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Full length Research paper

Response to selection for maize streak resistance, grain yield, and secondary traits in three quality protein maize populations in Zimbabwe

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Maize Streak Virus disease (MSVD) is a major problem in quality protein maize (QPM) in Mozambique. Recurrent selection was applied to improve MSVD resistance in three QPM populations, Sussuma, ZM521Q and Pop62SRQ at CIMMYT-Harare Research Station in Zimbabwe, during 2003-2006. Maize streak virus disease incidence and severity were rated at four weeks after emergence and at flowering stage based on visual assessment of the whole plot. Two selection cycles were formed and evaluated. Selection intensity was 50%, and 25% in cycle 1 (C1) and cycle 2 (C2), respectively. The C1 and C2 were evaluated in a randomized complete block design with three replications in 2005/6 season. Results showed significant improvement in MSVD resistance from C1 to C2, with scores of 3.4-2.9 in Sussuma, 2.7-2.3 in ZM521Q and 3.47-3.0 in Pop62SRQ, respectively. Results also indicated increase in genetic variances (σ^2_G) for MSVD from C1 to C2, from 0.314 in C1 to 0.559 in C2 in Sussuma; from 0.519 in C1 to 0.640 in C2 in ZM521Q, and from 0.135 in C1 to 0.781 in C2 in Pop62SRQ. Broad sense heritability estimates (H^2) ranged from moderate to high and increased from C1 to C2 in all populations. The H^2 estimates were 0.83-0.94 in Sussuma; 0.70-0.88 in ZM521Q and 0.65-0.87 in Pop62SRQ. This was associated with an increase in yield of about 4.57% in Sussuma, 4.62% in ZM521Q and 4.37%) in Pop62SRQ. There was also an improvement in flintiness of the grain with texture scores of 2.7-1.5 in Sussuma, 2.9-1.9 in ZM521Q and 2.5-1.7 in Pop62SRQ. There were no significant changes in anthesis-silking interval, plant height and number of ears plant^{-1}. This study showed that S1 recurrent selection was effective in improving QPM populations for MSVD resistance, increasing genetic variances and broad sense heritability estimates without compromising grain yield, texture, and other important characteristics.

Keywords: Maize Streak Virus disease, quality protein maize, recurrent selection, genetic variances, grain yield.

INTRODUCTION

Maize streak virus disease (MSVD) is one of the most important diseases affecting quality protein maize (QPM) in Mozambique. It is the second most important disease in cereal crops in Africa (Engelbrecht, 1975) and causes severe damage to maize in the mid-altitude and highland areas in Mozambique (DINA, 1995). Breeding for resistance to MSVD in maize is therefore important in northern and central Mozambique (DINA, 1995), where it is most prevalent. The disease is also important in other Countries in sub-Saharan Africa and causes yield losses reaching 100% (Mzira, 1984; Bjarnason, 1986; Bosque-Perez, 2000). van Rensburg (1991) reported that yield reduction due to MSVD was higher when young plants are infected.

Different methods can be used to control the disease. Insecticides can be used to control leafhoppers which transmit the disease, but the chemicals are not always available in Africa due to limited resources. Outbreaks of MSVD is associated with the behaviour of the Cicadulina vector species in Southern African (Pham 1992), while it has been associated with drought, irregular and early rains in West Africa (Bosque-Pérez, 2000). High MSVD epidemics have also been associated with increasing

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intensity of maize production (Bosque-Pérez, 2000). Due to limitation of resources it sounds most economical to control MSVD by breeding for resistance in QPM varieties, since the crop is grown by subsistence farmers in Mozambique (Barrow, 1992; Bosque-Pérez, 1998; DeVries and Toenniessen, 2001).

There are few reports of recurrent selection for MSVD in QPM germplasm. However, resistance to MSVD can be improved by recurrent selection (RS) methods which have resulted in significant gains for yield and other traits in maize populations (Efron *et al.,* 1989), without compromising the genetic variation required for future improvement (Moll and Smith, 1981). Quality protein maize (QPM) varieties have been introduced in Mozambique but are very susceptible to MSVD. There is need to breed for durable resistance to MSVD in these populations.

Objective and research hypothesis of the study

The specific objectives of the study were:

a) To study the response to recurrent selection for MSVD resistance using full-sib and selfed progenies (S1) of three QPM populations.

b) To determine correlated responses of the three populations for yield, ASI, grain texture, grain moisture and other important characteristics after two cycles of recurrent selection.

The hypothesis tested was:

Resistance to MSVD in QPM populations can be improved by using recurrent selection, and genetic variability of important traits remains high after cycles of recurrent selection.

MATERIAL AND METHODS

Location of the experiment

The experiments were conducted at International Maize and Wheat Improvement Centre (CIMMYT) in Harare, Zimbabwe, test plots located on the University of Zimbabwe Farm, about 13 km North of Harare.

Germplasm

The three quality protein maize populations Sussuma (S_2 generation), ZM521Q and Pop62SRQ (Table 3.1) were used in this study. They are high grain yielding and highly susceptible to maize streak virus (MSV). These populations were designated Sussuma, ZM521Q and Pop62SRQ, respectively, in this study. All three populations were originally developed at the International Maize and Wheat Improvement Centre (CIMMYT) in Harare. All the populations were adapted to tropical environments in East and Southern Africa. They were improved for QPM at Instituto de Investigação Agrária de Moçambique (IIAM), in Mozambique.

Establishment of screening nurseries, artificial inoculation for Maize Streak Virus Disease and formation of the cycles

At CIMMYT-Harare Research Station, in November 2003, November 2004, and November 2005 MSVD nurseries were established every season to screen the progenies. Selected ears from selfed seeds of each population were planted for screening for MSVD resistance. The population size of plants was established and was equal number of that used for screening to DM, around 5.000 plants for each population.The progenies of the selected plants were planted in an ear-to-row method in which progenies of each plant were planted in one row only. Screening nurseries were laid out in three blocks for each population on one row plots of 5 m long. The blocks were made up of 275 rows. Virus-free leafhoppers were allowed to acquire the virus on stocks of infected MSVD susceptible maize plants for 2 d. Maize streak virus inoculum source was a composite of isolates obtained from infected maize sampled throughout Zimbabwe. Three to five leafhoppers were dropped into the plant whorl at the V3 stage (Efron *et al.,* 1989), about 3 weeks after planting. When streak symptoms appeared, plants were thinned to one plant per hill. All plants per row were individually rated two times at biweekly intervals beginning 2 weeks after infestation. The numbers of diseased and healthy plants were recorded and percentage of plants with systemic MSVD was calculated. Agronomic practices included fertilizer application at planting with NPK (120:60:60), herbicide application with glyphosate before planting followed by weeding and top dressing with urea (46% of N) during the vegetative stage. Stalk borer control was done by spraying with insecticide Decis (pyrethroid) at regular intervals to reduce crop loss.

During flowering time, all selected plants had their ear shoots covered. The ears of the selected progenies were self-pollinated to provide S1 seed, and other ears of other selected progenies were also cross-pollinated using pollen from the selfed plants to form FS seed. Selfed S1 progenies from the best FS were used to advance to the next generation. To keep the protein quality, the best S1 progenies were also again selected in laboratory, using ELISA test. Although FS and S1 progenies from an equal number of plants in each of the three populations were sought, the proportion of plants obtained was 50% (around 2658 plants), 25% (around 665 plants) and 25% (around 166 plants) for the populations Sussuma, ZM521Q and Pop62SRQ, respectively. These were plants with adequate FS seed with resistance to MSVD used to form the base population referred to herein as a cycle 1.

In November 2005, a trial was planted for evaluation of the two cycles of each population in the season 05/06. A lattice design with nine blocks and three replications was used. Selected high yielding progenies of full-sib families were randomly assigned to each block planting density was 53,333 plants ha^{-1}. Plot size was one row of 5m length with hills spaced 80cm between rows and 25cm within rows. The hills were over planted and thinned to one plant per hill. Additional variables, such as days to 50% pollen shedding, plant height and ear height were recorded for each plot. Plots were hand harvested and shelled grain weight recorded.

Grain moisture at harvest was determined and plot yields adjusted to 13.5% moisture level converted to yield. Data were analyzed on a per block basis and individual analyses of variance pooled over blocks for a trial. Selection was based on FS performance within blocks. Only those FS that yielded above their respective block means and were equal to or below the average grain moisture at harvest and with quality protein content were selected. Selfed (S1) progenies of superior FS families were advanced to the next generation.

Selection method

The selection method used was the same for DM selection process. It was based on single plant selection. This was done just before flowering stage (because of cross and self pollination). Best rows were selected and in each row the best five plants were selected. The best plants were those that showed resistance to maize streak virus.

The selected progenies were self-pollinated to generate selfed progenies, and crossed to form full-sib progenies formation using the same selected plants. Although the resistance to maize streak virus disease was the principal criterion of the progenies selection, grain yield, ASI, grain moisture and grain texture were also considered during selection.

The full-sib families were also selected at harvest for yield and other environmental responses. Selection of plants for advancement to the next generation was conducted in stages: First, plants with zero (0) severities were not selected and only those that showed symptoms with severity scores of 2 and 3 were selected. About 10% (510/5,316) of the plants with scores of 2 to 3 (rating scale 0-5) were selected, equivalent to a selection intensity of 1.74 (Falconer, 1981). Second, the self-pollinated progenies of each population were again selected during harvest time and taken to the laboratory for the tryptophan analysis. Selected progenies with resistance to MSVD were also selected on the basis of grain texture. Selection for grain texture was based on levels of flintiness of the grain using a scale of 1 (flint) to 5 (completely dent). Only plants showing grain texture scores between 1.9 and 2.8, were selected and advanced to the next generation of selection.

Experimental layout of yield trial

For yield evaluation and other agronomic characteristics full-sib families formed through cross pollination of the selected progenies were used. Cycles C1 and C2 were evaluated at CIMMYT-Harare Research Station (planted in November 2005 -season 05/06). Trials were laid out as a randomized complete block design with three replications. Each entry was planted in two rows: 5m long with 80cm between rows and 25cm between hills within rows. All entries were over planted and later thinned to one plant per station to give 53 333 plants ha^{-1}.

Data collection

Disease development was monitored throughout the growth cycle, and the data recorded. Maize streak virus disease incidence and severity were scored twice; at four weeks after emergence and at flowering (critical stages for MSVD effect on yield) based on visual assessment of the whole plot. Disease incidence was scored by recording the number of plants in each population showing MSVD symptoms and expressing that as a percentage of the total plant population. Disease severity was scored on the whole plant as a proportion of total leaf area diseased using a scale of 0 to 5. Details of the rating scale were as follow: 0= no visible disease symptoms, 1 = very few streaks on some leaves, 2 = light streak symptoms on most leaves, 3 = moderate streak symptoms on most leaves, 4 = abundant symptoms on all leaves (≥60%) leaf area affected, 5 = severe symptoms on all leaves (≥80%) of leaves affected with no yield (Bosque-Perez, 1998). The rating scale was used to evaluate the disease at CIMMYT-Harare Research Station during 2004/05 to 2005/06 seasons. The number of days to mid-silking (DMS) and anthesis (DMP) were estimated as number of days from planting to 50% plants with silks emerged and tassels shedding pollen, respectively. Plant and ear height were measured as the distance from the base of the plant to the height of the first tassel branch and the height of the node bearing the uppermost ear, respectively. Grain weight and moisture content per plot were obtained at harvest and values obtained were used to estimate grain yield (t ha^{-1}) adjusted to 13.5% moisture content.

Data analysis

Quantitative data generated from 2006 infected trials were each subjected to a separate ANOVA using REML tool in Field book. Data were analyzed using the following model: $\mathbf{Y_{ijk} = \mu + \beta_i + g_j + e_{ijk}}$, where μ is the general mean, β_i the effect of $_i$th block, g_j the effect of $_j$th genotype and e_{ij} the error associated with particular measurement.

Response to selection was determined using the following formula: $R = iH^2\sigma^2_P$ (Falconer, 1961), where i =

Table 4.1 Skeleton analysis of variance when *g* genotypes are raised in RCBD with *r* replications

Source	Df	S.S	MS	Expected Mean square
Replications	(r-1)			
Among genotypes	(g-1)	$r\Sigma\ (yi-y.)^2$	M1	$\sigma^2e + \sigma^2g$
Within genotypes	(r-1)(g-1)	$\Sigma(yij-yi.)^2$	M2	σ^2e
Total	(rg-1)			

selection intensity of 50 and 25%; H^2 = broad sense heritability; and σ^2_P = phenotypic variance. Broad-sense heritability estimates were calculated using the following formula: $H^2 = \sigma^2_g/\sigma^2_P \times 100$ (Falconer, 1961). Genetic covariance between FS was estimated as: *Covg (FS) = t (1/2VA + 1/4VD + VEc*) (Lonnquist *et al., 1967)*; Genetic coefficient of variation for DM and yield were obtained using the following formula: *GCV = √σ/X x 100 (*Eberhart *et al.,1973)*; and the correlations for the FS were obtained using the following formula *t = (1/2VA + 1/4VD + VEc)/VP* (Falconer, 1961).

RESULTS

Variances associated with differences among FS families in three QPM populations were highly significant (Tables 4.3, 4.4, and 4.5). Responses to selection per cycle^{-1} in C1 and C2 for all three QPM populations are presented in Table 4.2.

Maize Streak Virus

Maize streak virus disease rating decreased by 0.35 in Sussuma, 0.15 in ZM521Q, and 0.25 in Pop62SRQ per cycle (Table 4.2). The gain cycle^{-1} had reduced by 4.26% for Sussuma, 3.88% for ZM521Q, and 4.32% for Pop62SRQ (Table 4.2). Mean square for maize streak virus disease scores were highly significant ($P \leq 0.01$) among full-sib families in all QPM populations (Appendices 4.1, 4.2, and 4.3). Genetic variances for MSVD increased from 0.314 in C1 to 0.559 in C2 in Sussuma, from 0.519 in C1 to 0.640 in C2 in ZM521Q, and from 0.135 in C1 to 0.781 in C2 in Pop62SRQ (Tables 4.3, 4.4, and 4.5). Comparatively, higher heritability estimates for MSVD were observed in C2 in Sussuma (0.94) than in ZM521Q (0.88) and Pop62SRQ (0.87) (Tables 4.3, 4.4 and 4.5). Genetic coefficients of variation (GCV) for MSVD in Sussuma changed very little from C1 to C2, compared with that in Pop 62 SRQ (Tables 4.6).

Using a selection intensity of 50% in C1 and 25% in C2 selection intensities (from the Table of Falconer, 1981) respectively, the response to selection was 0.41 in C1 and 0.92 in C2 for Sussuma, 0.53 in C1 and 0.86 in C2 for ZM521Q, and 0.24 in C1 and 1.0 in C2 for Pop62SRQ (Table 4.8).

Grain yield

The gain cycle^{-1} of grain yield of each selection cycle contributed in 150 kg in Sussuma, 180 kg in ZM521Q and 200 kg in Pop62SRQ (Table 4.2). Mean squares for grain yield were highly significant ($P \leq 0.01$) among full-sib families in all populations (Appendices 4.1, 4.2, and 4.3). Similarly the heritability estimates were higher in Sussuma population (0.64 in C1, and 0.81 in C2) , followed by ZM521Q (0.64 in C1 and 0.70 in C2), and, and Pop62SRQ (0.51 in C1 and 0.59 in C2) (Table 4.3, 4.4 and 4.5). Genetic variances for grain yield increased from 0.209 in C1 to 0.347 in C2 in Sussuma, from 0.116 in C1 to 0.172 in C2 in ZM521Q; and 0.197 in C1 to 0.728 in C2 in Pop62SRQ (Tables 4.3, 4.4, and 4.5). Genetic coefficients of variation (GCV) for yield in Sussuma and ZM521Q changed very little from C1 to C2, than in Pop 62 SRQ where GCV values on C2 were approximately two times higher compared to the C1 (Tables 4.6). Little increase was observed in genetic covariance (Covg (FS-S1) for yield from C1 to C2 in ZM521Q but higher increase of these variances were achieved from C1 to C2 in Pop 62SRQ (Table 4.6).

Using a selection intensity of 50% in C1 and 25% in C2 the response to selection was 0.29 in C1 and 0.67 in C2 for Sussuma, 0.22 in C1 and 0.44 in ZM521Q, and 0.24 in C1 and 0.89 in C2 for Pop62SRQ population (Table 4.9).

Plant height

The gain per cycle^{-1} for plant height was negligible in all the three populations (Table 4.2). Mean squares among full-sib families (Appendices 4.1, 4.2, and 4.3) were significant ($P \leq 0.01$) for plant height in all three QPM populations. Similarly estimates of heritability for plant

Table 4.2 Means and response to selection for MSVD rating, yield and other agronomic traits of different cycles of selection in three QPM population

	SUSSUMA					**ZM 521Q**					**Pop 62 SR Q**			
Trait	**C0**	**C1**	**C2**	**+Resp. cycle^{-1}**	**LSD**	**C0**	**C1**	**C2**	**+Resp. cycle^{-1}**	**LSD**	**C0**	**C1**	**C2**	**+Resp Cycle^{-1}**
MSV rating (1-5)	3.4	3.25	2.9	-0.35	0.8	2.70	2.45	2.3	-0.15	1.3	3.47	3.25	3.0	-0.25
Yield (t ha^{-1})	3.18	3.38	3.58	0.20	0.9	4.30	4.40	4.70	0..30	1.65	2.75	2.95	3.15	0.20
Plant height (cm)	187.6	185.7	183.8	-1.9	13.8	185.8	184.9	183.8	-1.1	12.3	189.2	187.6	186.3	-1.3
Ear height (cm)	83.3	82.7	81.1	-1.6	0.34	87.6	85.8	84.8	-1.0	0.27	93.6	92.8	92.4	-0.4
Days to 50% silking	88.7	87.7	85.6	-2.1	0.17	87.5	86.3	84.7	-1.6	0.14	89.2	88.0	86.3	-1.7
Days to 50% pollenshed	85.3	84.5	82.5	-2.0	0.13	83.9	82.9	81.4	-1.5	0.11	86.6	85.6	84.1	-1.5
Anth-Silk Interval (ASI)	4.10	3.30	2.50	-0.8	3.1	4.6	4.10	3.20	-0.9	2.0	2.60	2.40	2.20	-0.20
Ear per plant	0.9	1.07	1.20	0.13	2.3	0.94	1.07	1.16	0.12	2.1	0.89	1.06	1.20	0.14
Grain moisture (%)	12.90	12.60	12.22	-0.38	1.6	14.90	14.40	13.80	-0.60	1.0	17.90	17.50	17.00	-0.5
Grain Texture (1-5)	2.7	2.1	1.5	-0.6	0.8	2.9	2.4	1.9	-0.5	0.9	2.5	2.0	1.6	-0.4

+ Response to selection cycle^{-1} = C2-C1

Table 4.3 Estimated variance components of the Sussuma related to the different agronomic traits in cycles C1 and C2

	SUSSUMA					
		C1			**C2**	
Traits	**σ^2_g**	**Se**	**H^2**	**σ^2_g**	**Se**	**H^2**
Maize Streak Virus	0.314	0.139	0.83	0.559	0.164	0.94
Yield	0.209	0.132	0.64	0.347	0.132	0.81
Plant height	14.22	10.80	0.36	10.85	6.920	0.86
Ant-silking Interv	0.047	0.037	0.63	0.135	0.053	0.79
Grain moisture	0.038	0.056	0.71	1.043	0.378	0.82

Table 4.4 Estimated variance components of the ZM521Q related to the different agronomic traits in cycles C1 and C2

			ZM 521 Q			
		C1			**C2**	
Traits	**σ^2_g**	**Se**	**H^2**	**σ^2_g**	**Se**	**H^2**
Maize Streak Virus	0.640	0.150	0.70	0.519	0.171	0.88
Yield	0.116	0.066	0.64	0.172	0.104	0.70
Plant height	4.660	4.460	0.26	16.67	9.190	0.77
Ant-silking Interv	0.149	0.096	0.58	0.199	0.060	0.86
Grain moisture	1.426	0.696	0.68	7.201	2.347	0.75

Table 4.5 Estimated variance components of the Pop 62 SRQ related to the different agronomic traits in cycles C1 and C2

			Pop 62 SRQ			
		C1			C2	
Traits	$\sigma^{2}_{g\ g}$	**Se**	H^{2}	σ^{2}_{g}	**Se**	H^{2}
Maize Streak Virus	0.135	0.042	0.65	0.781	0.840	0.87
Yield	0.197	0.146	0.51	0.728	0.211	0.59
Plant height	19.13	15.73	0.54	28.86	12.53	0.70
Ant-silking Interv	0.239	0.556	0.71	1.894	0.507	0.72
Grain moisture	0.032	0.047	0.52	0.298	0.018	0.87

height were higher and are presented in Table 4.3, 4.4, and 4.5. Heritability estimates were 0.36 in C1 and 0.86 in C2 for Sussuma, 0.54 in C1 and 0.70 in C2 and C2 for Pop62SRQ, and 0.26 in C1 and 0.77 in C2 for ZM521Q. Genetic variances increased from 10.85 in C1 to 14.22 in C2 in Sussuma, from 4.660 in C1 to 16.67 in C2 in ZM521Q, and from 19.13 in C1 to 28.86 in C2 in Pop62SRQ (Tables 4.3, 4.4, and 4.5).

Anthesis-Silking Interval

The ASI was reduced by 0.8 day in Sussuma; 0.9 day in ZM521Q and 0.2 day in Pop62SRQ populations (Table 4.2). Mean squares for ASI (Appendices 4.1, 4.2, and 4.3) were significant ($P \leq 0.01$) among full-sib families in all three QPM populations. Similarly estimates of heritability for ASI were higher and are presented in Table 4.3, 4.4, and 4.5. Heritability estimates were 0.63 in C1 and 0.79 in C2 for Sussuma, 0.58 in C1 and 0.86 in C2 for ZM521Q, and 0.71 in C1 and 0.72 in C2 for Pop62SRQ.
Genetic variances showed an increase from C1 to C2 for ASI from 0.047 to 0.135 in Sussuma higher increase from 0.239 to 1.894 in Pop62SRQ and from 0.1490 to 0.1990 in ZM521Q (Tables 4.3, 4.4, and 4.5).

Correlations

In Sussuma population high correlations coefficients were observed between grain moisture and MSV. Grain yield also exhibited correlations with grain texture. ASI and MSV were less correlated (Table 10).

In ZM521Q population significant correlation coefficients were observed between grain moisture and ASI and grain texture with ear per plant. Grain yield was also correlated with grain texture. (Table 4. 11). In Pop62SRQ population Grain yield was highly correlated with ear per plant and grain moisture. Plant height exhibited high correlation with grain yield and grain texture (Table 4.12).

DISCUSSION

Sussuma, ZM521Q and Pop62SRQ populations

Conventional breeding methods are among some of the practical tools used by breeders to develop cultivars resistant to maize streak virus disease. In this study recurrent selection method was utilised to select for resistance to MSVD in three QPM populations.

All selected progenies that had low incidence also experienced low disease severity. This observation appeared to suggest preferences by leafhoppers to feed on some plants. Higher MSVD decrease severity was recorded in C1 than in C2 indicating that recurrent selection method was effective in improving resistance to MSVD. These observations conform with finding reported in earlier studies (Dudley, 1984; Lamkey *et al.,* 1993). High heritability estimates for MSVD were shown in all the three populations.

This indicates that once MSVD disease occurs it would be easy to score, the symptoms are highly evident and easy to score. These results ‘’]\\ support earlier reports by Welz et al. (1998); Kyetere et al. (1999), and Pernet et al. (1999). All QPM populations under study had highly significant variations among progenies. In the current study, two cycles of recurrent selection for MSVD resistance significantly reduced the infection in Sussuma, ZM521Q and in Pop62SRQ.

It was concluded that all QPM populations were responsive to selection for MSVD resistance. Analysis of variance of full-sib progenies indicated the presence of

Table 4.6 Genetic parameter estimates for FS families of the three QPM populations

	YIELD					
	SUSSUMA		**ZM 521 Q**		**Pop 62 SRQ**	
Parameter	**C1 FS**	**C2 FS**	**C1 FS**	**C2 FS**	**C1 FS**	**C2 FS**
GCV	12.76	17.17	7.49	8.82	14.10	28.43
σ^2_G	0.208	0.347	0.116	0.172	0.197	0.728
Covg(FS-S1)	14.89	15.07	8.37	10.37	16.87	78.14
H^2	0.64	0.81	0.64	0.70	0.51	0.59

GCV = Genetic coeficient of variation; Covg = genetic covariance; σ^2G = genetic variance; H^2 = broad-sense heritability

Table 4.7 Genetic parameter estimates for FS families of the three QPM populations on cycles C1 and C2

	Maize Streak Virus					
	SUSSUMA		**ZM 521 Q**		**Pop 62 SRQ**	
Parameter	**C1 FS**	**C2 FS**	**C1 FS**	**C2 FS**	**C1 FS**	**C2 FS**
GCV	15.66	21.81	15.84	17.03	12.23	28.06
$\sigma 2_G$	0.314	0.559	0.519	0.640	0.135	0.781
Covg(FS-S1)	13.12	16.81	18.65	38.52	9.28	29.06
H^2	0.83	0.94	0.70	0.88	0.65	0.87

GCV = Genetic coefient of variation; Covg = genetic covariance; σ^2G = genetic variance; H^2 = broad-sense heritability

Table4.8 Response to selection for MSV on three QPM populations in C1 and C2

			Maize Streak Virus			
	Sussuma		**ZM 521Q**		**Pop 62 SR**	
	C1	**C2**	**C1**	**C2**	**C1**	**C2**
i	0.798	1.271	0.798	1.271	0.798	1.271
H^2	0.83	0.94	0.70	0.88	0.65	0.87
σ_P	0.617	0.772	0.956	0.769	0.453	0.950
RS	0.41	0.92	0.53	0.86	0.24	1.0
RS = $ih^2\sigma_P$						

RS = response to selection; i= selection intensity
H^2 = broad-sense heritability; σ_P = standard error of phenotypic variance

Table 4.9 Response to selection for yield on three QPM populations in C1 and C2

	Yield					
	Sussuma		**ZM 521Q**		**Pop 62 SR**	
	C1	**C2**	**C1**	**C2**	**C1**	**C2**
i	0.798	1.271	0.798	1.271	0.798	1.271
H^2	0.64	0.81	0.64	0.70	0.51	0.59
σ_P	0.569	0.654	0.426	0.495	0.581	1.189
RS	0.29	0.67	0.22	0.44	0.24	0.89
$RS = iH^2\sigma_P$						

RS = response to selection; i= selection intensity
H^2 = broad-sense heritability; σ_P = standard error of phenotypic variance

Table 4.10 Correlations coefficients among measured parameters (below) and probabilities (above) of Sussuma population in C 2

	ASI	**Maize Streak Virus**	**Ear per Plant**	**Grain Moisture**	**Grain Texture**	**Grain Yield**	**Plant Height**
ASI							
Maize Streak Virus	-0.2800						
Ear per Plant	-0.0880	0.1210					
Grain Moisture	0.0180	0.3320*	-0.0244				
Grain Texture	0.0550	0.0060	-0.0350	-0.0180			
Grain Yield	0.0690	-0.1590	-0.1200	-0.0420	0.0740		
Plant Height	0.1000	0.0640	0.0460	0.0090	0.0090	0.0350	

Table 4.11 Correlations coefficients among measured parameters (below) and probabilities (above) of ZM521Q population in C 2

	ASI	**Maize Streak Virus**	**Ear per Plant**	**Grain Moisture**	**Grain Texture**	**Grain Yield**	**Plant Height**
ASI							
Maize Streak Virus	-0.1231						
Ear per Plant	-0.1640	-0.0420					
Grain Moisture	0.2610*	-0.0180	0.0740				
Grain Texture	-0.1451	0.0350	0.3440*	0.0090			
Grain Yield	-0.1123	0.0180	0.0690	0.0550	0.1000		
Plant Height	0.2020	-0.2440	-0.1211	-0.0350	0.0460	-0.0812	

Table 4.12 Correlations coefficients among measured parameters of Pop62SRQ population in C 2

	ASI	Maize Streak Virus	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Maize Streak Virus	0.0155						
Ear per Plant	-0.0880	-0.0521					
Grain Moisture	0.0180	0.0320	-0.2440				
Grain Texture	0.0550	-0.1423	-0.0350	-0.0180			
Grain Yield	0.0690	0.1350	0.3200**	0.4200**	0.0740		
Plant Height	0.1000	-0.3020	0.0460	0.0350	0.3440*	0.3652**	

Table 4.13 Correlations coefficients among measured parameters and probabilities of Pop62SRQ population in C 2

	ASI	**Maize Streak Virus**	**Ear per Plant**	**Grain Moisture**	**Grain Texture**	**Grain Yield**	**Plant Height**
ASI							
Maize Streak Virus	0.0133						
Ear per Plant	-0.7540	-0.241					
Grain Moisture	0.0580	0.0430	-0.2654				
Grain Texture	0.0350	-0.234	-0.3860	-0.480			
Grain Yield	0.0480	-0.350	-0.3420	0.2400*	0.0740		
Plant Height	0.0127	-0.320	0.0654	0.0350	0.1880*	0.2565*	

highly significant (P≤0.01) genetic variation in all populations for tasseling, silking and pollen shedding.

CONCLUSIONS

Breeding for resistance to MSVD using recurrent selection method was highly effective.

Two cycles of S1 recurrent selection significantly improved MSVD resistance in the three QPM populations although the basic levels differed.

There was concurrent improvement in grain yield performance, ASI, grain texture, grain moisture, ears per plant and other desirable characteristics.

Genetic variances and heritability estimates for MSVD resistance and other important characteristics generally increased or remained unchanged which was important for future continued selection within these populations.

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Appendix 4.1 Means of MSVD, grain yield and secondary traits of Full-Sib families of Sussuma population in cycle two

Entry Sussuma	Maize Streak Virus	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
	(1-5)	t ha^{-1}	Rank	d	Cm	#	%
		Bottom Ten					
5	3.0	2.5	30	2.5	204.9	1.05	13.0
41	3.8	2.6	29	4.3	178.0	1.09	10.4
40	3.4	2.7	28	3.0	149.0	1.01	12.3
43	2.0	2.8	27	4.3	174.0	1.14	12.4
29	2.8	2.8	26	0.8	166.8	1.13	12.1
25	3.1	2.9	25	3.4	174.1	1.21	12.6
22	2.9	3.1	24	3.3	188.5	1.04	12.6
38	1.4	3.3	23	2.7	189.7	0.86	12.4
8	3.3	3.3	22	1.4	181.4	1.31	10.8
30	1.4	3.4	21	6.1	175.1	1.14	12.0
		2.5					
		Top Ten					
4	3.0	5.6	1	2.3	169.1	1.45	11.8
3	2.9	4.8	2	3.7	175.8	1.28	11.3
11	3.0	4.6	3	4.1	173.5	1.24	12.6
18	4.1	4.5	4	3.1	176.4	1.06	12.6
1	2.4	4.5	5	5.3	173.6	1.02	12.3
42	2.9	4.5	6	3.3	165.4	1.14	13.2
32	3.8	4.3	7	2.2	176.3	1.32	12.1
34	3.1	4.2	8	3.6	172.5	0.76	11.6
7	3.3	4.2	9	4.0	198.1	1.04	13.0
12	1.7	4.0	10	2.4	186.9	1.24	12.8
Mean	**2.9**	**3.58**		**2.5**	**183.8**	**1.20**	**12.2**
LSD (0.05)	**0.8**	**0.9**		**3.1**	**13.8**	**0.34**	**1.6**
MSe	**0.2**	**0.80**		**3.0**	**285.0**	**0.04**	**1.0**
CV	**17.1**	**25.05**		**52.0**	**9.5**	**18.18**	**8.3**
P	**0.000**			**0.361**	**0.000**	**0.024**	**0.002**
P	***	Ns		Ns	***	*	**
Min	**1.4**	**1.89**		**0.8**	**149.0**	**0.76**	**9.9**
Max	**4.4**	**5.64**		**6.1**	**204.9**	**1.45**	**13.2**
Standard Error	0.3971	0.7597		1.5	6.765	0.1676	

Appendix 4.2 Means of MSVD, grain yield and secondary traits of Full-Sib families of ZM521Q population in cycle two

Entry	Maize	Grain	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist

	Streak Virus	Yield					
ZM 521 Q							
	(1-5)	$t\ ha^{-1}$	Rank	D	cm	#	%
		Bottom Ten					
9	3.5	4.0	30	3.2	163.8	1.10	14.2
32	2.7	4.0	29	3.3	152.8	1.18	12.9
13	2.5	4.1	28	3.3	157.4	1.18	13.5
18	3.2	4.1	27	3.7	218.7	1.44	14.8
7	3.3	4.2	26	3.1	165.4	1.13	13.9
2	2.8	4.3	25	3.2	177.6	1.42	13.6
15	3.4	4.5	24	3.8	169.8	1.04	14.0
6	3.1	4.5	23	3.7	184.4	1.37	13.6
23	3.0	4.5	22	3.9	163.7	1.28	14.3
22	2.4	4.6	21	4.0	162.1	1.13	14.0
		Top Ten					
14	1.1	7.6	1	3.4	164.4	1.16	14.6
3	1.4	6.2	2	2.8	179.1	1.20	13.9
21	1.6	6.0	3	4.5	174.5	1.18	13.3
33	1.7	5.6	4	4.0	179.9	1.08	14.1
16	1.8	5.5	5	5.3	190.5	1.06	12.7
10	1.9	5.3	6	3.3	176.0	1.15	13.3
24	2.1	5.2	7	3.7	144.1	1.03	15.0
8	2.2	5.2	8	3.9	190.8	1.37	14.3
11	1.5	5.1	9	4.4	173.2	1.10	14.2
4	1.2	5.1	10	3.5	162.1	1.09	13.2
Mean	**2.3**	**4.70**		**3.2**	**173.0**	**1.16**	**13.8**
LSD (0.05)	**1.3**	**1.65**		**2.0**	**12.3**	**0.27**	**1.0**
Mse	**0.6**	**1.06**		**1.5**	**216.4**	**0.03**	**0.4**
CV	**33.5**	**21.93**		**33.1**	**8.5**	**14.79**	**4.3**
P	**0.118**	**0.001**		**0.435**		**0.158**	**0.000**
P	Ns	**		Ns	ns	ns	***
Min	**1.1**	**4.0**		**2.6**	**144.1**	**1.00**	**12.7**
Max	**3.5**	**7.6**		**5.6**	**218.7**	**1.44**	**15.0**
Standard Error		0.8093					

Appendix 4.3 Means of MSVD, grain yield and secondary traits of Full-Sib families of Pop62SRQ population in cycle two

Entry	**Maize Virus**	**Streak**	**Grain Yield**	**Rank**	**ASI**	**Plant Height**	**Ears/ Plant**	**Grain Moist**
Pop 62 SR								
	(1-5)		$t\ ha^{-1}$	Rank	D	Cm	#	%
			Bottom Ten					
5	4.3		2.98	30	2.5	154.0	0.92	17.0
41	3.0		3.04	29	2.4	142.9	0.88	16.1
40	3.3		3.11	28	1.0	141.9	0.88	15.9
43	3.1		3.14	27	2.1	142.5	0.72	16.6
29	3.0		3.19	26	1.9	145.9	0.83	14.9
25	3.2		3.28	25	2.0	146.5	0.97	17.0

22	2.9	3.29	24	2.5	143.6	0.93	17.1
38	3.1	3.33	23	4.0	159.4	0.99	16.6
8	2.5	3.34	22	2.4	156.5	0.86	17.3
30	2.2	3.34	21	3.0	160.7	1.02	17.0
		Top Ten					
4	2.0	4.85	1	2.4	164.1	1.00	15.7
3	3.1	4.60	2	2.5	161.7	0.88	16.0
11	2.5	4.57	3	2.4	151.3	0.90	24.6
18	2.1	3.98	4	2.0	162.6	0.85	16.5
1	3.5	3.84	5	2.5	148.6	0.99	25.5
42	3.1	3.80	6	1.5	146.4	0.97	17.4
32	3.2	3.79	7	2.5	145.2	0.75	16.0
34	2.5	3.75	8	2.0	153.9	0.89	16.3
7	3.2	3.70	9	2.5	143.1	0.98	16.3
12	3.2	3.69	10	3.4	156.9	1.05	16.3
Mean	**3.0**	**3.15**		**2.2**	**144.1**	**1.20**	**17.0**
LSD (0.05)	**1.0**	**1.52**		**2.0**	**22.0**	**0.22**	**4.3**
MSe	**0.3**	**0.54**		**1.1**	**273.6**	**0.03**	**5.3**
CV	**18.0**	**23.45**		**42.9**	**11.0**	**17.64**	**13.7**
P	**0.001**	**0.025**		**0.883**	**0.067**		**0.013**
P	**	*		ns	+	Ns	*
Min	**2.0**	**2.98**	**1**	**-2.0**	**141.9**	**0.61**	**14.5**
Max	**4.3**	**4.85**	**49**	**4.0**	**164.1**	**1.21**	**25.5**
Standard Error	0.5	0.76		0	10.7	0.16	2.1

Appendix 4.4 Means of MSVD, grain yield and secondary traits of Full-Sib families of Sussuma population in cycle one

Entry **Sussuma C 1**	**Maize Streak Virus**	**Grain Yield**	**Rank**	**ASI**	**Plant Height**	**Ears/ Plant**	**Grain Moist**
	(1-5)	t ha^{-1}	Rank	d	Cm	#	%
		Bottom Ten					
5	3.0	2.5	30	2.5	204.9	1.05	13.0
41	3.8	2.6	29	4.3	178.0	1.09	10.4
40	3.4	2.7	28	3.0	149.0	1.01	12.3
43	3.0	2.8	27	4.3	174.0	1.14	12.4
29	2.8	2.8	26	0.8	166.8	1.13	12.1
25	3.1	2.9	25	3.4	174.1	1.21	12.6
22	2.9	3.1	24	3.3	188.5	1.04	12.6
38	3.4	3.3	23	2.7	189.7	0.86	12.4
8	3.3	3.3	22	1.4	181.4	1.31	10.8
30	2.4	3.4	21	6.1	175.1	1.14	12.0
		2.5					
		Top Ten					

4	3.0	5.6	1	2.3	169.1	1.45	11.8
3	3.0	4.8	2	3.7	175.8	1.28	11.3
11	3.0	4.6	3	4.1	173.5	1.24	12.6
18	3.9	4.5	4	3.1	176.4	1.06	12.6
1	3.4	4.5	5	5.3	173.6	1.02	12.3
42	2.9	4.5	6	3.3	165.4	1.14	13.2
32	3.8	4.3	7	2.2	176.3	1.32	12.1
34	3.1	4.2	8	3.6	172.5	0.76	11.6
7	3.3	4.2	9	4.0	198.1	1.04	13.0
12	2.7	4.0	10	2.4	186.9	1.24	12.8
Mean	**3.25**	**3.38**		**3.3**	**185.7**	**1.07**	**12.6**
LSD (0.05)	**0.8**			**3.1**	**13.8**	**0.34**	**1.6**
MSe	**0.2**	**0.80**		**3.0**	**285.0**	**0.04**	**1.0**
CV	**17.1**	**25.05**		**52.0**	**9.5**	**18.18**	**8.3**
P	**0.000**			**0.361**	**0.000**	**0.024**	**0.002**
P	***	Ns		ns	***	*	**
Min	**1.4**	**1.89**		**0.8**	**149.0**	**0.76**	**9.9**
Max	**4.4**	**5.64**		**6.1**	**204.9**	**1.45**	**13.2**
Standard Error	0.3971	0.7597		1.5	6.765	0.1676	

Appendix 4.5 Means of MSVD, grain yield and secondary traits of Full-Sib families of ZM521Q population in cycle one

Entry	**Maize Streak Virus**	**Grain Yield**	**Rank**	**ASI**	**Plant Height**	**Ears/ Plant**	**Grain Moist**
ZM 521 Q C1							
	(1-5)	t ha^{-1}	Rank	D	cm	#	%

		Bottom Ten					
8	3.5	2.8	30	3.2	163.8	1.10	14.2
29	3.7	3.0	29	3.3	152.8	1.18	12.9
17	3.5	3.2	28	3.3	157.4	1.18	13.5
21	3.2	3.8	27	3.7	218.7	1.44	14.8
12	3.3	3.9	26	3.1	165.4	1.13	13.9
15	2.8	4.1	25	3.2	177.6	1.42	13.6
19	3.4	4.2	24	3.8	169.8	1.04	14.0
7	3.1	4.4	23	3.7	184.4	1.37	13.6
32	3.0	4.4	22	3.9	163.7	1.28	14.3
21	2.4	4.5	21	4.0	162.1	1.13	14.0
		Top Ten					
9	2.1	5.6	1	3.4	164.4	1.16	14.6
45	1.4	5.2	2	2.8	179.1	1.20	13.9
53	1.6	5.0	3	4.5	174.5	1.18	13.3
6	1.7	4.6	4	4.0	179.9	1.08	14.1
23	1.8	4.5	5	5.3	190.5	1.06	12.7
43	1.9	4.3	6	3.3	176.0	1.15	13.3
26	2.1	4.2	7	3.7	144.1	1.03	15.0
14	2.2	4.2	8	3.9	190.8	1.37	14.3
11	1.5	4.1	9	4.4	173.2	1.10	14.2
4	1.2	4.1	10	3.5	162.1	1.09	13.2
Mean	**2.45**	**4.40**		**4.1**	**184.9**	**1.07**	**14.4**
LSD (0.05)	**1.3**	**1.65**		**2.0**		**0.27**	**1.0**
Mse	**0.6**	**1.06**		**1.5**	**216.4**	**0.03**	**0.4**
CV	**33.5**	**21.93**		**33.1**	**8.5**	**14.79**	**4.3**
P	**0.118**	**0.001**		**0.435**		**0.158**	**0.000**
P	Ns	**		Ns	ns	ns	***
Min	**1.1**	**2.95**	**1**	**2.6**	**144.1**	**1.00**	**12.7**
Max	**3.5**	**7.62**	**35**	**5.6**	**218.7**	**1.44**	**15.0**
Standard Error		0.8093					

Appendix 4.6 Means of MSVD, grain yield and secondary traits of Full-Sib families of Pop62SRQ population in cycle one

Entry	**Maize Virus**	**Streak**	**Grain Yield**	**Rank**	**ASI**	**Plant Height**	**Ears/ Plant**	**Grain Moist**
Pop 62 SR C1								
	(1-5)		t ha^{-1}	Rank	D	Cm	#	%
			Bottom Ten					
5	4.3		2.98	30	2.5	154.0	0.92	17.0
41	3.0		3.04	29	2.4	142.9	0.88	16.1
40	3.3		3.11	28	1.0	141.9	0.88	15.9
43	3.1		3.14	27	2.1	142.5	0.72	16.6
29	3.0		3.19	26	1.9	145.9	0.83	14.9
25	3.2		3.28	25	2.0	146.5	0.97	17.0
22	2.9		3.29	24	2.5	143.6	0.93	17.1

38	3.1	3.33	23	4.0	159.4	0.99	16.6
8	2.5	3.34	22	2.4	156.5	0.86	17.3
30	2.2	3.34	21	3.0	160.7	1.02	17.0
		Top Ten					
4	2.0	4.85	1	2.4	164.1	1.00	15.7
3	3.1	4.60	2	2.5	161.7	0.88	16.0
11	2.5	4.57	3	2.4	151.3	0.90	24.6
18	2.1	3.98	4	2.0	162.6	0.85	16.5
1	3.5	3.84	5	2.5	148.6	0.99	25.5
42	3.1	3.80	6	1.5	126.4	0.97	17.4
32	3.2	3.79	7	2.5	145.2	0.75	16.0
34	2.5	3.75	8	2.0	153.9	0.89	16.3
7	3.2	3.70	9	2.5	143.1	0.98	16.3
12	3.2	3.69	10	3.4	156.9	1.05	16.3
Mean	**3.25**	**2.95**		**2.4**	**187.6**	**1.06**	**17.5**
LSD (0.05)	**1.0**	**1.52**		**2.0**	**22.0**		**4.3**
MSe	**0.3**	**0.54**		**1.1**	**273.6**	**0.03**	**5.3**
CV	**18.0**	**23.45**		**42.9**	**11.0**	**17.64**	**13.7**
P	**0.001**	**0.025**		**0.883**	**0.067**		**0.013**
P	**	*		ns	+	Ns	*
Min	**2.0**	**1.63**		**-2.0**	**126.4**	**0.61**	**14.5**
Max	**4.4**	**4.85**		**4.0**	**164.1**	**1.21**	**25.5**
Standard Error	0.5	0.76		0	10.7	0.16	2.1

The correlation coefficients in Sussuma population showed grain yield highly correlated with ear per plant and grain texture.

Appendix 4.7 Correlations coefficients among measured parameters and probabilities of Sussuma population in C 1

	ASI	**Maize Streak Virus**	**Ear per Plant**	**Grain Moisture**	**Grain Texture**	**Grain Yield**	**Plant Height**
ASI							
Maize Streak Virus	-0.2612						
Ear per Plant	-0.3464	-0.0240					
Grain Moisture	-0.2310	-0.0380	0.0740				
Grain Texture	-0.2451	0.0350	0.0440	0.0790			
Grain Yield	-0.2330	0.0189	0.1900*	0.0450	0.1430*		
Plant Height	-0.2020	-0.2640	-0.2211	-0.3800	0.0460	0.0182	

The correlation coefficients in ZM521Q population showed grain yield highly correlated with ear per plant.

Appendix 4.8 Correlations coefficients among measured parameters and probabilities of ZM521Q population in C 1

	ASI	**Maize Streak Virus**	**Ear per Plant**	**Grain Moisture**	**Grain Texture**	**Grain Yield**	**Plant Height**
ASI							
Maize Streak Virus	-0.0680						
Ear per Plant	-0.0380	0.1240					
Grain Moisture	0.0197	-0.3120	-0.0468				
Grain Texture	0.0650	0.0760	-0.0345	-0.1180			
Grain Yield	0.0670	-0.1890	0.1320*	-0.0450	0.02400		
Plant Height	0.0187	0.0680	0.0460	0.0190	0.0860	0.0370	