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Response to two cycles of S_1 recurrent selection for turcicum leave blight in an open pollinated maize variety population (Longe 5)

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ABSTRACT

Farmers have shown preference for the maize variety Longe 5 because of its quality protein nature, easy access to seed and high adaptability. However production of Longe 5 is constrained by endemic foliar diseases including turcicum leaf blight. The current study determined the effectiveness of two cycles of S_1 recurrent selection towards improvement of resistance to turcicum leaf blight as well as improvement of yield and the associated traits. Selections were made by identifying and self pollinating foliar diseases-free plants from the base population of Longe 5 (the original cycle i.e. C_0) grown at the National Crops Resources Research Institute (NaCRRI), Namulonge in Uganda. Over 400 selfed ears were obtained and evaluated under artificial inoculation for turcicum leafblight. Remnant seeds of 80 selected S_1 lines were grown in isolation to reconstitute a new population of Longe 5 (C_1). Individuals in subsequent cycles were not selfed, instead in 2012A, 200 families of C_1 were grown in isolation to generate C_2. The cycles were evaluated in 2012B following a randomized complete design with split plot arrangement replicated 10 times. Highly significant variations were observed among the S_1 lines for turcicum leaf blight (TLB), grain yield (GY), plant height (PH), ear height (EH), ear aspect (EA), days to an thesis (DTA) and days to silking (DTS). Selection differential was positive for GY (0.12), PH (3.89) and EH (1.69) while it was negative for AUDPC (-2.98), EA (-0.085) and DTS (-0.83) as desired. The gain per cycle from C_0 to C_2 was -3.75% for DTA,-4.88% for DTS, -20.16% for EA, and -26.43% for AUDPC reflecting a significant reduction in the disease severity and significant improvement in the other traits. Positive significant gain was realised for grain yield (8.35%), 12.61% for EH and 0.21% for PH. There was a higher % gain cycle^{-1} realised for AUDPC in C_1 (-18.21%) than in C_2 (-10.07). Similar positive trends were realised for GY, DTA and DTS. The results indicate that the S_1 recurrent selection method employed was effective in improving Longe 5 for TLB, grain yield and the associated traits.

Keywords: Longe 5, *Exserohilum turcicum*, S_1 recurrent selection, grain yield, Uganda.

INTRODUCTION

Maize is an important crop in Eastern Africa as source of food, feed and household income for most smallholder families. In Eastern Africa, it is planted on more than 15 million hectares covering approximately 38% of the cultivated land [9]. Maize is also a principal and popular component of the diets across the region. The crop provides 50% of the calories with about 100 kg of per capita consumption per year in the region while in Central Africa the per capita consumption is 23 kg per year and provides 13% of the calories [15]. It is largely used directly for human food but increasing quantities are used for animal feed. Maize production, processing and utilisation provide vital employment and income generation activities for a large cross-section of the population including men, women and children. In spite of the high potential for maize production in the region, grain yield remains low (less than 3tha^{-1}). The low yields are attributed to prevalent use of unimproved varieties and low adoption of new stress tolerant germplasm that combines resistance to major foliar diseases, abiotic stresses such as drought and biotic stresses such

as Turcicum leaf blight, maize streak virus, gray leaf spot, insect pests and more recently, Maize lethal necrosis caused by synergistic effect of Maize Chlorotic Mottle Virus and Sugarcane Mosaic Virus [33]. The humid and wet environment in the mid altitude zone also presents favourable conditions for occurrence of the biotic stresses.

Although most of the maize produced in the region (about 85%) is consumed as food at household level, the regular or normal maize has low levels of essential amino acids, especially lysine and tryptophan [24, 18]. This means for humans and monogastric animals like pigs that depend on maize for their major food and feed, their diet has to be supplemented by other sources rich in essential amino acids, making it costly. Quality Protein Maize (QPM) with enhanced levels of essential amino acids was developed in 1970's to address this deficiency. Indeed, several countries invested in development and dissemination of QPM varieties to farmers. Accordingly, Ghana was the first country in Africa to release QPM open pollinated maize variety, OBATANPA. Similarly in Uganda, the improved version of this variety was released in 2000 as Longe 5 and is popularly known as Nalongo. Farmers in Uganda have shown preference for the variety because of its quality protein nature, easy access to seed and good adaptability [8]. However Obatanpa originally developed under lowland tropics in West Africa is susceptible to a number of foliar diseases, especially Turcicum leaf blight under the mid-altitude environment in Eastern Africa. This necessitated the improvement of this variety for Turcicum leaf blight and maize streak virus by crosses and selections between original Obatanpa and Ssusuma, an improved version for MSV from Mozambique to form the Longe 5.

Turcicum leaf blight was first reported in Uganda in early 1990's but still remains a serious challenge for maize production due to farmers growing susceptible varieties and the favourable conditions including high humidity, extended leaf wetness in some areas and moderate temperatures (17-27°C) [2]. Turcicum leaf blight causes yield loss of 50%, especially when disease sets early in the season. *Exserohilum turcicum* is known to survive on maize residue [20, 25, and 31]. Given the nature of farming practices carried out by farmers in the region, it is easy to perpetuate the pathogen season after season by farmers practice of repeated planting of maize in a given year and leaving crop debris in the field. The recommended practices for control of TLB include: 1) use of resistant hybrids, 2) spraying with fungicides, 3) eradication of crop debris after harvesting. However, host resistance through deploying resistant varieties remains the most economical and sustainable control of TLB. Moreover, it ensures environment safety. Therefore, maize improvement for yield and resistance to turcicum leaf blight remains an important strategy to improve production and productivity especially in endemic areas.

In the case of populations and open pollinated varieties, recurrent selection has been widely used by maize breeders for crop improvement [7]. It increases the favourable alleles in maize pools [13] especially for traits of quantitative nature. The goals of recurrent selection are to improve the mean performance of a population of plants and to maintain some level of genetic variability present within the population. Progress in selection is based on the heritability of the trait and the types of genetic variation controlling the trait in the particular population under selection and on the selection differential. Given the economic importance of turcicum leaf blight and the role of S_1 line recurrent selection, the current study was conducted to determine the effectiveness of two cycles of selection in improving host resistance to the *E. turucium*in Longe 5, a popular OPV on the market as well as other desirable agronomic traits. The specific study objectives were to: 1) determine the possible genetic gains in TLB resistance, 2) determine the potential gain in grain yield and secondary traits, 3) determine the improvement in resistance against TLB after two cycles of S_1 recurrent selection and 4) estimate heritability for various morphological and yield traits in Longe 5.

MATERIALS AND METHODS

3.2.1: Population Development and Experimental Design

The study was conducted at National Crops Resources Research Institute (NaCRRI), Namulonge, located at 0° 32'N, 32°35'E with altitude of 1140 m above sea level. An open pollinated Quality Protein Maize (QPM) variety (Longe 5) was used as the source population from which S_1 families and cycles C_1 and C_2 were derived.To start an S_1 line (first selfed generation) recurrent selection, the source population was planted in isolation at Namulonge during the second rains of 2010 (2010B). Each family was planted in single rows of 5m long comprising of 17 plants at a spacing of 0.75m between rows and 0.30m within rows. The whole plot comprised of 10 decks of 30 rows each. Fertilisers were applied in form of urea and diammoniumphosphate (DAP) at the rate of 45 and 30 kg ha^{-1},respectively. Entire DAP was applied at planting time while urea was side dressed when plants were at V7 growth stage [26]. Selection criteria included early pollen shade accompanied with early silking in addition to optimum plant height and ear placement. At flowering, ear shoots were bagged for selected plants with good agronomic traits in time to avoid cross pollination on the desired plants. Plants showing TLB symptoms were avoided while carrying out self-pollination to produce S_1 progeny. This aimed at selecting plants with tolerance to TLB. At physiological maturity, the selfed ears were individually harvested, threshed and numbered separately. A total of 350-450 selfed progenies were produced by controlled self-pollination.

During the first season of 2011 (2011A), 400 selfed progenies were evaluated ear-to-row. The progenies were of 2-row plots of 5m long each with spacing of 0.75m between rows, replicated twice. The recurrent S_1 selection was conducted under artificial inoculation for turcicum leaf blight. Ten plants with desirable traits in each family were inoculated with turcicum infested sorghum seeds at V6-7 stage. The same cultural practices were followed for the S_1 evaluation as discussed earlier. Half the seed was stored for recombination of selected S_1 lines to make a source population for the next cycle as described by Hallauer and Martison [14].

Data was recorded on Days to silking (DTS), Days to Anthesis (DTA), Plant Height (PH), Ear Height (EH), Ear Aspect (EA), Disease severity and grain yield (GY).

After evaluation, remnant seeds of 80 S_1 lines selected on basis of yield superiority, early maturity and resistance to turcicum leaf blight were planted in isolation to allow random mating by open pollination [35]. The recombination phase was carried out during the second rain season of 2011 (2011B) at NaCCRI. This reconstituted a new population which was C_1 of Longe 5.

Individuals in subsequent cycles were not selfed due to time constraint instead in 2012A season, 200 families of isolation seed (C_1 seed) were planted in isolation. The usual spacing of 75*30 m was followed. Every fifth entry formed the male row that provided the bulk pollen, and was made up of seeds from all the entries (male bulk=C_1 bulk), the other 4 rows formed the female plants which were detassled and pollinated with the bulk pollen. Weak or bad plants were eliminated and pollen collected from disease free vigorous, early silking and early flowering male plants. Pollen from desired plants was combined to pollinate the plants in female rows. At harvest, ears from female rows were handpicked and seeds combined to form C_2.

Evaluation of the cycles C_0, C_1 and C_2 was during 2012 B season, under field conditions at NaCRRI Uganda. The experimental design was a randomised complete block design with split plot arrangement, replicated 10 times. The inoculum formed the main plot while the sub plots were the cycles. The main plots were separated by 4 rows of Longe 6H and boarded by 4 rows of also Longe 6H on either sides. The cycles were 2- row plots of 5m long, at spacing of 0.75m x 0.03m. TLB inoculum was administered at 6-7V growth stage.

3.2.2Pathogen culture and inoculation

E. turcicum inoculum was produced from isolates obtained from infected maize leaves from Namulonge for inoculation of plots. Portions of infected leaf tissues were surface sterilized in 1% sodium hypochloride for 30 secs, rinsed in distilled water, and placed in high humidity under fluorescent light for 3 days to initiate sporulation. Single conidia were then picked from conidiophores with sterile glass needle and placed on lactose casein hydrolysate agar (37.5 g lactose, 3 g caseinhydrolysate, 1g $KH2PO_4$, 5 g $MgSO_4$, 2 ml microelements, 15 g agar dissolved in 1 litre of de-ionized water) in Petri plates. Cultures were maintained at room temperature for 15 days until the plates were fully colonized. Colonized media sections from the culture were placed onto sorghum seeds in 1000 ml autoclavable plastic containers filled half-full. The containers were shaken once a week to loosen the inoculated seeds and facilitate uniform colonization. Infested seeds were air-dried on green house benches for 3 to 4 days and thereafter kept dry at 10^oC until used. The colonized seeds were used for inoculation. Treatment materials were inoculated at V6-V7 growth stage, by placing approximately 5-15 infested sorghum seeds into the leaf whorls of all plants.

3.2.3 Disease severity assessment and scoring for other traits

Disease assessment for TLB was made on a whole plot basis commencing 3 weeks after inoculation. A scale of 0-5 was used to estimate severity of TLB following the CIMMYT procedure, i.e. 0 for no lesion and 5 for heavily blighted leaves. The scale assigns a percentage leaf area affected (PLAA) score based on visual estimates of the percent leaf surface area covered by lesions on single plants. Instead of individual plant assessments, visual estimates were made on whole-plots because each plot constituted a family and reaction of the plants within a family to infection was similar. A total of four assessments were made at one-week intervals. The four scores were used to calculate the area under disease progress curves as AUDPC = $\sum[(X_i + X_i+1)/2](t_i+1-t_i)$[5] and they were standardized by dividing by the total number of days used for disease assessment, where X_i is disease rating on date i, and t_i is the time in days on which X_i was recorded.

Several traits were evaluated but data on days to 50% silking (DTS), days to 50% anthesis (DTA), plant height (PH), ear height (EH) and grain yield (GY) only are presented in this paper. Days to 50% anthesis (DTA) and DTS were recorded as the number of days from planting to when 50% of plants in a plot had shed pollen, and had emerged silks, respectively. Ear height (cm) was measured from the ground level to the node bearing primary ear as an average of five randomly selected plants in each row per entry [12]. Plant height (cm) of each plant was measured as the distance from the ground level to the base of the flag leaf then, averaged for five randomly selected plants in each row as mentioned by Guzman and Lamkey [12]. Ear aspect (EASP) was visually rated on a scale of 1 to 5,

where 1 = clean, uniform, large and well filled ears and 5 = rotten, variable, small and partially filled ears. All ears harvested from each plot were weighed and shelled to determine grain weight and a representative sample was taken to determine percent moisture. Grain yield, measured in tones ha^{-1} adjusted to 12.5% moisture content was calculated from grain weight and percent moisture using the following formula relationship [6].

Grain yield ha^{-1}= [(FW*0.8) x ((100-M) /87.5) x (10,000 m^2ha^{-1}/ 7.5m^2)]

Where:
FW = Field weight of ear in kg / plot at the time of harvest
0.8 = threshing percentage
M = Percentage grain moisture at harvest
87.5 = 100 – Standard Moisture (12.5)
7.5 = Plot area per row per cycle (2x5mx0.75m)

3.2.5 Data Analysis
Disease severity data (PLAA) was used to calculate the area under disease progress curve (AUDPC) for TLB using Microsoft Excel 2007 (Microsoft Corporation) and subsequently subjected to analysis of variance (ANOVA) of the Genstat Discovery edition 4, using the appropriate method for randomised complete block split plot design for TLB and other traits. Estimates of genotypic and phenotypic variance components were calculated from ANOVA and used to calculate heritability. The following formula were used to estimate $\mathbf{h^2_{BS}}$, **S** and $\mathbf{R_e}$

Broad Sense Heritability ($\mathbf{h^2_{BS}}$) = $\boldsymbol{\delta^2_G}$/ ($\boldsymbol{\delta^2_E}$+ $\boldsymbol{\delta^2_{G)}}$
Where:
$\mathbf{h^2_{BS}}$ = broad sense heritability
$\boldsymbol{\delta^2_G}$ = Genetic variance
$\boldsymbol{\delta^2_E}$ = Environmental variance

Selection differential (S) = $\boldsymbol{\mu_{S1} - \mu}$
Where: $\boldsymbol{\mu_{S1}}$ = mean of the selected S_1 lines
μ= Population mean (comprising all S_1 lines)

Expected response (Re) =S **x** $\mathbf{h^2_{BS}}$
Percent deviation of inoculated from uninoculated was calculated by the formula:

$$\mathbf{PercentDeviation} = \frac{(\mathbf{Inoculated} - \mathbf{Uninoculated}) * \mathbf{100}}{\mathbf{Uninoculated}}$$

$$\mathbf{PercentgainCycle^{-1}} = \frac{(\mathbf{Cycle_2} - \mathbf{Cycle_1}) * \mathbf{100}}{\mathbf{Cycle_{12}}}$$

RESULTS AND DISCUSSION

3.3.1 AUDPC (TLB)
The data revealed that S_1 lines differ significantly ($P<0.01$) for AUDPC. Population mean including selected S1 lines (33.3) was greater than the mean of selected S_1 lines (30.34) resulting in negative selection differential of -2.98 which was in the desired direction and at the same time with a negative response of -0.98 AUDPC value. These results are supported by those of Jinahyon and Russell [16] who reported reduction in mean disease score for stalk rot from 3.7 to 1.7 with three cycles of S_1 recurrent selection.

Moderate estimates of heritability for AUDPC (0.33) was observed in Longe 5 population (table 1). The mean squares in table 2 indicated significant differences ($P<0.001$) in cycles regarding AUDPC. The results for the mean performance of cycles C_O, C_1 and C_2 as regards AUDPC are presented in tables 4 and 5.The mean score for AUDPC in C_2 (25.81) was significantly less than that of C_0 (35.09) while C_1 with a mean score of 28.3 performed better than C_2 as regards AUDPC. The lower AUDPC value in C_2 as compared to C_1 reflects the genetic improvement of the population against Turcicum leaf blight as well as efficacy of the recurrent selection method. These results are supported by those reported by Ceballos *et al* [7], De Leon *et al* [10], who also observed reduction in maydis leaf blight severity in advanced cycles of recurrent selection in maize populations.

Cycle means and gain cycle $^{-1}$ for AUDPC are presented in tables 4 and 5 and figure 1. A higher percentage gain $cycle^{-1}$ (-18.21%) was realised for AUDPC in C_1 than in C_2 (-10.07%).The two cycles of recurrent selection for TLB resistance significantly reduced the infection, (AUDPC) from 35.09 to 25.81 probably because of the negative

selection differential. The negative value of selection differential indicated that additive genes control the disease. Sheih and Lu [29] reported that additive genetic effects accounted for a major part of the total variation in resistance among the genotypes. Another possibility might be that the S1 lines have high concentration of proteins, lignins, phenolic and callose, providing extra source of resistance to turcicum leaf blight. Smith and Cordova [30] reported significant improvement from 4.5 to 3.7 and from 3.8 to 2.9 across two locations using three cycles of S_1 recurrent selection. The lower severity of infection in C_2 as compared with C_1 possibly reflects the effectiveness of recurrent selection for disease resistance in Longe 5 population.

Significant deviations were observed in scores for AUDPC between inoculated and non-inoculated plants among the cycles (Table 3). C_0 registered a higher (-26.533%) deviation than C_2 (0.661%) on the other hand C_1 scored a negative deviation of -3.626%.Lower deviation of inoculated and none inoculated for AUDPC in C_1 and C_2 revealed more resistance to the inoculum.

3.3.2 Grain yield

Recurrent selection based on S_1 progeny is a good method of achieving improvement within populations [23] and has been proposed as a particularly promising means of improving grain yield. The results indicate highly significant differences ($P<0.01$) among S_1 lines, similar to the findings of Shah *et al* [28] who also reported highly significant differences ($P<0.01$) among S_1 lines using S_1 line recurrent selection for grain yield and MLB resistance.

Population mean including selected S_1 lines (2.48 tha^{-1}) was less than the mean of selected S_1 lines (2.61 tha^{-1}) resulting in selection differential of 0.025. The expected response was 0.110 tha^{-1}. A high level of the selection differential was observed for several traits of economic importance. This showed the ability of diverse germplasm in any breeding program.

A very high estimate of heritability for grain yield (0.90) was observed in Longe 5 population (table 1). The high heritability value for this trait concurs with the findings of Saleh *et al* [27] who also reported moderate heritability for grain yield. The broad sense heritability of high magnitude regarding grain yield showed that this trait could be improved in the following generations.

The mean squares in table 2a indicated highly significant ($P<0.001$) differences in cycle regarding grain yield. The results for the mean performance of cycles C_O, C_1 and C_2 as regards grain yield are presented in tables 4 and 5. The mean grain yield in C_1 (2.575 tha^{-1}) was comparatively less than that of $cycle_2$ (2.609 tha^{-1}) while C_O performed least (2.408 tha^{-1}) of the cycles as regards grain yield. Cycle means and gain $cycle^{-1}$ of grain are presented in table 4 and figure 1. Increase in grain yield $cycle^{-1}$ was 6.685% and 2.01% for cycle C_1 and C_2 respectively. Our results are in agreement with those of De Leon *et al* [10] who also reported highly significant increase in grain yield i.e. 507 kg $cycle^{-1}$. Similarly, Vales *et al* [32] also reported significant increase in grain yield due to selection. Ceballos *et al* [7] reported 19% gain $cycle^{-1}$ in early and 7% gain $cycle^{-1}$ under intermediate disease pressure trials for grain yield in maize populations. Similarly Weyhrich *et al* [34] observed significant increase in grain yield in the BS II maize population .They reported 110 and 220 kg ha^{-1} gains per cycle after completing four cycles of S_1 progeny selection. A higher percentage gain (6.94%) was realised for grain yield in C_1 than in C_2 (1.32%).

Table 1. Mean square values (MS), Population mean (μ), mean of the selected S1 lines (μ_{S1}), selection differential (S), environmental variance (δ^2_E), genetic variance (δ^2_G), heritability values (h^2_{BS}) and expected response for various traits of Longe 5

Trait	MS	μ	μ_{S1}	S	δ^2_E	δ^2_G	h^2_{BS}	R_E
DTA	3.233^{***}	62.29	64.575	2.2850	2.099	0.567	0.21	0.56
DTS	4.086^{***}	65.462	64.628	-0.8340	2.104	0.991	0.32	-0.23
Plant Height	1122.2^{***}	183.41	187.3	3.8900	215.4	453.4	0.68	2.65
Ear Height	163.69^{***}	74.62	76.31	1.6900	50.25	56.72	0.53	0.89
Ear Aspect	0.3037^{***}	2.7114	2.626	-0.0850	0.14	0.08185	0.37	-0.03
AUDPC	120.27^{***}	33.3	30.34	-2.9800	60.19	30.04	0.33	-0.98
Grain Yield	0.5148^{***}	2.484	2.606	0.1224	0.0252	0.2448	0.91	0.11

**** Highly significant (P<0.001)*

Table 2a. Mean squares for EA, AUDPC, and G.Y over two cycles of S_1 recurrent selection in Longe 5 population evaluated for Turcicum leaf blight during 2012

Source	df	EA	AUDPC	G.Y
Cycle	2	1.9365^{***}	450.54^{***}	0.23124^{***}
Rep	9	0.0888	112.65^{ns}	0.04395^{ns}
Inoculum	1	2.904^{***}	90.04^{ns}	0.02225^{ns}
Cycle*Inoculum	2	0.1115	126.94^{ns}	0.00171^{ns}
Error	36	0.1249	49.13	0.03547

*** * highly significant (P<0.001), ns non-significant (P>0.05)*

Table 2b. Mean squares for DTA, DTS, PH and EH over two cycles of S_1 recurrent selection in Longe 5 population evaluated for Turcicum leaf blight resistance during 2012

Source	df	DTA	DTS	PH	EH
Cycle	2	32.6^{***}	52.917^{***}	925^{***}	431.67^{***}
Rep	9	4.25^{ns}	3.039^{ns}	789.2^{ns}	100.68^{ns}
Inoculum	1	15^{*}	20.417^{*}	2653.3*	770.42^{***}
Cycle*Inoculm	2	2.4^{ns}	1.617^{ns}	178.6^{ns}	13.07^{ns}
Error	36	2.519	3.026	147.6	28.74

*** * highly significant (P<0.001), * significant (P < 0.05) and ns non-significant (P > 0.05)*

Negative deviations were observed in grain yields of inoculated and non-inoculated plants among the cycles (Table 3). C_2 registered a higher (-2.274%) deviation than C_1 (-0.928%) on the other hand C_O deviated by -1.361%. In most inoculated plants, grain yield was reduced compared to uninoculated.

Table 3. Means and deviations of inoculated and Un- inoculated for various traits of Longe 5 evaluated for Turcicum Leaf Blight after 2 cycles of S1 Recurrent selection

Traits	Cycle 0			Cycle 1			Cycle 2		
	Ino	Unino	Dev (%)	Ino	Unino	Dev (%)	Ino	Unino	Dev (%)
DTA days	68	66.2	2.719	65.7	65.1	0.922	64.9	64.3	0.933
DTS days	66.9	66.2	1.057	65.7	63.9	2.817	63.8	62.8	1.592
PH Cm	186.4	192.8	-3.32	169.6	186.4	-9.02	181.6	198.3	-8.42
EH cm	67.3	75.4	-10.743	69.8	77.9	-10.398	77.7	83	-6.386
EA cm	3.3	2.8	17.857	3.1	2.55	21.569	2.57	2.3	11.739
AUDPC TLB	39.2	30.98	26.533	28.17	29.23	-3.626	25.9	25.73	0.661
Yield (Grains tha^{-1})	2.392	2.425	-1.361	2.563	2.587	-0.928	2.579	2.639	-2.274

3.3.3 Maturity Characteristics

Data concerning days to anthesis (DTA) and days to silking (DTS) revealed highly significant (P<0.01) variations among S_1 lines. Selected S_1 lines took fewer days (64.628) to silking than the unselected S1 lines (65.462) days. (Table 1). On the other hand, the selected S1 lines took more days (64.575) to anthesis than the unselected S_1 lines (62.29). The expected response for DTA was 0.56 while that for DTS was -0.27. Early maturing populations have the property of disease escape and could therefore be less amenable to disease development and hence can reduce yield losses. Our results revealed significant variations among S_1 lines. Abedon and Tracy [1] also observed significant differences for maturity traits using S1 line recurrent selection. Similarly, De Leon *et al* [10] observed significant differences for maturity in four tropical maize populations implementing S_1-S_2 line recurrent selection for downy mildew resistance. Using full Sib recurrent selection for northern corn leaf blight disease resistance in sub-tropical maize populations, Ceballos *et al* [7] reported a significant decrease in maturity traits. Heritability estimates for DTS and DTA were moderately low, 32 and 21 respectively. Selection differential for these traits were -0.834 for DTS and 2.285 for DTA.

Significant (P>0.001) differences were exhibited among cycles for DTA and DTS (Table 2a). The results of DTA and DTS showed that C_2 took least days (64.4) followed by C_1 with 65.4 while C_O took longest of days (67.1) to flower. The same trend was manifested for DTS whereby C_2 exhibited the least mean score of 63.3 followed by C_1, with a mean score of 64.8 and lastly C_0 with a mean score of 66.55.

Cycle means and gain $cycle^{-1}$ of DTA and DTS are presented in tables 4 and 5. A higher percentage gain $cycle^{-1}$ (-2.6%) was realised for DTA in C_1 than in C_2 (-1.24%). A similar trend was manifested for DTS whereby C_1 exhibited a higher percentage gain (-2.65%) than C_2 (-2.315%). The percentage gain per cycle in Longe 5 for DTA and DTS were 3.474% and 1.721% for C_1 and C_2 respectively while they were 1.69% and 1.244% for C_1 and C_2 respectively for DTA. Martin and Russell [21] observed that recurrent S_1 selection was effective for maturity characters in SW population. Similarly, Johnson *et al* [17] reported earlier flowering with a 4.4% increase in grain yield $cycle^{-1}$ after conducting 15 cycles of full sib recurrent selection in one low land tropical maize population.

Significant deviations were observed in DTA and DTS of inoculated and non-inoculated plants among the cycles (Table 3). C_O registered a higher (2.719%) deviation than C_1 (0.922%) and C_2 (0.933%) for DTA. As regards DTS, C_1 registered a higher (2.817%) deviation followed by C_2 (1.592%) while C_O deviated by 1.057%.

3.3.4 Agronomic Traits

Data showed highly significant variations (P<0.01) for plant height, ear height and ear aspect, among the S_1 lines .The average plant height of selected S_1 lines was higher (187.3 cm) than that S_1 lines (183.4 cm), resulting in selection differential of 3.89 with expected response of 2.65 cm. The same trend was manifested for ear height and ear aspect. The average ear height for selected S_1 was higher (76.31) than that for S_1 lines (74.62 cm) resulting in selection differential of 1.69. The expected response was 0.89 cm. As regards ear aspect, the results were in the desired direction where selected S_1 score was less (2.626) than that of S_1 line (2.714) resulting in a negative selection differential of -0.085 with expected response of -0.03.Ear height, plant height and ear aspect are important agronomic characters. They play a key role in the plants tolerance to a plants tolerance to lodging and can affect yield considerably. Lower plant height and near central placement of top ear on plant are desired because such plants are more resistant to lodging [4]. The S_1 lines varied significantly (P<0.01) in regard to plant and ear height and ear aspect. Abedon and Tracy [1] reported significant differences for plant and ear height while using full sib recurrent selection in maize.

Heritability for plant height, ear height and ear aspect was 0.68, 0.53 and 0 .37 respectively (Table 1). The low heritabilities indicate high environmental influence on plant and ear height. Ahsan and Mehdi [3] reported low heritability value (0.56) for plant height using S_1 family selection in maize for higher green fodder yield. On the contrary, Mihaljevic *et al* [22] obtained high heritability values (0.90) for plant height. The greater the heritability of a particular trait, the lesser will be the environmental effect.

Significant (P>0.001) differences were exhibited among cycles for Plant height, ear height and ear aspect (table2b). The results of plant height showed non directional trend where C_2 mean score was the highest (190 cm) followed by C_O (189.6 cm) while C_1 exhibited the lowest (178 cm) mean score for plant height. As regards ear height and ear aspect, the results exhibited desirable direction whereby for ear height, C_2 exhibited the highest (80.5 cm) mean score followed by C_1 with a mean score of 73.85 cm and lastly C_O with a mean score of (71.35 cm. For ear aspect, C_2 exhibited a mean score of 2.43 that was significantly better than C_O with a mean score of 3.05 and C_1 with a mean score of 2.82.Significant differences were observed for plant morphology regarding cycles. The positive deviations of ear and plant height cycle^{-1} indicated increase (6.5cm and 120cm in ear and plant height respectively. Devey*et al* [11] reported significant increase in ear and plant height with 40% reduction in grain yield after conducting seven cycles of S_1 recurrent selection in Lancaster maize population for stalk quality. In this study, the selected S_1 lines had higher ear and plant height than the population mean. Likewise, C_2 had higher ear and plant height than C_1. Lamkey and Dudley [19] reported significant increase in ear and plant height, using mass selection in three autotetraploid maize synthetics. They observed 39cm, 15cm and 29 cm increase in plant height in the three populations. It was inferred from the results that the selection method was not very effective to characters related to plant morphology, because of low heritability, high instability and increased environmental influences.

Cycle means and gain cycle $^{-1}$ for plant height, ear height and ear aspect are presented in tables 4 and 5. The results indicate that a higher percentage gain cycle-^{1} was realised in C_2 than in C_1 for the three traits. A higher percentage gain of 6.065 was realised in C_2 than in C_1 (-6.065) for plant height and for ear height, the gain per cycle in C_2 was 8.8% which is higher than that in C_1 (3.5%).The same trend was exhibited for ear aspect whereby C_2 scored a higher gain (-13.805%) than C_1 (-7.377%)

Table 4. Cycle means for various traits of Longe 5 population evaluated after 2 cycles of S_1 line recurrent selection at NaCRRI during 2012A

Cycles	Traits						
	DTA(days)	DTS (days)	PH (cm)	EH (cm)	EA (1-5)	AUDPC (TLB)	G.Y(tha^{-1})
C_0	67.1	66.55	189.6	71.35	3.05	35.09	2.408
C_1	65.4	64.8	178.1	73.85	2.824	28.7	2.575
C_2	64.6	63.3	190	80.35	2.435	25.81	2.609
LSD	1.018	1.116	7.8	3.438	0.227	2.217	0.121

Table 5. Selection gain (%) cycle^{-1} exhibited of various traits of Longe 5 population evaluated after 2 cycles of S_1 recurrent selection at NaCRRI during 2012B

Cycles	Traits						
	DTA (days)	DTS (days)	PH (cm)	EH (cm)	EA (1-5)	AUDPC (TLB)	G.Y (tha^{-1})
C_0-C_2	-3.73	-4.88	0.21	12.61	-20.16	-26.45	8.35
C_0-C_1	-2.53	-2.63	-6.07	3.50	-7.41	-18.21	6.94
C_1-C_2	-1.22	-2.31	6.68	8.80	-13.77	-10.07	1.32

Significant deviations were observed in plant height, ear height and ear aspect of inoculated and non-inoculated plants among the cycles (Table 3). For plant height, C_1 registered a higher (-9.013%) deviation than C_2 (-8.422%)

and C_O with the least percentage deviation of -3.32%. As regards ear height C_O and C_1 did not differ significantly, with C_O registering slightly higher percent deviation (-10.743%) than C_1 (-10.398%). C_2 registered the least percentage deviation (-6.386%). For ear aspect, C_1 registered a higher percent deviation (21.569%) than C_O (17.875%) while C_2 scored the least percent deviation by 11.739%.

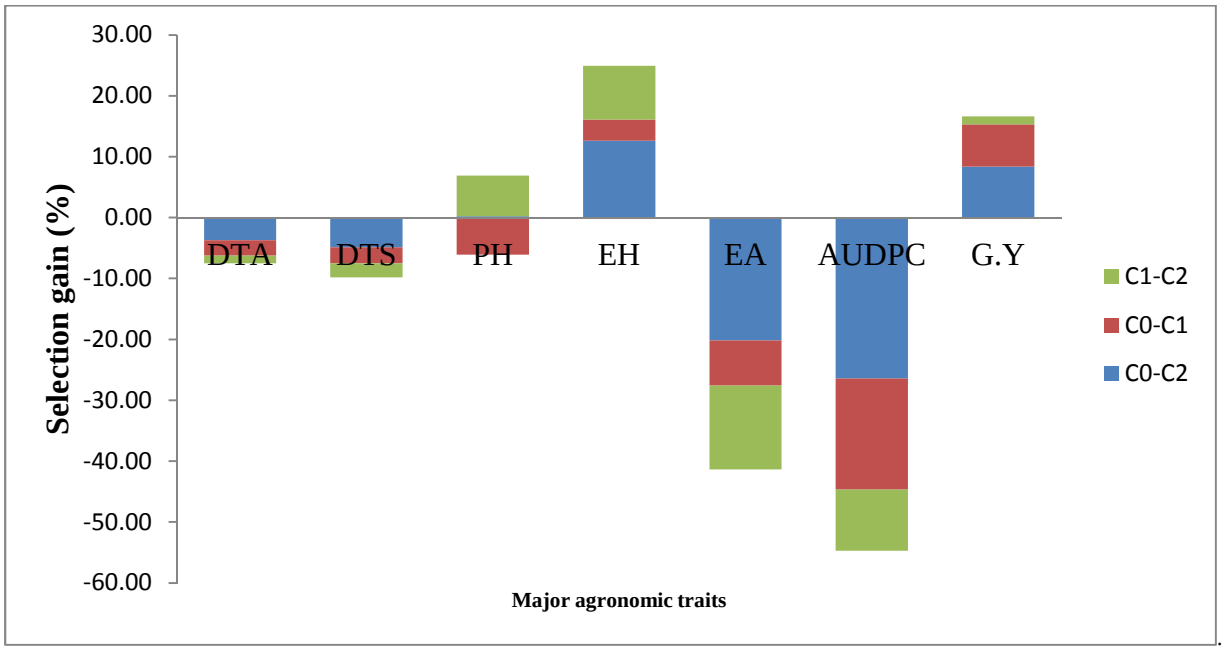

Figure 1 : Percentage selection gain exhibited among the three cycles

CONCLUSION

Moderate heritabilities, desirable selection differentials and significant improvement in TLB disease resistance indicate that the recurrent S_1 selection was effective in improving the Longe 5 population used in this study. The improvement in yield was probably partly, the result of the desirable decrease in ear aspect and the maturity traits. The higher percentage gain cycle^{-1} in C_1 than in C_2 suggests that selections in early cycles is crucial, although some additional cycles of selection would still be necessary to further improve resistance to TLB and grain yield, including the associated traits.

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