

EVALUATION OF TWO CYCLES OF MASS SELECTION IN
YZ COMPOSITE POPULATIONS OF SORGHUM
(Sorghum bicolor. (L). Moeneh)

BY

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DECLARATION

I hereby declare that this thesis is a documentation of my own research findings. It has not been presented before in any previous application for a higher degree.

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DEDICATION

This work is dedicated to my family: Mrs. Juliana D. Aba, Mr. Aluwong D. Aba, Miss Emily D. Aba and Mr. Tache D. Aba, for their patience throughout the period of research work.

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ABSTRACT

A random-mating population of sorghum (Sorghum bicolor. (L) Moenob)YZC composite, was being improved for yield using recurrent mass selection. The results from the evaluation of the data showed significant improvement for yield, in the individual as well as in the combined locations. Significant associated response was observed for plant height, emergence count and count at harvest. There was a significant reduction in maturity. Analysis of variance for the individual as well as for the combined data was done. Observed vs expected genetic change was also computed.

After two cycles of selection, a gain of 24.39% and 54.05% in head weight per plot and grain weight per plot were observed respectively. This means an average of 12.2% and 27.03% gain per cycle, respectively. From the combined analysis of variance, highly significant different ($p = 0.01$) between locations for all traits except for count: at thinning and head width. Highly significant population mean squares were also recorded for all traits except head width and number of grains per plant. Non--significant genotype x environment interaction mean squares were observed for all traits except days to 50% flowering which showed a highly significant ($p = 0.01$) mean square.

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INTRODUCTION

Population improvement is a long term breeding approach which offers opportunities for maintaining genetic variability, inspite of selection, after a long period. Frequent inter-crossing results in new recombinants that enhance selection opportunities cycle after cycle. Recurrent selection not only improves the performance of the population par se but the performance of lines derived from them are also improved.

Development and use of large random mating populations has been an important foundation of the population improvement at Institute for Agricultural Research, Samaru. With the discovery of the male-sterile gene ms_7 from an indigenous sorghum cultivar, and the subsequent generation of breeding populations at Samaru from them, it has been possible to start a continuous population improvement and recurrent selection program.

Recurrent selection has been a successful method in improving yield of sorghum populations. Effectiveness of mass selection in improving sorghum populations has been demonstrated in early maturing sorghum populations with different genetic base in Uganda, East Africa, U.S.A. and India. Such successes have also been shown in a few long-season populations in Nigeria by Obilana and EL-Rouby, (1980a) and Obilana (1981a&b).

This study is to evaluate two cycles of mass selection in a photosensitive, long season Yz composite population.

CHAPTER 2

LITERATURE REVIEW

The practice of mass selection for population improvement in crop plants dates back to the time when corn was first domesticated. Selection at that time was restricted to open-pollinated varieties and was a common practice before the concept of hybrid corn. The development of many adapted strains of corn can be attributed to successful selection by farmers and plant breeders (Allard 1960).

Smith (1909) gave an excellent example of how successful mass selection was for morphological characters. He showed that there were correlated effects on plant height, number of internodes below ear and total number of internodes; differences increased from 28.96cm to 88.14cm, 1.3 to 3.5 and 1.5 to 4.0 for the traits, respectively. Reports of the effectiveness of mass selection for the improvement of characters in the early part of the 20th century were not consistent, depending, in part, on the character under selection. Cortez-Mendoza (1977) and some corn breeders contended that mass selection was not an effective breeding method because of inadequate genetic variability. In most instances, however, faulty plot techniques and inadequate parental control restricted progress from mass selection, particularly for complex traits, such as yield, that have a relatively low heritability, (Cortez-Mendoza, 1977).

Later a mass selection program was initiated at Nebraska station in 1956 with the object of improving yield

in adapted varieties of corn. Results obtained showed that in few cases the data were consistent with those expected and also indicated an increase in yield than the earlier-practiced mass selection programmes.

Gardner (1961) reviewing early work in corn, was of the view that for yield, mass selection and its modification called ear-to-row selection have been ineffective in most instances.

After 1960, several programmes on mass selection, involving the use of the method described by Gardner in 1961, were initiated. Refinement of the techniques for mass selection as described by Gardner (1961) included; minimizing the environmental effects by timely irrigation; stratification of the field into small uniform of 4 by 5 hill grids so as to provide some control over soil fertility and moisture gradients and selecting the highest yielding plants within each block; and by drying the selected ears to a constant moisture level before the final selections are made. He stated that in this way one should expect to make progress in selecting for yield of grain in genetically variable populations of corn under irrigation.

Results of initial four cycles of mass selection for yield in Hays Golden were reported by Gardner (1961); his material consisted of an irradiated and a control population. An average gain in yield of 3.9% per generation was realized, he concluded that faulty techniques could easily account

for the ineffectiveness of mass selection reported in the past.

Johnson (1963) achieved a 33% improvement in a Mexican corn variety after three generations of mass selection.

According to Gardner (1961) and Lonquist (1967), mass selection for population improvement has the following advantages; minimum duration of cycles, maximum recombination opportunity, maximum utilization of genetic variability; maximum selection intensity possible, not only are the populations improved but also their crosses, as evident by diallel experiments. Varieties of highest yield usually gave the highest yielding hybrids (Lonquist, 1967).

Gardner (1969) used a linear relationship between grain yield and generation for selection as a measure of progress after 13 generations of recurrent mass selection. For a C¹³ population there was an increase in mean yield per cycle by 2.93% in relation to the original variety Hays Golden.

Lonquist (1967) reported results of five generations of mass selection for prolificacy in the Hays Golden variety of corn. This was the same variety used by Gardner (1961). The regression for gain in yield per cycle of selection relative to the parental variety was 6.28%. The greater effectiveness of selection where prolificacy was the primary trait was believed to be due to the higher selection intensity used as well as to high heritability of the trait under selection.

Hallauer and Sears (1969), following procedures similar to those used by Gardner (1961), conducted mass selection for yield improvement in Krug and Iowa Ideal open-pollinated varieties of corn. They made yield evaluations of six cycles of selection in Krug and five cycles in Iowa Ideal. They did not find significant improvement for yield in either variety by mass selection. The lack of significant progress was attributed to one or more of the following reasons: inadequate additive genetic variance in the varieties; imprecise plot techniques to minimize the confounding effects of the environment; insufficient testing to detect the small differences and to estimate the true value for the different cycles of selection, particularly in the later cycles, a low intensity of selection because of the exclusion of stalk-lodged plants in the basic units of selection, and plant density was too high in the plots under selection, a factor which prevented the phenotypic expression of yield for individual plant genotypes that could be selected visually.

Doggett (1972) discussed recurrent mass selection in mostly self-pollinating crops such as sorghum. The intercrossing required is achieved by the use of male sterility, and seed set deficiencies are avoided by using the method of female choice recurrent mass selection. He outlined a procedure that allows for continued improvement of a

population and at the same time ensuring the development of good parents to be used in hybrid production. He argued that traditional methods like mass selection were good for characters controlled by few genes. But since yield is controlled by many genes, it may be increased by recurrent selection method.

In a sorghum improvement programme in East Africa, Doggett and Eberhart (1968) used the genetic sterile ms_3 , for obtaining the intercrosses. After establishing 8 random mating populations they chose four of these which they labelled RS_1 to RS_4 , the other four he labelled PRS_1 to PRS_4 . The RS_1 to RS_4 population were based on 158 distinct sorghum varieties. The results from 3 cycles of mass selection showed that under female choice mass selection, there was some increase in yield over the mean of all the populations as a whole. Population RS_1 showed a 20% increase in yield over the three generations, which in view of the rather low selection intensities employed is a satisfactory result. Population RS_3 showed an even greater increase of 32%, but the base population yields were low, and it was probable that a simply inherited leaf disease factor was responsible for the behaviour of this population. The most interesting results came from the S_1 testing data. It was shown that the mean increase in yield obtained was 25%. Population PRS_1 , again most responsive, showed a yield increase of almost 33% in three generations. The most striking feature of the results obtained was the fact that the mean grain

yield from four populations under S_1 -testing of 6,980 kg/ha was significantly higher than the best Serena control-yield of 6,495 kg/ha while population PRS1 with 7,315 kg/ha was 13% above the best Serena control. Serena and Dohbs are the best yielding varieties in East Africa, yet these populations under the S_1 -testing system out yielded them after only 3 generations of selection.

Arboleda-Rivera and Compton (1974) used mass selection in developing three samples of a maize population for prolificacy and grain yield under three different seasonal conditions (1) rainy season (2) dry seasons, and (3) both rainy and dry seasons. Mass selection in the rainy seasons resulted in an increase in grain yield and ears per plant of 10.5% and 8.8% per cycle, respectively when tested in the rainy season. When tested in dry seasons, gains were 0.8% per cycle for yield and 1.0% per cycle for number of ears per plant. The direct response in grain yield in the population selected in the dry seasons was only 2.5% per cycle whereas it was 7.6% when tested in the rainy season. The gain in ears per plant was 11.4% when tested in the rainy season, but the direct response was 4.4% per cycle. In the population selected under both seasons, there was a gain in grain yield of 5.3% and 1.1% per cycle in the tests in the rainy and dry seasons, respectively. For prolificacy, the respective gains were 7.0 and 3.3% per cycle.

Devera and Bhatt (1972) used mass selection to improve the grain weight in wheat crosses. The results on 100 kernel weight for the third and fourth parent showed that after one cycle of mass selection, there was significant shift in the mean value for kernel weight in the positive direction for large seed size populations and a significant shift in the negative direction for the small seed size populations. Except for one cross, as compared with the mean of the unselected control populations. It was also observed that there was a significant reduction in the variances of the mass-selected populations as compared with the unselected control, in each cross studied. On the average the plants retained after applying this selection level for ear size were 41.16% for large seed size populations, 25.52% for the small seed size populations, and 30.20% for the control populations. Thus the chances of retaining the derived segregates among large seed size populations increased by 10.96% and among small seed populations they decreased by 4.73%.

One or two cycles of mass selection in parental material did not cause any appreciable differences in grain yield, compared with the grain yield of control populations. The cross N68.42 responded better to mass selection for seed size than cross N68.1 and N68.53. In general, mass selection for large seed size in heterogeneous populations gave a 33.8% higher yield than controls in the first cycle and a 32.5% higher yield in the second cycle. The reduction in yield due to selection for small seed size in these populations compared

with the controls was 7.7 and 6.8% for one and two cycles, respectively. In homogeneous parental material, selection for large seed size gave a nominal increase of 7.4% over the controls for one cycle and a reduction of 0.9% for the second cycles. Reduction in yield for small seed size in these populations was 3.7 and 4.4% for one and two cycles, respectively. Knott and Talukdar (1971) have shown that increasing seed weight in wheat is conducive to higher grain yield. Bhatt (1972) studied the inheritance of kernel weight in two spring wheat crosses. He found that the estimates of heritability and genetic advance for seed yield were high and this character should be easily amenable to improvement by mass selection.

Forster and Weng (1979) evaluated 10 cycles of mass selection in an inbred population of grain sorghum. Selection gains were evaluated by comparing non-selected and ten cycle selected populations grown in replicated experiments at three locations in 1979. Mean per cycle selection response expressed as a percentage of non-selected population mean over 10 generations ranged from 0.25 for flowering to 3.40% for seed weight. The results suggest that sorghum populations may respond to directional selection despite apparently restricted mating systems.

Obilana and EL-Rouby (1980) reported on an improvement program for yield abilities of two composite populations by mass selection. The report included evaluations of the

original populations and subsequent cycles of mass selection within the populations. The mean performance of the original populations (Co) and those of the three advanced generation cycles C₁, C₂ and C₃ showed that after three cycles of mass selection in the B composite, the C₃ population was significantly higher yielding with 2.63 kg/plot and with more fertile tillers (54 heads) than the Co population with 1.90 kg/plot and 44 heads. The associated changes observed for days to 50% heading and plant height were not significant. Similar changes were observed in the Y composite. Significant increases were shown by the C₃ for yield with 2.50 kg/plot and fertile tillers (48 heads) over the Co that gave yield of 1.78 kg/plot and 32 heads. Associated change observed for days to 50% heading was not significant but was significant for plant height. However, the amount of progress due to female choice mass selection was different in the two composites. The observed gain in yield after three cycles of selection in B composite was 38.40% as compared to the expected gain of 29.40%. This high observed value more than the expected, they explained may be due to a compensation for the initial drop in the C₁. This initial drop could be due to slight inbreeding depression complicated with head and leaf diseases and insect pest in the C₁ population. On the other hand, the observed gain in yield in Y composite was 40.40% after three cycles of mass selection similar to the expected 41.80%. The pattern of increase was also different. The high percentage increases for this study were probably due to the high selection intensity used (K = 2.06). Thus, they reported, it was evident that

female choice mass selection has effectively increase yield in two sorghum populations, B and Y composites, at an average rate of 12.80% and 13.50% per cycle respectively. The general response due to selection for major genes was substantial due to the amount of genetic variability and diversity present within the composites and use of high selection intensities coupled with appropriate plant population size.

MATERIALS AND METHODS

3.1. Genetic background of material investigated

Six random-mating populations (composites) were developed for the Nigerian Sorghum Improvement Programme. Two of these heterogeneous populations, Y and B composites, served as the base populations in this study. The Y composite, mainly of local germplasm, was found to be more adapted than the B composite, although the B composite had better quality heads. However, both populations had generally low yield. Therefore, the two composites were combined into one (Z composite) and then backcrossed to Y composites to form the YZ composite which was used in this study. It is a genetically broadbased, diverse and variable population developed from a mixture of exotic and indigenous germplasm crossed to non-restorer "A" lines (Obilana and El-Rouby, 1980a). The male sterile gene ms_7 was used to effect random-mating in this base population.

Stratified mass selection was practiced among male sterile plants (female choice.) in the YZ composite base population. At each generation, 53,333 plants were established in rows which were spaced 75cm apart and plants were spaced 25cm within the rows. The field was divided into 150 grids (sub-plots) each containing 100 plants. At anthesis all sterile plants were tagged for identification. At harvest the highest yielding 20% of the sterile plants which were visually identified in each sub-plot were harvested and in the seed

house, the best 10% were selected. Equal quantity of seed were bulked from selected plants to form the next cycle. Two cycles of mass selection have been completed in this composite. The original (Co) and two advanced generations were evaluated in randomized and replicated experiments in Samaru and at Mokwa in 1983. Two elite lines, L.187 and L.243, were used as checks in the evaluation trials.

3.2 Experimental Layout

The resulting two generations including the original YZ composite (Co) and the C₁ and C₂ with the two check varieties were planted in Samaru on 15 June and at Mokwa on the 20th July 1983. At preparation of the field, split application of nitrogenous fertilizer (Nitro-chalk) was broadcast with compound fertilizer (15:15:15). After thinning and just before heading, the second dose of same fertilizers was applied at the rates of 125 and 251 kg per hectare, respectively. The fertilizer was top dressed on each split application. A randomized complete block design was used (RCBD) with five replications. Each plot of 6 rows (gross plot) and 6m long was over planted and thinned after three weeks to 25 plants per row. Data were taken on the inner 4 rows (net plot), thus having 100 plants per plot. Seeds were treated with Amdex-T before planting. Missing hills were compensated for in most plots by transplanting during thinning. The rows were spaced 75 cm apart and hills within the rows were spaced 25 cm apart, to give approximately 53,333 plants/ha.

3.3. Observations

Data were collected on 100 plants per plot whenever possible for 12 quantitatively inherited traits as follows.

(1) Plant count at emergence: The whole seedlings on a hill were counted as one and either 100 or less per plot were recorded.

(2) Plant count after thinning: All rows were thinned to a maximum of 25 plants per row, where possible, but in cases where germination was poor less than 25 plants were recorded.

(3) Days to 50% flowering: The number of days from planting to 50% heading was recorded when 50% of the plants in a plot showed anthesis.

(4) Plant height: The height of each plant was measured (to the nearest cm) from ground level to the base of the flag leaf.

(5) Head length: The total head length of all harvested heads was obtained to the nearest cm. The head length was then divided by the number of heads per plot to obtain average head length per plant.

(6) Head Width: The total head width was obtained to the nearest cm. This width was then divided by the

number of harvested heads to obtain the average head width of the head per plant.

(7) Head Weight: The total head weight per plot was obtained to the nearest 0.01 kg. This weight was divided by the total number of heads to obtain the average weight of the head per plant.

(8) Grain yield: Total grain weight was measured on per plot and per plant basis and was recorded to the nearest 0.01 kg and 0.1 gm, respectively.

(9) Plant count at harvest: All plants that produced heads were counted for each plot and the number was recorded.

(10) 1000 grain weight: 1000 grains were counted from each plot after threshing and weighed to the nearest 0.01 gm.

(11) Head Count at harvest: All heads produced in each plot were counted and recorded.

(12) Number of seeds per plant: These were obtained by calculation using grain weight per plant and 1000 grain weight as described by Jan-Orn (1973). Thus

$$1000 \text{ grain weight} = X \text{ gm}$$

$$1 \text{ grain weight} = \frac{X}{1000} \text{ gm}$$

If $\frac{X}{1000}$ is weight of 1 grain

∴ Y gm is the weight of $Y \times \frac{1000}{X}$ grains

Where

X is 1000-grain weight and

Y is grain weight per plant.

3.4. Statistical analyses:

Two generations of the YZ composite and their data were used for analysis, using plot means. The same design was used for the single, and combined analysis of variance, over the two environments. Check entries were removed from the analyses.

The statistical model used for the combined analysis of variance (ANOVA) was:

$$Y_{ijk} = \mu + E_i + R_{ij} + G_k + (GE)_{ik} + e_{ijk}$$

where

μ = overall mean

E_i = The effect of the i th environment; $i = 1, 2$.

R_{ij} = the effect of the j th replication in the i th environment $j = 1, 2, 3, 4, 5, 6$.

G_k = the effect of the k th generation;

$(GE)_{ik}$ = the interaction effect between k th generation in the i th environment; and

$E_i \sim$ NID $(0, \sigma^2_E)$

$G_k \sim$ NID $(0, \sigma^2_G)$

$e_{ijk} \sim$ NID $(0, \sigma^2_e)$

Analysis of variance was performed for each trait in each experiment. The analysis for each character was computed using plot means, as well as family means. The latter was used to obtain the within plot variation, σ^2_w .

Generations and environments were treated as fixed and random effects. The form of analyses of variance, with the expected mean squares which were used for the estimation of genetic parameters, is shown in table 1.

Table 1. Form of ANOVA with expected mean square (EMS) in one environment for each character.

Sources of variation	d.f.	M.S.	EMS
Replications	(r-1)		
Generations	(g-1)	M_g	$\sigma^2 + r\sigma^2_g$
Error	(r-1)(g-1)	M_e	σ^2

r = number of replications

g = number of generations

σ^2 = error variance

σ^2_g = total genetic variance among generations

M subscript = the observed mean squares for the subscripted effect.

For each experiment, components of variance were estimated from the expected mean square for each trait by

$$\sigma^2 = m_e \text{ and}$$

$$\sigma^2_g = \frac{M_g - M}{r}$$

A combined analysis of variance for the two experiments in the YZ composite for each character provided more valid estimates of variance components, including the generation X environment interaction (Table 2).

Table 2. Form of ANOVA with expected mean square (EMS) in two environments for each character.

Sources of variation	d.f.	M.S.	EMS
Environment	(E-1)		
Reps/environment	E(r-1)		
Generations	(G-1)	M _g	$\sigma^2 + r\sigma_{ge}^2 + re\sigma^2$
Generations x Environment	(G-1)(E-1)	M _{ge}	$\sigma^2 + r\sigma_{ge}^2$
Pooled Error	E(G-1)(r-1)	Me	σ^2
Within plot error	(G x r x n)-1	M _w	σ_w^2

E = number of environments

r = number of replications

G = number of generations

n = number of plot samples

M Subscript = observed mean square for the subscripted effect.

σ_{ge}^2 = generation x environment interaction variance.

σ^2 = error variance

σ_w^2 = Within plot variance, computed from sample means.

The components of variance and their standard errors were estimated from expected mean squares using observed mean square values for each character, thus:

$$\sigma^2 = Me \text{ with S.E. } = \frac{2(Me)^2}{d.f. + 2}$$

$$\sigma_{ge}^2 = \frac{M_{ge} - Me}{re = 12} \text{ with S.E. } \frac{2(M_{ge})^2}{d.f. + 2} + \frac{2(M_{ge})^2}{d.f. + 2}$$

To determine if the variations among generations and their interaction with the environment were significantly

different from zero, F tests were used for both single and combined ANOVA as follows:

$$F = \frac{M_g}{M_e} \text{ with } (g-1), (r-1)(g-1) \text{ degrees of freedom} \\ \text{for one environment.}$$

$$F = \frac{M_g}{M_e} \text{ with } (g-1), E(r-1)(g-1) \text{ degrees of freedom} \\ \text{and}$$

$$F = \frac{M_{ge}}{M_e} \text{ with } (g-1)(e-1), E(r-1)(g-1) \text{ degrees of} \\ \text{freedom for two environments.}$$

Heritability (H) estimates were calculated on entry mean and plot bases over one environment and also for the two environments. They were computed from variance components estimates by using the formula for heritability based on entry means.

$$H = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/r}$$

Where σ_g^2 and σ_e^2 are estimates of generation and environmental variances respectively, r is the number of replications.

Heritabilities based on plot means were obtained from the formula:

$$H = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

Where σ_g^2 and σ_e^2 are generation and environmental variances respectively.

Expectations of mean squares in the combined analysis of variance were used to calculate the predicted genetic gain from mass selection per cycle, thus:

Expected genetic gain ($\Delta G = \text{progress}$) in yield as (Eberhart, 1970):

$$\Delta G = \frac{K.C.O^2A}{\sqrt{\frac{1}{re} \left(\frac{\sigma^2_w}{n} + \sigma^2 \right) + \frac{\sigma^2_{ge}}{e} + \sigma^2_A}}$$

Where K is the selection intensity, C. is parental control (= $\frac{1}{2}$ female choice mass selection), r, is replications, e is environment, σ^2_A is additive genetic variance, n is the number of random plants per plot sample, σ^2_w is the within plot variance, σ^2_{ge} is the generation x environment interaction variance, and σ^2 is the plot component expressed as $\frac{\sigma^2_e - n\sigma^2_w}{n^2}$ where σ^2_e is the error variance.

F tests were used to obtain significance of mean squares and the L.S.D. was used to compare generation means. $\sigma^2_A = \sigma^2_g$, in the formula used by Eberhart (1970) because σ^2_g is the portion of genetic variance among individuals or families due to additive effects. However, because only individuals were selected in mass selection procedure, $\sigma^2_g = \sigma^2_g' = \sigma^2_h$ in this study. This relationship assumes negligible dominance deviation σ^2_D .

RESULTS

4.1 Population means

The grand means of 12 traits measured in the two locations, separately and combined, including their standard deviations, ranges and their coefficients of variation are given in Table 3. The C.V's range from 1.79% for head length to 32.60% for grain weight per plot in Samaru. Whereas in Mokwa it ranges from 1.60% for days to 50% flowering to 12.70% for number of heads per plot. For the combined locations, the C.V's range from 0.80% for days to 50% flowering to 19.00% for grain weight per plot. Wide ranges were also observed for plant height (140.00 - 208.30 cm), number of grains per plant (3157 - 3871) and number of heads per plot (52.30 - 83.70) in Samaru. The same traits showed wide variation in Mokwa, (185.00 - 233.80), (1861.00 - 3068.00) and (92.80 - 176.20) for plant height, number of grains per plant and number of heads per plot, respectively. As for the combined locations, wide ranges were obtained for plant height (124.86 - 244.86 cm), count at harvest (29.40 - 91.40), head weight per plot (2.95 - 10.95 kg), grain weight per plot (0.61 - 8.96 kg), number of grains per plant (1285.50 - 3531.70) and number of heads per plot (30.38 - 187.30). In all cases the standard errors of the means were lower than the means. In general, the traits showed a wide range of phenotypic variation.

Table 3. Mean (\bar{X}), standard error of the mean (S.E. \bar{X}), range and coefficient of variability (C.V.%) for 12 traits of 3 generations in YZC population for Samaru, Mokwa and the two locations combined.

Trait	Mean	S.E. \bar{X}	Range	C.V.%
Count at Emergence (%)				
Samaru	93.10	± 7.90	82.20-100.10	8.50
Mokwa	91.50	± 5.89	79.80-99.50	6.40
Combined	89.80	± 8.07	64.03-91.93	7.00
Count after Thinning(%)				
Samaru	83.50	± 11.16	76.70-94.50	13.40
Mokwa	91.70	± 5.60	80.30-99.00	6.20
Combined	85.10	± 9.60	47.40-90.40	10.30
Days to 50% flowering				
Samaru	120.00	± 7.30	118.00-126.00	0.00
Mokwa	94.07	± 1.40	92.33-95.17	1.60
Combined	107.70	± 0.90	90.10-125.09	0.80
Plant height (cm)				
Samaru	177.70	± 10.70	140.00-208.30	6.00
Mokwa	216.30	± 17.10	185.00-233.80	7.90
Combined	212.10	± 15.14	124.86-244.86	7.10
Count at harvest(%)				
Samaru	66.00	± 9.50	57.50-79.70	14.00
Mokwa	91.00	± 5.20	79.50-98.67	5.70
Combined	75.90	± 8.60	29.40-91.40	11.40
Head length (cm)				
Samaru	29.90	± 1.79	27.80-31.90	6.00
Mokwa	33.05	± 1.70	30.48-34.91	5.30
Combined	32.39	± 1.75	22.25-36.25	5.40

Table 3. (Contd.)

Trait	Mean	S.E. \bar{X}	Range	C.V.%
Head Width (cm)				
Samaru	9.60	± 0.85	8.41-10.39	8.90
Mokwa	8.90	± 1.20	7.94-11.13	12.60
Combined	9.30	± 1.20	6.30-12.17	10.30
Head Weight/plot (kg)				
Samaru	6.05	± 1.50	4.58-7.19	25.10
Mokwa	8.90	± 0.70	7.59-10.57	8.90
Combined	7.59	± 1.20	2.95-10.90	16.10
No. of grains/plant				
Samaru	3346.80	± 509.70	3157-3871	14.70
Mokwa	2556.00	± 329.50	1861-3068	12.90
Combined	3275.00	± 461.00	1285-3335	13-10
Grain Weight/plot (kg)				
Samaru	3.11	± 1.00	2.30-3.64	32.60
Mokwa	6.37	± 0.59	5.21-7.78	10.90
Combined	4.83	± 0.91	0.61-8.96	19.00
1000 grain Weight (g)				
Samaru	25.14	± 2.30	23.52-26.77	9.30
Mokwa	30.85	± 1.80	27.22-35.83	6.10
Combined	27.70	± 1.90	16.31-35.56	7.10
No. of heads/plot				
Samaru	70.30	± 11.40	52.30-83.70	16.30
Mokwa	119.90	± 15.19	92.80-176.20	12.70
Combined	85.80	± 12.70	60.30-187.30	14.80

4.2. Population variability

Mean squares for 12 traits in the individual locations are shown in Table 4. At Samaru, significant ($p = 0.05$) entry mean squares were shown for only five traits, including plant height, harvest count, head length, head width and number of heads per plot. On the other hand Mokwa, entry mean squares for all traits showed significant variation at $p = 0.01$, except days to 50% flowering which was significant at $p = 0.05$.

The combined analysis of variation (Table 5) shows highly significant differences ($p = 0.01$) between locations for all traits except count at thinning and head width. Highly significant population mean squares were also recorded for all traits except head width and number of grains per plant. Non-significant genotype x environment interaction mean squares were observed for all traits except days to 50% flowering which showed a highly significant ($p = 0.01$) mean square.

4.3. Genetic variance components

Estimates of components of genetic variation were calculated from the combined analysis (Table 6). All estimates were positive and significant for genetic variance (σ^2_G) for all traits except for head width and number of grains per plant. All the σ^2_G estimates were also larger than twice their standard errors. Relative values of the σ^2_G show low genetic variation for number of heads per plot (0.71) and harvest count (0.71). Most other traits showed

Table 4: Analysis of variance of 12 traits obtained from 3 generations of Yzc population grown in Samaru and MOKWA

Sources of Variation	D.F.	Count at emergence	Count after thinning	Days to 50% flowering	plant height	Count at harvest	MEAN SQUARES											
							SAMARU						MOKWA					
					Head Length	Head width	Head weight per plot	Number of grains/plant(x10 ³)	Grain weight per plot	1000 grain weight	Number of heads/							
Replicates	5	55.26	261.3	0.00	115.3	37.23	5.61	0.49	2.10	45.427.00	1.85	17.39	76.70					
Populations	2	112.38	342.9	7.68	4763.3	569.62*	13.70*	3.49*	5.33	477.943.00	1.53	9.72	850.10*					
Error	10	63.04	124.60	0.00	115.30	90.62	3.21	0.73	2.30	259.845.00	1.02	5.45	131.00					
						MOKWA												
Replicates	5	57.13	271.30	3.14	121.30	41.13	7.40	2.31	3.80	47.132.00	2.23	20.90	79.80					
Populations	2	604.37**	544.13**	7.05*	2303.6**	550.75*	17.14*	5.32*	7.01**	1687.949.00**	5.38**	59.59*	6477.50					
Error	10	34.64	31.89	2.14	295.3	27.16	3.04	1.51	1.63	108.567.00	0.48	3.55	230.60					

* Significant at 0.05% level.
 ** Significant at 0.01% level.

Table 5: Combined analysis of variance for 12 traits from 3 generations in Yzc population grown in Samaru and Mokwa

Sources of Variation	D.F.	MEAN SQUARES											
		Count at Emergence	Count at Thinning	Days to 50% Flowering	Plant Height	Count at Harvest	Head Length	Head Width	Head Weight per plot	No of grains per plot (x10 ³)	Grain Weight per plot	1000 grain weight	No of heads per plot
Reps/Loc	10	57.49	125.62	0.92	314.29	44.38	4.70	0.85	1.30	291.23	0.69	9.68	224.00
Loc (1)	1	367.36*	169.00	7310.00*	9216.00*	4096.00*	90.92*	2.07	87.42*	457.14*	106.60*	263.60*	1181.00*
Populations (G)	2	831.69**	1231.85*	75.25**	1500.00**	1574.19*	11.46*	1.07	23.87*	23.93	11.85*	17.07*	2007.20
G X L	2	64.36	6.08	27.25**	141.10	20.58	0.35	1.56	0.16	531.67	1.29	2.45	420.60
Pooled Error	35	65.15	92.74	0.32	229.30	75.52	3.07	1.61	1.49	212.51	0.84	2.83	161.50

* Significant at the 0.05% level.
 ** Significant at the 0.01% level.

Table 6: Estimates of genotypic variance (σ^2_G), genotype x environment interaction (σ^2_{GL}), phenotypic variance (σ^2_{ph}), and environmental variance (σ^2_e) with their respective standard errors

Character	σ^2_G	σ^2_{GL}	σ^2_{ph}	σ^2_e
Count at Emergence	831.69±147.46 (2.82)*	64.36±32.38 (0.99)	896.85±147.00 (3.05)	65.16±19.61 (1.65)
Count after thinning	1231.86±217.76 (2.82)	6.08±14.14 (0.214)	1324.60±217.76 (3.04)	92.74±27.96 (1.65)
Days to 50% flowering	75.25±14.14 (2.66)	22.25±0.81 (13.73)	76.06±13.30 (2.85)	0.81±0.24 (1.68)
Plant height	1500.00±266.42 (2.82)	141.10±60.69 (1.16)	1229.30±265.25 (2.31)	229.30±69.13 (1.65)
Count at harvest	1574.19±1113.21 (0.71)	20.58±13.51 (0.76)	1649.71±278.28 (2.31)	75.57±22.77 (1.65)
Head length	11.46±2.03 (2.82)	0.35±0.95 (0.18)	14.52±2.02 (3.59)	3.06±0.92 (1.66)
Head width	1.06±0.33 (1.60)	1.56±0.60 (1.30)	2.66±0.19 (7.00)	1.60±0.48 (1.66)
Head weight/ plot	23.78±4.20 (0.32)	0.15±0.23 (3.00)	25.76±4.20 (3.00)	1.48±0.44 (1.68)
No. of grains/ plant	23.93±4.28 (2.82)	531.67±285.00 (9.32)	236.45±4.23 (2.79)	212.51±64.07 (1.65)
Grain weight/ plot	11.85±2.13 (2.78)	1.20±0.86 (0.70)	12.69±2.09 (3.03)	0.84±0.25 (1.68)
1000 grain weight	17.06±3.04 (2.80)	2.45±1.04 (1.17)	20.88±3.01 (3.43)	3.87±1.15 (1.66)
No. of heads/ plot	2007.20±1421.25 (0.706)	420.60±150.68 (1.39)	2168.70±354.82 (3.05)	161.50±48.69 (1.65)

*() Values in parenthesis are relative values of variances for the traits studied obtained as variance $\frac{\sigma^2}{2(S.E.)}$

similar amounts of relative genetic variation (2.78 - 2.82) which are mostly larger than their relative σ^2_{GL} and σ^2_{Ge} . Two traits, days to 50% flowering and number of grains per plant, however, had very high relative σ^2_{GL} estimates (13.73 and 9.32 respectively) which were significantly higher than their respective σ^2_G estimates. All traits had similar relative amounts of σ^2_{ph} with their respective error variances, σ^2_e , being more similar and mostly less than their respective σ^2_G values. Environmental variance estimates were found to be higher than genotype x environment interaction variance estimates for all traits except number of heads per plot.

Estimates of genetic variance components were also obtained for individual locations. Table A₂ in appendix shows the estimates of genetic variance (σ^2_G), phenotypic variance (σ^2_{ph}), error variance (σ^2_e) and their standard errors for the individual locations compared with those of the two locations combined. The genotypic, phenotypic and error variances were large for count at emergence, count after thinning (establishment count), plant height, count at harvest, number of grains per plant and number of heads per plot. Phenotypic variance estimates in the individual locations and for the combined data analysis were higher than all the genotypic and error variances. The standard errors for the individual locations for all estimates were low except those for number of grains per plant which were very high. In all these cases the standard errors were lower than their corresponding

estimates. Standard errors for the combined estimates were comparatively high for count at emergence, count after thinning, plant height, count at harvest, number of grains per plant and number of heads per plot. All other standard errors were quite low. Standard errors for the combined analysis were lower than all their corresponding variance estimates.

4.4. Heritability estimates

Since all the traits measured had positive σ^2_G , it was possible to compute heritabilities (H) using the components of variance estimates from individual as well as for the combined analysis of variance. For Samaru the H ranges from 59% for grain weight per plot to 99% for days to 50% flowering table 7. The heritabilities for Mokwa range from 78% for days to flowering to 96% for number of heads per plot. For the combined estimates the H range from 34% for head width to 71% for 1000 grain weight. Heritability estimates for the individual locations were all higher than those of the combined estimates except for 1000 grain weight for Samaru which was lower than that of the combined. The results showed that the estimates of H for the combined locations are more reliable than for the individual locations since it was possible to obtain genotype x environment interaction variance. This is not possible in a single environment thus biasing the estimates of H upwards. The results obtained (Table 7) showed that all estimates based on family means for the

individual locations and for the combined analysis were higher than all their corresponding estimates based on the plot means.

Estimates based on family means for the individual locations and for the combined were very high, ranging from 76.90% for head width in the combined analysis to 99.00% for plant height and days to flowering at Samaru, and for count at emergence, count after thinning, 1000 grain weight and number of heads per plot for Mokwa. These high estimates were expected since most of their estimated σ^2_G were fairly high, while the σ^2_{GE} and σ^2_e estimates were relatively low. Estimates based on plot means in the individual locations and for head width to 99.90% for days to 50% flowering for both locations and plant height in Mokwa. It is possible to group the H estimates based on plot means into three categories, very high for those that fall between 70% and 100%, moderately high for those that fall between 50% and 70% and low for those between 25% and 40%. All standard errors were lower than their corresponding estimates.

4.5. Correlations

All possible phenotypic correlations were computed among the 12 traits from their means for the three generations of YZC population studied. In general all traits were positively correlated (Table 8) with days to 50% heading being highly correlated with all traits except count at emergence,

Table 7: Heritability estimates (H%) of 12 traits from 3 generations of Yzc grown in Samaru and Mokwa and combined over locations, with their standard errors.

Character	H %					
	Samaru		Mokwa		Combined	
	Plot	Family	Plot	Family	Plot	Family
Count at emergence	67.93±2.00	92.70±0.83	94.66±0.43	99.06±0.82	46.87±0.59	84.11±0.81
Count after thinning	73.34±0.45	94.99±0.41	94.46±0.50	99.03±0.83	57.52±0.51	89.00±0.82
Days to 50% flowering	99.00±0.49	99.00±1.00	98.54±0.49	95.17±0.90	52.86±1.06	87.00±0.99
Plant Height	97.600±2.06	99.59±0.96	88.63±0.49	97.90±0.95	57.81±1.15	89.15±0.95
Count at harvest	86.07±0.19	97.30±0.78	95.30±0.50	99.18±0.86	37.00±0.41	77.90±0.99
Head length	81.01±0.04	96.24±0.86	84.90±0.49	97.12±0.94	60.50±1.00	90.19±0.98
Head width	82.70±0.50	96.63±0.93	86.33±0.50	97.43±0.95	34.73±1.73	76.15±0.80
Head weight/plot	69.80±0.50	93.32±0.77	91.66±0.49	98.50±0.97	46.64±1.00	84.00±0.98
Number of grains/plant	64.78±0.20	91.69±0.51	93.05±0.43	98.90±0.82	57.80±0.15	89.10±0.72
Grain weight/plot	59.83±0.04	89.93±0.57	91.74±0.49	98.50±0.97	45.38±1.01	83.39±0.98
1000 grain weight	64.07±0.50	91.45±0.83	94.35±0.50	99.50±0.96	71.67±1.00	93.80±0.94
Number of heads/plot	86.57±0.50	97.49±0.94	94.56±0.49	99.40±0.89	58.10±0.40	89.27±0.94

Table 8: Phenotypic (rph) and some genotypic (rg) correlation coefficient of 12 traits in YZC populations.

Character	Count at emergence	Count after thinning	Days to 50% flowering	Plant height	Count at harvest	Head length	Head width	Head weight per plot	No of grains per plant	Grain weight per plot	1000 grain weight	No of heads per plot
Count at emergence	1.00											
Count after thinning	0.815**	1.00										
Days to 50% flowering	0.045	0.374	1.00									
Plant height	0.117	0.149	0.577* (0.079)	1.00								
Count at harvest	0.420	0.717**	0.786**	0.421	1.00							
Head length	0.650**	0.159	0.603* (0.191)	0.587* (0.436)	0.463	1.00						
Head width	0.748	0.176	0.055	0.336	0.112	0.530	1.00					
Head weight/plot	0.129	0.353	0.758**	0.518	0.685*	0.599*	0.22	1.00				
Number of grains/plant	0.141	0.418	0.633*	0.177	0.631*	0.056	0.462	0.270	1.00			
Grain weight/plot	0.053	0.341	0.867** (0.043)	0.594*	0.721**	0.629*	0.185	0.956** (0.727)	0.392	1.00		
1000 grain weight	0.105	0.125	0.679* (0.002)	0.513	0.500	0.490	0.134	0.585* (0.254)	0.514	0.651* (0.312)	1.00	
Number of heads/plot	0.308	0.535	0.708**	0.742	0.749**	0.219	0.319	0.685*	0.679*	0.712**	0.307	1.00

* Significant at 0.05% level
 ** Significant at 0.01% level
 Correlations for synthesis
 The upper and lower correlations refer to phenotypic and genotypic correlations in each cell respectively.

count after thinning and head width. The most highly correlated traits were grain weight per plot and head weight per plot ($r = 0.96$) while the least correlated was emergence count with days to 50% heading ($r = 0.05$). Emergence count and establishment count (count after thinning) showed very high relationship ($r = 0.82$). Days to 50% heading was most highly correlated with grain weight per plot ($r = 0.86$), count at harvest ($r = 0.79$), head weight per plot ($r = 0.79$) and number of heads per plot ($r = 0.71$). Plant height showed average correlations with most of the head traits including head length ($r = 0.60$), head weight per plot ($r = 0.52$) grain weight per plot ($r = 0.60$) and 1000 grain weight ($r = 0.51$).

Among the head traits and grain-yield components, head length and number of grains per plot were least correlated ($r = 0.06$) while head weight per plot and grain weight per plot were the most highly correlated ($r = 0.96$). In general, head width showed least correlation with other head and yield traits except for head length ($r = 0.50$).

4.6. Observed changes in mean performance of YZC population due to selection

The observed changes in mean performance for 12 traits in two advanced generations over the base population are shown in Table 9. From this table it is evident that after two cycles of mass selection in YZC population the C_1 and C_2 are significantly ($p = 0.01$) higher yielding than the C_0 , with 20.94% and 54.05% more grain weight of C_1 and C_2 over the

Table 9. Observed genetic changes for 12 traits in three generations of YZC due to mass selection

Characters	Means	L.S.D.	% Observed change Over Co	Over C1
Count at Emergence	Co 85.20a	7.61	-	-
	C1 84.80a		-0.46	-
	C2 99.40b		16.66	17.23
Count after thinning	Co 79.50a	9.08	-	-
	C1 78.90a		-0.75	-
	C2 96.80b		21.76	22.68
Days to 50% flowering	Co 110.70a	0.85	-	-
	C1 107.90b		-2.59	-
	C2 105.10c		-5.05	-2.59
Plant height	Co 199.60a	14.28	-	-
	C1 215.70b		8.06	-
	C2 221.10b		10.71	2.50
Count at harvest	Co 96.60a	8.19	-	-
	C1 69.10a		-0.71	-
	C2 89.20b		28.16	29.08
Head length	Co 31.50a	1.64	-	-
	C1 32.20ab		2.22	-
	C2 33.40b		6.03	3.72
Head width	Co 9.90a	1.19	-	-
	C1 10.49a		5.92	-
	C2 10.50a		6.06	0.095
Head weight/plot	Co 6.09a	1.15	-	-
	C1 7.80b		11.65	-
	C2 8.88b		24.39	13.84
Number of grains/ plant	Co 3273a	434.74	-	-
	C1 3321a		1.46	-
	C2 3232a		-2.25	-2.67
Grain Weight/plot	Co 3.70a	0.87	-	-
	C1 5.03b		20.94	-
	C2 5.70b		54.05	13.32
1000 grain weight	Co 26.68a	1.85	-	-
	C1 29.02b		8.77	-
	C2 27.40a		2.69	-5.58
Number of heads/ plot	Co 76.90a	11.96	-	-
	C1 79.90a		3.90	-
	C2 100.70b		3.9	26.03

* Means with similar alphabets are not significantly different.

Co respectively. The 13.32% increase grain weight of C_2 over the C_1 was however not significant. Similarly increases were observed for head weight (11.65% C_1 over Co, 24.39% C_2 over Co and 13.84% C_2 over C_1) and number of heads (30.95% C_2 over C_1 , 31.90% C_1 over Co, and 26.00% C_2 over C_1). The observed increase in 1000 grain weight was only significant from Co to C_1 (8.77%) and dropped in the C_2 with only a slight increase over Co. The changes in number of grains per plant were not significantly different in the three generations, though the grain number decreased slightly in the C_2 . Head length and width did not show any appreciable increase.

Associated changes observed for other traits were variable for the different traits. There was no significant change from Co to C_2 in head width although the head increased by 6.06 cm after two cycles of selection. Emergence count, establishment count (after thinning) and harvest count, all increased significantly only at the C_2 generation with 16.66%, 21.16 and 28.16% respectively, over the Co. Plant height also significantly increased at the C_1 (8.06%) and at the C_2 (10.71%) over the Co. There was no significant increase for this trait from C_1 to C_2 . Days to 50% heading was reduced significantly from Co to C_1 by 2.59% and from C_1 to C_2 by 2.59%. A total reduction in maturity of 5.05% was recorded after two cycles in the C_2 .

4.7. Observed versus expected genetic change (ΔG) for eight traits in 2 cycles of YZC population

Observed genetic changes were highest for head weight per plot (24.39%) and grain weight per plot (54.05%) as compared to their respective expected genetic changes, which were 4.26 and 2.94 for the same traits. Reduced genetic changes were observed for days to 50% flowering (5.05) and number of grains per plant (2.25) as opposed to their expected genetic changes of 7.08 and 152.00, respectively. Four traits had similar observed changes as their expected. Plant height, head length, head width and 1000 grain weight had observed changes of 10.71, 6.03, 6.06, and 2.59% as compared to their expected changes of 8.06, 2.94, 0.60, and 3.49% respectively. It was not possible to calculate the expected genetic changes for the remaining four traits due to the inability to get the component σ^2_w used in the formula for computing the expected changes. σ^2_w was derived from individual plant data within a plot, but this was not possible for these traits.

Table 10. Observed versus expected genetic change (ΔG) for eight traits in 2 cycles of YZC populations

Character	Means	Observed	Expected	% Change	
				Observed	Expected
Days to 50% flowering	Co	110.70	-		
	C ₂	105.10	117.78	-5.05	7.08
Plant Height	Co	199.60	-		
	C ₂	221.10	207.66	10.71	8.06
Head length	Co	31.50	-		
	C ₂	333.40	34.44	6.03	2.94
Head Width	Co	9.90	-		
	C ₂	10.50	9.96	6.06	0.60
Head Weight/plot	Co	8.88	-		
	C ₂	10.35	24.39	4.26	
Number of grains/ plant	Co	3273	-		
	C ₂	3232	3425	-1.25	152.00
Grain weight/plot	Co	3.70	-		
	C ₂	5.70	6.64	54.05	2.94
1000 grain weight	Co	26.68	-		
	C ₂	27.40	30.17	2.69	3.49

DISCUSSION

The present study was carried out in Samaru and Mokwa, which represent two different ecological zones in the Savannah region. It will allow for the evaluation of the YZ composite population in the individual locations and for the two locations combined, which is expected to give a better estimation of genetic variance components and their heritabilities than in only one location as was observed by Frey and Horner (1955). Randomized complete block design was used for the experimental layout and also for the analysis of the data. The objective of this evaluation was to estimate the amount of improvement in terms of yield that has been achieved after 2 cycles of mass selection and also, to determine the effectiveness of recurrent mass selection as a method of population improvement in sorghum populations.

From the mean performance of the 2 cycles of mass selection (Appendix A₁), it is observed that the advanced generations showed higher means in all the traits than the check varieties. This means that there has been an increase in yield from C₀ to C₂. These observations are in agreement with those of Obilana and El-Rouby (1980a&b), Obilana (1981a&b) and Lukhele and Obilana (1982). Most of the traits in C₁ performed lower than the check varieties. This might be due to low yield potential of the base population coupled with few additive genes in the C₀ population that could contribute to improvement in C₁ population. With more random

mating in the C_1 , more of these additive genes were exposed which were selected for in the C_1 population to enhance improvement in the C_2 population.

From the results of this study, it is obvious that considerable variation still exists in these advanced generations of the YZ population. The large ranges and means of traits (Table 3) and the significant means squares observed (Table 4) have revealed the presence of variability within the populations. These compare very well with results of Obilana and El-Rouby (1980a&b), Obilana (1981a&b) and those of Lukhele and Obilana (1982). Many other workers have reported the existence of variability in other sorghum populations (Swarup and Chaugale, 1962; Basu, 1971; Vasudeva, 1973; Naphade and Ailwalar, 1978; Bittinger and Cantrel, 1979) and Cortez-Mendoza (1977) Ph.D. Thesis).

The combined analysis of variance showed that there was significant difference among the populations and non-significant genotype x environment interaction for all traits except for days to 50% flowering. This observation compares well with the findings of Obilana and El-Rouby (1980a&b), Ross and Hookstra (1983). Obilana (1980b) explained this situation to be that, irrespective of the type of environment, the original populations (C_0) and the advanced generations of selection performed significantly different. The significant genotype x environment interaction variance for days to 50% flowering indicates that it will vary in

different environments, as was mentioned earlier. To the breeder the presence of variability in a population indicates a sure source of improvement, genetic variances as well as phenotypic and environmental variances were obtained to assess the available variability of the populations. Table 7 shows that large genotypic, phenotypic and environmental variance exists for count at emergence, days to 50% flowering, plant height, count at thinning (establishment), count at harvest, head weight per plot, number of grains per plant, and number of heads per plot. The genotype x environment interaction was high for only days to 50% flowering. This indicates that this trait will tend to change with change in environment. On the other hand, Cockerham (1963) indicated that a large interaction component of variance could be due to genetic component being larger in one environment than the other, which is actually true in this investigation (Appendix A₂). Ten out of twelve traits have higher genotypic variances than their respective environmental variances, this indicates that there is high possibility for improving these traits. Relative values of variances (Table 6) clearly show that genetic variability exists in all traits except for number of heads per plot at harvest. This may be expected since these are not tillering populations. Phenotypic variation exists for all traits with that of head width being the largest (7.00) and plant height being the smallest (2.31). Relative error variances indicate that variations due to unspecified sources are very small,

which indicates the reliability of our estimates. The genetic variance estimates in this study are total genetic variance because it was not possible to partition it into its component parts (additive, dominance and epistatic variances) due to the experimental design used.

Most of the genetic variance estimates for the traits were quite high, higher than their corresponding coefficients of variability. Coefficient of variability (C.V) were low, ranging from 0.80 for days to 50% flowering to 19.00 for grain weight per plot.

Estimates of heritability for all traits from this study were relatively high and compares well with those reported by Liang and Walter (1968), Ali-Khan and Weibel (1969), Basu (1971) Mandouh *et al.* (1971), Vasudeva (1973), Jan-Orn *et al.* (1976), Ekebil *et al.* (1977) and Panchal *et al.* (1979). It has been shown by Johnson *et al.* (1955a) that heritability estimates along with genetic advance are more useful in predicting the resultant effect of selecting the best individuals in a given population than heritability estimates alone. It has also been observed that high heritability is not always accompanied with high genetic advance (Swarup and Chaugale, 1962). If heritability is mainly due to non-additive gene effects, the expected genetic advance would be low, and if there are additive gene effects, high genetic advance may be expected (Panse, 1940; Obilana and Fakorede 1981). Broad sense heritability estimates are useful

when high genetic gain in a particular trait is also possible (Kaul and Balm, 1974). Thus high heritability estimate considered along with estimates of genetic advance are more effective for selection purposes. In general we had high heritability estimates in this study. This may be due to non separation of the non-additive effects from the additive effects which biases the H value upwards.

The mean performances of the original populations and those of the two advanced generations C_1 and C_2 are shown in Table Appendix A2. From this table it is observed that after two cycles of mass selection in YZ composite the C_2 population was significantly ($p = 0.01$) higher yielding in terms of head weight per plot (8.88 kg/plot and grain weight per plot (5.70 kg/plot and with more fertile tillers (100.70 heads) than the C_0 population (6.09 kg/plot, 3.70 kg/plot and 76.90 tillers respectively). This finding is similar to those of Obilana and El-Rouby (1980b). The associated changes observed for days to 50% flowering (-5.05 days) and plant height (10.71 cm) were not significant. This also compares well with the observations of Obilana and El-Rouby (1980b). Other traits that might be associated with yield but do not show any appreciable increase in C_1 over the C_0 population include head length (33.40 cm), head width (10.50 cm), number of grains per plant (3232) and 1000 grain weight (27.40g), while the C_0 is 31.50 cm, 9.90 cm, 3273 and 26.68cm respectively) for the same traits. Increase in yield due to female choice mass selection was 24.39% for head weight

per plot and 54.05% for grain weight per plot as compared with their expected values of 2.94% and 4.76% respectively. This higher observed values than their expected might be contributed to the efficiency of the selection method as well as the diversity of the population.

Observed versus expected genetic change (ΔG)

The observed versus the expected genetic change (ΔG) for eight quantitative traits from the three cycles of selection in YZ population when the highest 10% of the population are selected for yield is shown in table 10. It shows that the present gain in four out of the eight traits were highly significant ($p = 0.01$) which includes head length, head width, head weight per plot, and grain weight per plot. 1000 grain weight was significant ($p = 0.05$). The other three traits, days to 50% flowering, plant height and number of grains per plant showed no significant increase. It was not possible to calculate the expected genetic change for the other four traits, count at emergence, count after thinning, count at harvest and number of heads per plot in that the formula used for calculating the genetic change has a component σ^2_w which is derived from observations based on individual plant data within a plot which was not possible with these traits, as earlier mentioned.

From some table 10, it is observed that there is little increase or even a decrease in some cases in the means for days to 50% flowering, head length, head width, number of grains per plant and 1000 grain weight. This might have been compensated for by the large increases in head weight per plot and grain weight per plot. This could imply that the reduction in grain number per plant resulted in an increase in grain size. There was an increase in number of tillers from C_1 to C_2 and because tillers produce smaller grains than the mother plant, 1000 grain/plot is expected to reduce accordingly. A decrease in days to 50% heading (maturity period) and average plant height seemed to favour increase in yield. This could be that selection for average and early maturing plants in these advanced generations of YZ composite may give better yields in advance generations.

The theoretical expected genetic gains ΔG calculated from this selection method are very similar to the actual observed gains from selection in four out of the eight traits. This shows that there was no form of biasing in our estimates due to the dominance deviation O^2D , which was assumed to be negligible in using the formula for obtaining ΔG , Eberhart (1970). When one looks at the expected and observed genetic gain due to selection in the other four traits, the above statement will seem not to be true since the values are quite different. For head weight and grain weight per plot, the high values more than the expected

might be due to inefficient measurement techniques which could be improved upon, low values for days to 50% heading, could be actual reduction in maturity period, number of grains per plant could also be due to the increases in grain weight as a compensation. Further improvement could be achieved by using the same female choice mass selection in the advanced generations.

The percent gain in yield observed here are higher than those observed by Doggett (1972a&b) in Sorero, Uganda, who obtained 32% in head weight in RS3 and 20% for PRS1 populations. The higher percentage increase in this study might be due to higher selection intensity used ($K = 1.75$) as compared to that used by Doggett ($K = 1.4$). The value here is higher than those got by Obilana and El-Rouby (1980) who got 23.40% and 0.60% for B and Y populations after three cycles of mass selection, though they used a higher selection intensity ($K = 2.06$). This could be attributed to high genetic diversity in YZC population. From this result it is evident that female choice mass selection has effectively increased yield in YZ composite population at an average rate of 27.025% per cycle. This is a high value when compared with previous investigations, thus there is high probability for increasing yield with further selection in these advanced populations of YZ composite.

Correlations

Most of the characters of economic importance such as yield, are complex in inheritance and might involve many

related characters (Robinson, Comstock and Harvey, 1951) and hence the degree of phenotypic and genotypic correlations of these characters is important. Genetic correlations are a measure of the association of genes controlling two characters. That is to say, if two characters have no genes in common, their genetic correlation would be expected to be zero (Mace and Robinson 1959). The plant breeder is mostly concerned with correlations between yield and other traits. Besides the quantitative inheritance of these characters, they are also used as criteria for selection, since selection involves the changing of two or more traits at the same time. In other words, when a character is selected for, it results in a simultaneous change in all traits correlated with it either negatively or positively. It is therefore important to compute phenotypic and genotypic correlations for all possible pair of traits (Table 5). High phenotypic correlations were observed between head weight per plot (yield) and grain weight per plot ($r_{ph} = 0.95\%$), days to 50% heading ($r_{ph} = 0.758$), plant height ($r_{ph} = 0.518$). Grain weight per plot (another yield component) was highly correlated to days to 50% heading ($r_{ph} = 0.862$), average correlation to plant height ($r_{ph} = 0.594$). Another yield component 1000 grain weight was averagely correlated to plant height ($r_{ph} = 0.513$). Average maturity plants with average heights could be selected for as an indirect way of improving yield in YZC populations.

CHAPTER 6

SUMMARY

Two advanced populations from a photosensitive randomizing population of sorghum, YZC, were grown along with the original population in Samaru and Mokwa in 1983 for evaluation. Two elite lines were used as checks; these were L. 243 and L. 187. A randomized complete-block design was used at each site and each plot consisted of 6 rows (gross plot) and 4 rows (net plot) spaced at 75 cm apart and 25 cm within the row. There were a maximum of 100 plants in each net plot. The two outer rows served as boarder rows. Data were collected on all the 100 plants wherever possible for 12 quantitative traits; namely, count at emergence, count after thinning, days to 50% flowering, plant height, count at harvest, head length, head width, head weight per plot, number of grains per plant, grain weight per plot, 1000 grain weight and number of heads per plot. Analysis of variance for the combined data was computed for all traits.

Considerable and significant variation was observed for all traits. The traits that showed high variation include count at emergence, count after thinning, days to 50% flowering, plant height, count after harvest, head weight per plot, 1000 grain weight and number of heads per plot. Significant differences were also observed for locations. Non-significant genotype x location interaction was found for all traits except days to 50% flowering.

Genetic variance estimates obtained were positive for all the traits studied. Genetic variance estimates were highest for count at emergence, count after thinning, plant height, count at harvest and number of head per plot, while head width, head length and grain weight per plot had the lowest.

Population and environment means were significantly different for each trait. There was non-significant interaction between the generations x environments for all traits except for days to 50% flowering. Population means for C_2 were higher than those of the C_0 population for all traits.

Coefficients of variations (C.V.%) ranged from 0.80 for days to 50% flowering to 19.00 for grain weight per plot. Head weight per plot, number of grains per plant and number of heads per plot also showed high coefficients of variation (16.10, 14.10 and 14.80, respectively).

Heritability estimates were quite high ranging from 34.73 for head width to 71.67% for 1000 grain weight. This was expected since the genetic variance estimates were high and genotype x environment interaction and error variance estimates were low.

The mean performance of the C_2 over the C_0 population was quite encouraging. Head weight per plot was 24.39% for C_2 better than the C_0 , and grain weight was 54.05%

higher than the Co. This shows that the YZ composite C₂ population has been improved much better than the Co. Female choice mass selection can be said to be a good method for population improvement in sorghum, and can be used to continue to improve the YZ composite.

Head weight per plot was positively and significantly correlated with grain weight per plot and days to 50% flowering. Grain weight was also found to be positively and significantly correlated with days to 50% flowering. Head weight was averagely correlated to plant height, count at harvest, head length and 1000 grain weight. This trait could be used as selection index for improving yield in YZ composite.

Observed genetic gain were quite high for the yield components, head weight per plot (24.39%) and grain weight per plot (54.05%) than their expected (2.99% and 4.26% respectively for the two traits. This points out that improvement has been achieved in the YZ composite population using female choice mass selection. It is envisaged that this rate of improvement would be maintained with further selections using the same female choice mass selection. All traits that are positively and significantly correlated with yield and its components should be used together with the yield and its components for selection. This is expected to enhance progress in the more advanced generations of the YZ composite populations.

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APPENDIX A₁ : Mean performance of three cycles of Mass selection in YZC population grown in two locations with the checks

	Means			Checks	
	Co	C ₁	C ₂	1	2
<u>Count at emergence</u>					
Samaru	89.20	89.80	100.00	94.00	92.50
Mokwa	81.00	79.80	98.80	99.50	98.00
Combined	85.20	84.80	99.40	96.50	95.25
<u>Count after thinning</u>					
Samaru	75.70	77.50	94.50	88.10	81.30
Mokwa	82.30	80.30	99.80	98.70	93.30
Combined	79.50	78.90	96.80	93.40	87.30
<u>Days to 50% flowering</u>					
Samaru	126.00	122.00	118.00	118.00	118.00
Mokwa	94.30	93.80	92.30	95.17	94.67
Combined	110.70	107.90	105.10	106.50	106.30
<u>Plant height</u>					
Samaru	181.00	200.00	208.00	140.00	161.10
Mokwa	219.20	231.30	233.80	212.30	185.00
Combined	199.60	215.70	221.10	176.10	173.05
<u>Count at harvest</u>					
Samaru	57.50	58.70	79.70	72.80	61.50
Mokwa	81.50	79.50	98.57	98.67	96.50
Combined	69.60	69.10	89.20	85.70	79.00
<u>Head length</u>					
Samaru	30.00	30.00	31.00	29.50	27.50
Mokwa	33.02	34.02	34.90	33.85	30.40
Combined	31.50	32.20	33.40	31.67	28.90
<u>Head width</u>					
Samaru	10.05	9.08	10.39	9.40	8.40
Mokwa	9.90	11.13	10.67	9.19	7.94
Combined	9.90	10.49	10.50	9.20	8.20
<u>Head weight/plot</u>					
Samaru	4.58	6.32	7.02	6.20	5.90
Mokwa	7.59	9.28	10.57	8.52	8.89
Combined	6.09	7.80	8.88	7.30	7.30
<u>Number of grains/plant</u>					
Samaru	3871	3574	3449	3255	3152
Mokwa	2574	3068	3014	2161	1861
Combined	3273	3321	3232	2708	2506
<u>Grain weight/plot</u>					
Samaru	2.30	3.39	3.05	3.50	3.15
Mokwa	5.20	6.67	7.78	6.03	6.18
Combined	3.70	5.03	5.70	4.70	4.60
<u>1000 grain weight</u>					
Samaru	23.50	26.70	24.70	26.30	24.63
Mokwa	29.80	31.27	30.15	35.80	27.20
Combined	26.68	29.02	27.40	31.00	25.90
<u>Number of heads/plot</u>					
Samaru	52.30	67.00	83.07	70.70	77.70
Mokwa	101.50	92.80	117.70	111.20	175.20
Combined	76.90	79.90	100.70	90.90	126.40

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APPENDIX A₂ : Genetic (σ^2_g), phenotypic (σ^2_{ph}) and error variances (σ^2_e) for 12 traits of 3 generations in YZC population for Samaru, Mokwa and the two locations combined

Traits	σ^2_g	σ^2_{ph}	p^2_e	H% (Plot grains)
<u>Count at emergence</u>				
Samaru	63.04+16.22	71.26+8.11	8.22+19.00	67.93
Mokwa	95.02+7.60	126.66+17.44	34.64+9.79	94.66
Combined	831.69+147.46	396.85+2.47	65.16+1.96	46.87
<u>Count after thinning</u>				
Samaru	33.38+1.49	157.98+9.89	124.60+37.56	73.34
Mokwa	85.37+7.85	117.26+15.70	31.89+9.01	94.46
Combined	1231.85+217.76	1324.60+4.23	92.74+2.70	57.86
<u>Days to 50% flowering</u>				
Samaru	1.26+1.10	1.26+2.21	0.00+0.00	99.99
Mokwa	0.81+1.01	2.96+2.03	2.14+0.60	78.54
Combined	75.25+14.14	76.05+1.33	0.81+0.06	57.86
<u>Plant height</u>				
Samaru	77.66+13.75	889.96+6.67	115.30+3.47	97.60
Mokwa	334.70+33.24	630.01+66.49	295.30+8.35	88.63
Combined	1500.00+266.42	1729.00+265.2	229.30+69.13	57.81
<u>Count at harvest</u>				
Samaru	79.83+16.44	170.45+82.21	90.62+27.32	86.07
Mokwa	87.26+7.74	114.47+15.89	27.16+7.68	95.30
Combined	1514.79+11113.21	649.71+278+2875.52	22.77	37.00
<u>Head length</u>				
Samaru	1.74+0.19	4.96+3.95	3.21+0.18	81.01
Mokwa	2.35+2.47	5.39+4.95	3.04+0.86	84.90
Combined	11.46+2.03	14.52+0.95	3.06+0.92	60.50
<u>Head width</u>				
Samaru	0.46+0.50	1.19+1.00	0.73+0.22	82.70
Mokwa	1.34+1.38	2.86+2.76	1.51+0.42	86.33
Combined	1.06+1.03	2.66+2.19	1.60+0.43	34.73
<u>Head weight/plot</u>				
Samaru	0.50+0.77	2.81+1.54	2.30+1.33	69.80
Mokwa	1.06+1.02	1.70+2.02	0.63+0.18	91.60
Combined	23.78+4.20	25.26+4.20	1.48+0.44	46.64
<u>Number of grains/plant ($\times 10^2$)</u>				
Samaru	363.49+137.97	2961.94+689.85	2598.45+783.46	64.78
Mokwa	2637.30+2436.6	3717.97+5643.72	1085.67+3070.73	93.05
Combined	23934.07+2864.2	241448+2860.30	212514.60+6.40	57.80
<u>Grain weight/plot</u>				
Samaru	0.50+0.02	1.53+0.44	1.02+0.09	59.83
Mokwa	0.81+0.77	1.30+1.55	0.48+0.13	91.74
Combined	11.85+2.13	12.69+2.09	0.84+0.25	45.33
<u>1000 grain weight</u>				
Samaru	4.27+1.40	9.72+2.80	5.45+1.64	64.07
Mokwa	9.33+4.21	12.90+8.42	3.56+1.00	94.35
Combined	17.05+3.04	20.69+3.01	3.82+1.15	71.67
<u>Number of heads/plot</u>				
Samaru	119.85+122.70	250.85+245.00	131.00+39.4	86.57
Mokwa	1041.15+934.00	1271.75+1369.0	230.60+60+65.2	96.56
Combined	2007.20+1421.25	2168.70+354.8	161.50+48.6	58.10

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College of Arts, Science and Technology Zaria	1973	1975	I.J.M.B.
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