloyede-Kamiyo et al. 2013). However, limited work has been carried out on maize populations through recurrent selection for resistance to *B. fusca* and *C. partellus* stem borers in Kenya.

The objectives this study were to separately improve resistance to two stem borers *B. fusca* and *C. partellus* in two tropical maize populations through S1 progeny

recurrent selection. The test hypothesis was that both resistance improvement to two stem borers, *B. fusca* and *C. partellus* and grain yield could be achieved through cycles of S1 progeny recurrent selection.

Materials and methods

Germplasm

Two maize breeding populations used in this study were CML395/MBR C5 Bc F114-1-2-3-B-4-2-B-B (hereafter referred to as CML395/MBR C5 Bc) and CML444/MBR/MDR C3Bc F1-1-1-1-B-3-2-B-B (hereafter referred to as CML444/MBR/MDR C3Bc). These populations from CIMMYT-Nairobi are unrelated and originate from various nurseries. They have not been improved for resistance to *B. fusca* or *C. partellus* resistance through a recurrent selection scheme. The two populations were chosen for improvement because they are popularly grown as open pollinated varieties by farmers. Prior to this study the means of various agronomic and borer resistance traits were recorded from previous studies on these maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc.

Experimental sites

Experiments were established at Kakamega, Kiboko, and Embu locations in Kenya (Fig. 1). KALRO Kakamega (37°75′E 2° 15′S, 1585 m asl) centre is located in the moist transitional mid altitude agro–ecological zone of western Kenya and experiences mean annual temperatures of 25 °C. Kakamega lies within a high potential agro-ecological zone and receives a bimodal mean annual rainfall of approximately 1850–1916 mm. The soils in Kakamega are well drained, moderately deep to very deep, red to dark in colour and in some places shallow over petroplinthite (Jaetzold and Schmidt 1982).

KALRO-Kiboko (2°15′S 37°75′ E, 975 m asl) is located in the dry mid altitude agro-ecological zone of eastern Kenya and experiences mean annual temperature ranges of 28–37 °C, with February and October being the hottest months. Kiboko receives a mean annual rainfall of approximately 530 mm. The soils are well drained, Fluvisols, Ferralsols, and Luvisols with soil pH of about 7.9 (Jaetzold and Schmidt 1982; KARI Land Resources and Analytical Services 2007).
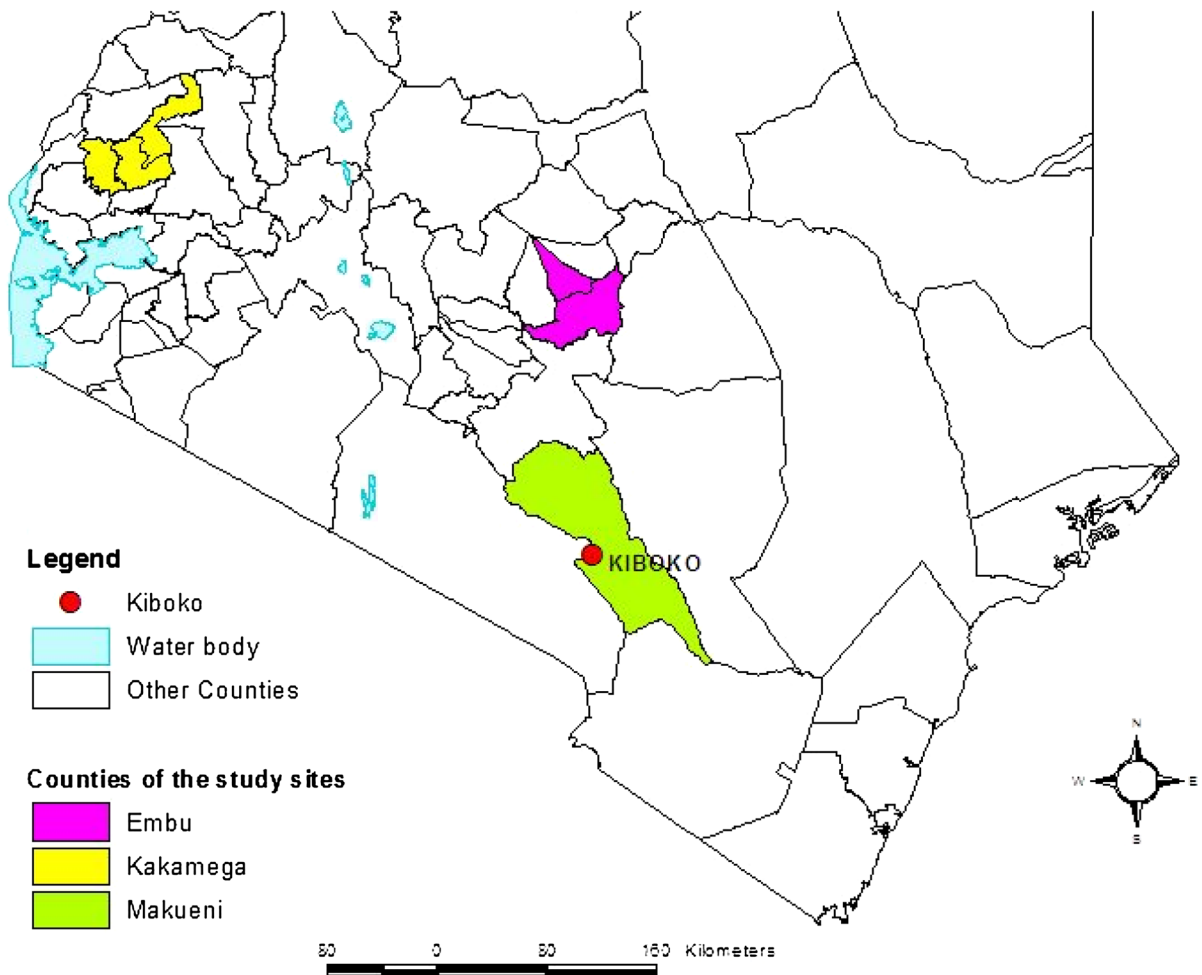
Fig. 1 Map of Kenya showing the locations Embu, Kakamega and Kiboko. Source: *KALRO* land resources and analytical services, 2013

KALRO-Embu centre (03°56′ 44′S and 39°46′ 00′E, 1510 m asl) is located in the moist transitional mid altitude agro-ecological zone of eastern slopes of Mt. Kenya and experiences mean annual temperature ranges of 14–25 °C. Embu lies within a high potential agro-ecological zone. Rainfall received is bi-modal ranging between 800 and 1400 mm annually. The soils are deep (about 2 m); well weathered Humic Nitisols with moderate to high inherent fertility (Jaetzold and Schmidt 1982).

Recurrent selection scheme for two populations

The recurrent selection scheme was applied separately to each of the two maize populations. One thousand and five hundred plants were established for each

population at each site between 2011B and 2012B and evaluated in 2013A season. The design was an un-replicated nursery with lines sown into 75 rows of 5 m lengths, with inter-row spacing of 0.75 m and inter–hills spacing of 0.25 m within the rows.

Plants were artificially infested in a controlled and uniform manner with *B. fusca* or *C. partellus* larvae respectively by placing 10 larvae in the maize whorl using a camel brush at two weeks after planting. Insect larvae were obtained from the International Centre for Insect Physiology and Ecology (ICIPE) and the Kenya Agricultural and Livestock Research Organization (KALRO) at Katumani stem borer insect pests mass rearing facility (Tefera et al. 2010, 2011). Plant evaluations on stem borer resistance as well as agro-nomic traits were measured as described in (CIMMYT

1989). After harvesting, a rank summation index (RSI) was constructed to determine the ranking of each line within each population for appropriate reaction. The index was obtained by the sum of the means of each of the leaf feeding damage score; number of dead-hearts; number of exit holes; and cumulative stem tunnel length for each line, to get its mean performance compared with other lines within the same population. An entry with the least value was ranked higher for the resistance traits (Mulamba 1978; Mutinda 2013).

The recurrent selection scheme for two maize populations under *B. fusca* and *C. partellus* infestation at three locations are described below.

Formation of S1 families

In the 2010B season, two cycle 0 (C_0) populations of CML395/MBR C5Bc and CML444/MBR/MDR C3Bc were established in rows in fields at Kiboko. Two seeds were planted per hill and later thinned to one. Recommended agronomic practices such as were implemented. About 1000 plants per population were selfed based on general performance to generate S_1 population. Only S_1 ears with sufficient seed were advanced.

Plant evaluations and selection criteria for the S_1 progenies

In the 2011A season, field evaluation of S_1 progenies under *B. fusca* and *C. partellus* infestation at Embu, Kakamega with 2 replications laid out in single rows in a 25×12 α-lattice design. The evaluations at Kiboko were exclusively under *C. partellus* infestation because the borer occurs in the region. Planting were ear-to-row to maintain genetic purity of the S_1 progenies. Two local (one resistant and the other susceptible) varieties were included as commercial checks. Remnant seed were stored. Data were collected on stem borer resistance traits on about 300 plants per population and grain yield to form the basis for selection. Fifty extra plants were sown to ensure a minimum of 300 healthy plants for advancement during selection. Divergent selection was carried out for *B. fusca* and *C. partellus* resistance and susceptibility at each site.

Recombination

In 2011B season, remnant seed of about 300 S_1 progeny rows showing resistance and susceptibility to stem borers were selected for recombination per population. Seed per progeny were reserved. Susceptible progeny were used as checks Recombination involved ear-to-row planting of the S_1 seed and hand-pollination using bulk pollen was carried out with one half pollinating the other to ensure random mating. Cycle 1 (C1S and C1R) seed was formed from this recombination per population (300 lines of C_1 seed expected/population).

Plant evaluations of advanced S_1 progenies

In 2012A season, field evaluation of advanced S_1 progenies under *B. fusca* and *C. partellus* infestation at Embu, Kakamega with 2 replications were laid out in single rows in a 25×12 α-lattice design. The evaluations at Kiboko were exclusively under *C. partellus* infestation. Evaluation of C_1 (C1S and C1R) seed was carried out in replication trials for resistance and susceptibility to stem borers, keeping remnant seed per ear. Two local (one resistant and the other susceptible) varieties were included as checks. The field design was laid out with two replicates in a 10×5 α lattice design. Twenty extra plants for each cycle were sown to ensure a minimum of 35 healthy plants for advancement during selection. Divergent selection was carried out for *B. fusca* and *C. partellus* resistance and susceptibility at each site.

Recombination

In 2012B season, remnant C_1 (C1S and C1R) seed from about 35 progenies showing similar characteristics of resistance and susceptibility to stem borers were selected for recombination per population. Recombination involved ear-to-row planting of the S_1 seed and hand-pollination using bulk pollen was carried out with one half pollinating the other to ensure random mating. Cycle 2 (C2R) seed were formed from this recombination (35 lines of C_1 seed expected/population).

Plant evaluations of all cycles for each population

In 2013A season, field evaluation of all cycles for each population, C_0, C_1 (C1S and C1R) and C_2 (C2R) of S_1 progenies under *B. fusca* and *C. partellus* infestation at Embu, Kakamega with 2 replications laid out in single rows in a 35×4 α-lattice design. The evaluations at

Kiboko were exclusively under *C. partellus* infestation. Seed from each location for each cycle for each population, C_0, C_1 (C1S and C1R) and C_2 (C2R) of S_1 progenies under *B. fusca* and *C. partellus* infestation was bulked separately. In addition to the cycles of the susceptible progeny per population, two local (one resistant and the other susceptible) varieties were included as checks.

Multi-site evaluations of the cycle 0 and the advanced cycles

The population cycles C_0, C_1S, C_1R and C_2R were evaluated in a 35×4 α-lattice design with two replications in each location. Each 6.75 m plot was divided into three parts namely, *B. fusca* and *C. partellus* infested on either side of the plot at Embu and Kakamega, while the middle part was protected using insecticide Bulldock® (active ingredient, *beta cyfluthrin 25 g/L*). At Kiboko, 5 m row plots were used, and were infested with *C. partellus* on half the plot while the remaining part was protected. Two seeds were sown per hill and later thinned to one. Inter-row spacing of 0.75 m and inter-hills spacing of 0.25 m within the rows was used. Recommended fertilizer application of nitrogen (60 kg N ha^{-1}) and phosphate (60 kg P_2O_5 ha^{-1}) and irrigation were applied as recommended for each location to ensure healthy and vigorous plants. Nitrogen was applied in two splits, while supplementary irrigation was applied when needed. The fields were kept free of weeds by hand weeding throughout the growth period.

Artificial infestation with insects

Insect larvae were obtained from the International Centre for Insect Physiology and Ecology (ICIPE) and KALRO Katumani stem borer mass rearing facilities. Plants were artificially infested in a controlled and uniform manner with the respective stem borer species by placing 10 larvae in the maize whorl using a camel brush at 2 weeks after planting.

Data collection

Plants in each population cycles C_0, C_1S, C_1R and C_2R were evaluated for leaf damage using a scale of 1 (resistant) to 9 (susceptible) (CIMMYT 1989). The number of dead-hearts was assessed as proportion of plants in the plot indicating death of the growing points. Other plant damage parameters were measured at harvest namely; cumulative tunnel length, number of exit holes, stalk strength, and number of larvae recovered per plant. Stalk strength was measured using a rind penetrometer 8 weeks after planting. Agronomic traits were measured following standard protocols used at CIMMYT (CIMMYT 1989). Grain yield (kg plot^{-1}) was obtained as grain weight adjusted for moisture content at 13 %, and converted to t ha^{-1}.

Data analysis

Analyses of variance (ANOVA) for all characters measured were computed using PROC MIXED procedures in SAS computer package, version 9.2 (SAS Institute, Inc. 2012) combined over locations and separately for each treatment with *B. fusca* and *C. partellus* using the following model:

$$Y = \mu + r + t + rt + c + ct + cr(t) + 1 + lr + lt + rtl + cl + tcl + lcr(t)$$

where; *Y* ie the detected value, μ is the overall mean, *r* is the replication effect with 2 levels, *t* is the treatment effect with 2 levels (*B. fuscaa* and *C. partellus*), *c* is the cycle effect with 4 levels (C_0, C_1S, C_1R and C_2R) and *l* is the location effect with 3 levels for *C. partellus* (Embu; Kakamega and Kiboko).

There were five error terms specifically;

(a) replication interaction with treatment effect—for testing significance of treatments

(b) cycle interaction with replication effects nested in treatment—for testing significance of cycles, and treatment × cycles interaction;

(c) location interaction with replication effects—for testing significance of locations;

(d) replication × treatment × location interaction effects—for testing significance of locations × treatment interaction;

(e) location × cycle × replication nested in treatment interaction—for testing significance of locations × cycle interaction, and locations × cycles × treatment interaction.

Population cycles C_0, C_1S, C_1R and C_2R were considered as fixed factors. The locations, replication

and interactions were considered random. Data on number of dead-hearts and cumulative stem tunnel length were transformed into arcsine values before subjecting them to analysis of variance (ANOVA). The C_1 susceptible progeny was used as the check. The response to selection was carried out by comparison of each population cycles C_0, C_1S, C_1R and C_2R.

The net genetic gain to selection was carried out by comparison of each population cycles C_0, C_0, C_1S, C_1R and C_2R. The net gain (%) was calculated using the formulae;

The percent net genetic gain to selection was calculated as:

$$\left[\frac{\mu C_n - \mu C_0}{\mu C_0} \right] \times 100$$

where, μC_0 and μC_n are means of the stem borer damage traits evaluated at cycles 0 and the nth cycle. The mean of cycle C_0 was used as the reference population.

PROC VARCOMP procedures in SAS computer package, version 9.2 (SAS Institute, Inc. 2012) were used for the estimation of the variance components. Each population was analyzed for the grain yield, stem borer resistance and agronomic traits to establish the genetic variance under *B. fusca* and *C. partellus* infestation. Broad sense heritability (H^2) was obtained using the formula $\sigma^2 g/\sigma^2 p$ (Dabholkar 1992; Falconer and Mackay 1996), where; $\sigma^2 g$—genotypic variance and $\sigma^2 p$—phenotypic variance. The standard error of broad sense heritability was calculated as;

SE $(H^2) = 2SE \{\sigma^2 g\}/\{\sigma^2 g + \sigma^2 p + \sigma^2 we\}$ and, $2SE\{\sigma^2 g\}$—square root of the genotypic variance and $\sigma^2 we$—is the within plot variance (Dabholkar 1992; Falconer and Mackay 1996).

Selection differential (S) was calculated by subtracting the populations mean for all S_1 progeny from the mean of the selected S_1s to be advanced;

(a) $S = \mu_{sel}2 - \mu_o$ for C_2
(b) $S = \mu_{sel}1 - \mu_o$ for C_1

where; $\mu_{sel}2$ is mean of the best 50 selected lines to advance to C_2R,; $\mu_{sel}1$ is mean of the best 100 selected lines to advance to C_1R,; μ_o is the mean of the original reference population prior to selection of the best stem borer resistant lines.

Results

Trait variations in cycles under *C. partellus* infestation

The mean squares of the populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc from analysis of variance for grain yield, stem borer resistance and agronomic traits for were significant ($p \leq 0.01$ to $p \leq 0.05$) for most traits under *C. partellus* infestation. In population CML395/MBR C5 Bc, the cycle main effects were significant ($p \leq 0.05$) for grain yield, plant height, plant and ear aspects, number of exit holes, and cumulative stem tunneling, and leaf feeding damage scores ($p \leq 0.05$). The location main effects were significant for all traits measured ($p \leq 0.01$). The location x cycle interaction effects were significant ($p \leq 0.05$) for grain yield, plant height, plant aspect, number of exit holes, and cumulative stem tunneling, and leaf feeding damage scores. In population CML444/MBR/MDR C3Bc, the cycle main effects were significant ($p \leq 0.05$) for grain yield, plant height, plant aspect, number of exit holes, cumulative stem tunneling, and leaf feeding damage scores ($p \leq 0.05$). The location main effects were significant for all traits measured ($p \leq 0.01$). The location x cycle interaction effects were significant ($p \leq 0.05$) for all traits measured.

Trait variations in cycles under *B. fusca* infestation

The mean squares of the populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc from analysis of variance for grain yield, stem borer resistance and agronomic traits were significant ($p \leq 0.01$ to $p \leq 0.05$) for most traits under *B. fusca* infestation. In population CML395/MBR C5 Bc, the cycle main effects were highly significant ($p \leq 0.01$) for grain yield, plant height, plant aspect, number of exit holes, and cumulative stem tunneling, and leaf feeding damage scores except days to anthesis under *B. fusca* infestation. The location main effects were significant for all traits measured ($p \leq 0.01$). The location x cycle interaction effects were highly significant ($p \leq 0.01$) grain yield, plant height, plant and ear aspects and cumulative stem tunneling, and leaf feeding damage scores. In population CML444/MBR/MDR C3Bc, the cycle main effects were highly significant ($p \leq 0.01$) for all traits except ear aspect. The location main

effects were significant for all traits measured ($p \leq 0.01$). The location × cycle interaction effects were highly significant ($p \leq 0.01$) for all traits measured.

Mean performance of cycles of two maize populations

Results from the evaluation of the reference cycle (C_0) and the advanced cycles (C_1R and C_2R) of two maize populations across locations under *B. fusca* and *C. partellus* infestation are shown. In population CML395/MBR C5 Bc, the overall mean grain yield was significantly ($p \leq 0.05$) higher in C_1R and C_2R compared to C_1S and C_0. Grain yield was higher under *B. fusca* infestation compared to *C. partellus* in C_1R and C_2R compared to C_0 and C_1S. No significant differences were detected for days to anthesis and silking. Cumulative stem tunneling was significantly ($p \leq 0.05$) lower in C_1R and C_2R compared to C_0 and C_1S. *B. fusca* caused more tunneling in the cycles than and *C. partellus*. The number of exit holes was significantly ($p \leq 0.05$) higher in C_0 and C_1S than in C_2R except under *C. partellus* infestation. Leaf feeding damage scores were significantly ($p \leq 0.05$) higher in C_0 and C_1S. Cycles C_1R and C_2R had similar mean leaf feeding damage scores under *B. fusca* infestation. Plant and ear aspects were significantly higher in C_1R and C_2R compared to C_0 and C_1S under both *B. fusca* and *C. partellus* infestation. However, plant height for all cycles was not significant under *B. fusca* and *C. partellus* infestation.

In population CML444/MBR/MDR C3Bc, the overall mean grain yield was significantly ($p \leq 0.05$) higher in C_1R and C_2R compared to C_1S and C_0. No significant differences were identified for days to anthesis and silking. Cumulative stem tunneling was significantly ($p \leq 0.05$) lower in C_1R and C_2R compared to C_0 and C_1S. Although there was a reduction in the level of cumulative tunneling from C_0 to C_2R, *B. fusca* caused more tunneling in the cycles compared to *C. partellus*. The number of exit holes was significantly ($p \leq 0.05$) higher in C_0 and C_1S than in C_2R except under *C. partellus* infestation. Leaf feeding damage scores were significantly ($p \leq 0.05$) higher in C_0 and C_1S in comparison with C_1R and C_2R. However, no significant differences were detected for

mean plant aspect and ear aspect, and plant height for all cycles under *B. fusca* and *C. partellus* infestation.

Genetic gains from selection in cycles

There were net genetic gains from selection in cycles under *B. fusca* and *C. partellus* infestation (Table 1 and Table 2). Under *B. fusca* infestation, in population CML395/MBR C5 Bc, the net genetic gain in grain yield was 43 %, cumulative stem tunneling −41 %, number of exit holes −35 %, and leaf feeding damage score 0 %. In population CML444/MBR/MDR C3Bc, the net genetic gain in grain yield was 25 %, cumulative stem tunneling −57 %, number of exit holes −69 % and leaf feeding damage score 10 %. For both populations, the other agronomic traits showed varied trends in the net genetic gain under *B. fusca* infestation (Tables 1, 2).

Under *C. partellus* infestation, in population CML395/MBR C5 Bc, the net genetic gain in grain yield was 70 %, cumulative stem tunneling −35 %, number of exit holes −35 %, and leaf feeding damage score 9 %. In population CML444/MBR/MDR C3Bc, the net genetic gain in grain yield was 36 %, cumulative stem tunneling −24 %, number of exit holes −15 % and leaf feeding damage score −29 %. For both populations, the other agronomic traits showed wide-ranging inclinations in the net genetic gain under *C. partellus* infestation (Tables 1, 2).

Broad sense heritability estimates

The broad sense heritability estimates of cycle 0 and the advanced cycles (C_1R and C_2R) of two maize populations across locations under *B. fusca* and *C. partellus* infestation (Table 3). Broad sense heritability estimates were high for all traits measured in both maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc (Table 3).

Under *B. fusca* infestation, in population CML395/MBR C5 Bc, the broad sense heritability estimates for grain yield were 95.7, 93.5 and 98.4 % for cycles 0, C1R and C2R, separately. In population CML444/MBR/MDR C3Bc under *B. fusca* infestation, the broad sense heritability estimates for grain yield were 99.1, 99.6 and 99.1 % for cycles 0, C1R and C2R,

Table 1 Means for selected traits in two maize populations under *B. fusca* and *C. partellus* infestation at Embu, Kakamega and Kiboko

Cycle	GY		LD		TL		EXH		AD		SD		PA		EA		PH	
	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp
CML395/MBR C5 Bc																		
C0(Reference)	0.81	0.64	2.68	2.78	12.91	6.67	11.24	8.12	72.19	67.95	72.69	68.87	3.16	2.37	3.19	2.37	154.60	176.80
C1 Susceptible	0.44	0.66	2.89	2.99	10.97	4.24	8.93	11.50	72.53	68.07	72.92	68.88	2.75	2.97	3.19	2.64	153.50	174.90
C1 Resistant	0.99	0.86	2.99	2.32	12.56	4.11	9.76	9.92	72.29	67.94	72.73	68.58	3.54	3.10	3.38	2.68	147.40	183.00
C2 Resistant	1.16	1.09	2.69	2.53	8.37	3.91	7.25	10.18	72.39	68.11	73.02	69.05	2.77	2.54	3.56	2.69	154.10	168.90
LSD(0.05)	0.02	0.03	0.08	0.12	0.41	0.62	0.82	0.78	0.81	0.91	0.76	0.86	0.11	0.17	0.12	0.18	6.47	9.71
Net gain (%)	43	70	0	−9	−35	−41	−35	25	0	0	0	0	−12	7	12	14	0	−4
CML444/MBR/MDR C3Bc																		
C0(Reference)	0.58	0.73	2.98	3.83	15.36	8.11	8.75	8.87	74.71	70.18	75.79	70.73	2.61	3.16	2.40	2.85	158.70	166.80
C1 Susceptible	0.61	0.84	3.12	3.43	14.57	6.77	7.73	8.37	75.31	69.06	76.81	70.52	2.79	3.28	2.78	2.94	182.20	175.10
C1 Resistant	1.23	0.86	3.62	2.90	16.51	7.66	4.19	9.04	76.85	69.20	76.62	70.18	2.62	3.46	2.56	2.83	159.10	172.60
C2 Resistant	1.28	1.15	3.28	2.71	10.49	6.18	2.69	7.55	75.34	70.42	76.56	70.97	2.77	2.88	2.38	2.89	173.00	171.40
LSD(0.05)	0.03	0.05	0.12	0.18	0.57	0.86	1.14	1.02	1.11	1.67	1.05	1.58	0.15	0.20	0.16	0.24	8.96	10.12
Net gain (%)	25	36	10	−29	57	−24	−69	−15	1	0	1	0	6	−9	−1	2	9	3

Bf B. fusca, *Cp C. partellus*, *GY* grain yield (t ha^{-1}), *AD* days to anthesis, *SD* days to silking, *PH* plant height, *PA* plant aspect, *EA* ear aspect, *EXH* number of exit holes, *TL* cumulative stem tunneling (cm), *LD* leaf feeding damage

Table 2 Genetic gains[§] for selected traits in two maize populations under *B. fusca* and *C. partellus* infestation at Embu, Kakamega and Kiboko

Cycle	GY		AD		SD		TL		EXH		LD		PA		EA		PH	
	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp	Bf	Cp
CML395/MBR C5 Bc																		
C_1R-C_0	0.18	0.22	0.1	−0.01	0.04	−0.29	−0.35	−2.56	−1.48	1.8	0.31	−0.46	0.38	0.73	0.19	0.31	−7.2	6.2
C_1R-C_1S	0.55	0.2	−0.24	−0.13	−0.19	−0.3	1.59	−0.13	0.83	−1.58	0.1	−0.67	0.79	0.13	0.19	0.04	−6.1	8.1
C_2R-C_1R	0.17	0.23	0.1	0.17	0.29	0.47	−4.19	−0.2	−2.51	0.26	−0.3	0.21	−0.77	−0.56	0.18	0.01	6.7	−14.1
Net Gain (C_2R-C_1S)	0.72	0.43	−0.14	0.04	0.10	0.17	−2.60	−0.33	−1.68	−1.32	−0.20	−0.46	0.02	−0.43	0.37	0.05	0.60	−6.00
Net Gain (C_2R-C_0)	0.35	0.45	0.20	0.16	0.33	0.18	−4.54	−2.76	−3.99	2.06	0.01	−0.25	−0.39	0.17	0.37	0.32	−0.50	−7.90
CML444/MBR/MDR C3Bc																		
C_1R-C_0	0.65	0.13	2.14	−0.98	0.83	−0.55	1.15	−0.45	−4.56	0.17	0.64	−0.93	0.01	0.3	0.16	−0.02	0.4	5.8
C_1R-C_1S	0.62	0.02	1.54	0.14	−0.19	−0.34	1.94	0.89	−3.54	0.67	0.5	−0.53	−0.17	0.18	−0.22	−0.11	−23.1	−2.5
C_2R-C_1R	0.05	0.29	−1.51	1.22	−0.06	0.79	−6.02	−1.48	−1.5	−1.49	−0.34	−0.19	0.15	−0.58	−0.18	0.06	13.9	−1.2
Net Gain (C_2R-C_1S)	0.67	0.31	0.03	1.36	−0.25	0.45	−4.08	−0.59	−5.04	−0.82	0.16	−0.72	−0.02	−0.40	−0.40	−0.05	−9.20	−3.70
Net Gain (C_2R-C_0)	0.70	0.42	0.63	0.24	0.77	0.24	−4.87	−1.93	−6.06	−1.32	0.30	−1.12	0.16	−0.28	−0.02	0.04	14.3	4.60

GY grain yield (t ha^{-1}), *AD* days to anthesis, *SD* days to silking, *PH* plant height, *PA* plant aspect, *EA* ear aspect, *EXH* number of exit holes, *TL* cumulative stem tunneling (cm), *LD* leaf feeding damage, *Bf B. fusca*, *Cp C. partellus*, § refers to the true means and their unit of measurement used to calculate the net genetic gain per cycle

Table 3 Estimates of genetic variances and broad sense heritability for grain yield, stem borer resistance and agronomic traits under *B. fusca* and *C. partellus* infestation at Embu, Kakamega and Kiboko

CML395/MBR C5 Bc

	GY			LD			TL			EXH		
	C_0	C_1R	C_2R	C_0	C_1R	C_2R	C_0	C_1R	C_2R	C_0	C_1R	C_2R
$\sigma^2 g$	409.9	678.59	660.65	6136.46	5325.9	4381.9	549,864.9	1,007,121.1	254,567.5	137,550.1	375.38	121,048.5
$H^2 Cp$	0.795	0.797	0.770	0.765	0.799	0.787	0.799	0.800	0.799	0.799	0.566	0.799
$H^2 Bf$	0.957	0.935	0.984	0.974	0.975	0.951	0.996	0.997	0.994	0.998	0.998	0.999

	AD			SD			PH		
	C_0	C_1R	C_2R	C_0	C_1R	C_2R	C_0	C_1R	C_2R
$\sigma^2 g$	253,756.90	267,619.30	247,718.50	205,825.30	242,765.10	212,634.90	6,921,878.70	17,941,363.00	2,893,750.50
$H^2 Cp$	0.800	0.800	0.800	0.800	0.800	0.800	0.800	0.800	0.799
$H^2 Bf$	1.000	1.000	1.000	1.000	1.000	1.000	0.994	0.995	0.993

CML444/MBR/MDR C3Bc

	GY			LD			TL			EXH		
$\sigma^2 g$	3315.31	2075.7	3236.03	10137.2	7269.3	4611.2	741840	1105263.3	255637.1	34226.33	332634.3	325475.3
$H^2 Cp$	0.791	0.799	0.788	0.800	0.800	0.800	0.800	0.800	0.799	0.647	0.800	0.800
$H^2 Bf$	0.991	0.996	0.991	0.981	0.978	0.965	0.999	0.998	0.998	0.885	0.871	0.877

	AD			SD			PH		
	C_0	C_1R	C_2R	C_0	C_1R	C_2R	C_0	C_1R	C_2R
$\sigma^2 g$	289104.10	846278.00	333503.70	361250.00	571555.00	429627.00	929757.00	2568774.00	35907.40
$H^2 Cp$	1.000	1.000	1.000	1.000	1.000	1.000	0.997	0.999	0.931
$H^2 Bf$	0.999	0.999	0.999	1.000	1.000	1.000	0.996	0.996	0.996

GY grain yield (t ha^{-1}), *AD* days to anthesis, *SD* days to silking, *PH* plant height, *PA* plant aspect, *EA* ear aspect, *EXH* number of exit holes, *TL* cumulative stem tunneling (cm), *LD* leaf feeding damage, *Bf B. fusca*, *Cp C. partellus*

respectively (Table 3). Similar trends were detected for leaf feeding damage, cumulative stem tunneling and number of exit holes. Other agronomic characters showed diverse trends for broad send sense heritability estimates (Table 3).

Under *C. partellus* infestation, in population CML395/MBR C5 Bc, the broad sense heritability estimates for grain yield were 79.5, 77.7 and 77.0 % for cycles 0, C1R and C2R, in that order. In population CML444/MBR/MDR C3Bc under *C. partellus* infestation, the broad sense heritability estimates for grain yield were 79.1, 79.9 and 78.8 % for cycles 0, C1R and C2R, individually (Table 3). Comparable tendencies were identified for leaf feeding damage, cumulative stem tunneling and number of exit holes.

Other agronomic traits displayed varied inclinations for broad send sense heritability estimates for

both maize populations the genetic variances showed less variation from cycles 0, C1R and C2R for most of the traits (Table 3).

Discussions

There were highly significant differences detected among the different cycles of the two maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc for the various stem borer resistance and agronomic traits showed the existence of significant variation among the populations that allows for selection of preferred resistant genotypes. The population studied exhibited wide genotypic variability and heritability estimates showing possible projections of selection gain for the subsequent cycles.

For the two maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc, the partition of treatments, cycles and locations and their interactions into variances provided a better insight of the dissimilar patterns among treatments and cycles, and their reaction across locations. In both populations, grain yield was significantly higher in cycles C2R than in C0 and C1S, indicating positive response to selection. Even though incessant genetic gains in successive cycles of recurrent selection has been argued among researchers, in population CML395/MBR C5 Bc, each cycle improved grain yield by 0.5 t ha^{-1}, while in population CML444/MBR/MDR C3Bc, each cycle improved grain yield by 0.8 t ha^{-1}. Similar findings have been reported in literature on maize (Ana Paula et al. 2013). These genetic gains may imply the losses incurred by farmers for not controlling the stem borers in the maize agro-ecologies where they exist. The reduction in the cumulative stem tunneling, number of exit holes per plant, leaf feeding damage scores, in both maize populations' for all cycles and for both *B. fusca* and *C. partellus* stem borers was an improvement in the mitigation of damaging effects of borers in maize plants. The days to anthesis and silking and plant height, plant and ear aspect marginally maintained the same values with the advancing cycles of selection. Similar findings have been reported from previous studies on maize (Ordas et al. 2012, 2013).

Under *B. fusca* infestation the net genetic gain in cumulative stem tunneling of −41 %, number of exit holes −35 %, and leaf feeding damage score 0 % in population CML395/MBR C5 Bc contributed towards the 43 % net genetic gain in grain yield. In this population the reduced stem tunneling and number of exit holes were crucial in the gains in the grain yield. However, in population CML444/MBR/MDR C3Bc, the net genetic gain in cumulative stem tunneling of 57 %, number of exit holes −69 %, and leaf feeding damage 10 % was important in the 25 % net genetic gain in grain yield. Similarly, reductions in cumulative stem tunneling, number of exit holes, and leaf feeding damage were of considerable importance towards grain yield gain in population CML444/MBR/MDR C3Bc (Ana Paula et al. 2013; Liberatore 2013). Under *C. partellus* infestation, in population CML395/MBR C5 Bc, the net genetic gain in cumulative stem tunneling of −35 %, number of exit holes −35 %, and leaf feeding damage score 9 % were attributable to the 70 % genetic gain grain yield. In population CML444/MBR/MDR

C3Bc, the net genetic gain in cumulative stem tunneling of −24 %, number of exit holes −15 % and leaf feeding damage score −29 % contributed towards the 36 % genetic gain in grain yield. For both populations, the other agronomic traits showed wide-ranging inclinations in the net genetic gain under *C. partellus* infestation (Tables 2, 3). Comparable outcomes on estimates of gains in selection for yield have been reported in the literature (Ana Paula et al. 2013; Liberatore 2013). Although, results with similar heritability values have been reported, the value of heritability for grain yield detected in this study is an estimate of high magnitude, considering the quantitative and polygenic nature of this trait (Hallauer 2010).

Although broad sense heritability estimates were high (>0.5) for most traits in both populations, they are not reliable (Falconer and Mackay 1996). The heritability estimates for the stem borer resistant parameters are specific to the populations and the mega environments under study, therefore predictions based on these estimates should be carried out with caution. The characters with low heritability estimates may require more cycles of selection. The variations detected among cycles for heritability estimates may be due to experimental error, genotype x environment interaction effects and possibly due to linkage disequilibrium leading to over estimation of genetic variances. Similar results were reported among cycles of maize populations (Sandoya 2008; Ana Paula et al. 2013). The improvement of grain yield and a reduction in the number of exit holes, cumulative stem tunneling, and leaf feeding damage scores is possible through the S1 progeny recurrent selection. The scheme may be effective for the accumulation of favourable alleles for breeding progress in maize for resistance to *B. fusca* and *C. partellus* attack. In the two populations studied, it is possible to conclude that the success of new selection cycles, which provides a continuous concentration of favorable alleles and the production of hybrids, is likely.

Conclusions

The study showed that the S1 progeny recurrent selection scheme is effective for the accumulation of favourable alleles for stem borer resistance and indirectly contribute towards genetic gain in grain yield. Through this scheme there was a reduction in

the injurious effects of *B. fusca* and *C. partellus* stem borers attributable to number of exit holes, cumulative stem tunneling, and leaf feeding damage scores in the maize populations. This was evident with the improvement of grain yield in the advancing cycles of maize through the S1 progeny recurrent selection scheme. These results suggest that further S1 progeny recurrent selection cycles may further improve the stem borer resistance. The S1 progeny recurrent selection scheme is useful in the development of improved populations and to borer resistance. The method is appropriate in making elite germplasm available for breeding. The advanced cycles of maize populations CML395/MBR C5 Bc and CML444/MBR/MDR C3Bc from the current study will be evaluated further for *B. fusca* and *C. partellus* stem borer resistance and grain yield to confirm their stability. The advanced cycles of these maize populations will be used in breeding with emphasis on borer resistance breeding programmes in the tropics.

Ethical statement I Murenga Mwimali declare that:

1. The research work reported in this manuscript, except where otherwise indicated, is my original investigation
2. This manuscript has not been submitted for any degree or examination at any other university.
3. This manuscript does not contain other persons' data, pictures, graphs or information unless explicitly acknowledged as being sourced from other persons.
4. This manuscript does not contain other persons' writing, unless explicitly acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

   (a) their words have been re-written but the general information attributed to them has been referenced;
   (b) where the exact words have been used, their writing has been placed inside quotation marks, and referenced.

5. This manuscript does not contain text, graphics or tables copied and pasted from the internet, unless specifically acknowledged, and the sources being detailed in the manuscript and the reference section.

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