Full length Research paper

Response to selection for downy mildew resistance, grain yield, and secondary traits in three quality protein maize populations in Mozambique.

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Downy mildew (DM) is a major problem in quality protein maize (QPM) varieties under cultivation in Mozambique. Recurrent selection was therefore initiated to improve DM resistance in three QPM populations, mainly Sussuma, ZM521Q and Pop62SRQ at Umbeluzi Research Station in Mozambique, during 2003-2006 seasons. Downy mildew disease incidence and severity were rated at four and eight weeks after infection (WAI) based on visual assessment of the whole plot. Selfed S1 progenies were selected based on FS progeny performance. 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 indicated significant improvement in DM resistance from C1 to C2, with scores of 4.6-3.9 in Sussuma, 3.0-2.3 in ZM521Q and 4.0-3.3 in Pop62SRQ, respectively. Results also indicated increase in genetic variances (σ^2_G) for DM from 0.069 in C1 to 0.119 in C2 in Sussuma; 0.054 in C1 to 0.1442 in C2 in ZM521Q, and from 0.097 in C1 to 0.313 in C2 in Pop62SRQ. Broad sense heritability (H^2) estimates ranged from moderate to high and increased from C1 to C2 in all populations. The H^2 estimates were 0.63-0.76 in Sussuma; 0.60-0.63 in ZM521Q and 0.60-0.63 in Pop62SRQ. These changes were associated with an increase in yield of about 4.67% in Sussuma, 4.68% in ZM521Q and 4.47% in Pop62SRQ. There was also an improvement in flint nature of the grain with texture scores of 2.7-1.4 in Sussuma, 2.9-1.8 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 DM resistance, increasing genetic variances and broad sense heritability estimates without compromising grain yield, texture, and other important characteristics.

Keywords: Downy mildew, quality protein maize, recurrent selection, progenies, genetic variances.

INTRODUCTION

The objective of QPM breeding is to improve the nutritional value of proteins in maize grain, which is only 40% of that of milk (Bressani, 1991). Maize is therefore recommended and consumed with other balancing proteins from legumes and animal products, which are not readily available to small-scall farmers. Most people in sub-Saharan Africa rely on a predominantly maize based diet hence cases of malnutrition abound. In Africa

for example, maize contributes 20% of total daily calories and accounts for 17 to 60% protein FAO (1995) requirements, yet it lacks in essential amino acids. QPM varieties would therefore address such inadequacy in maize .

Although the grain yield potential of QPM varieties has been improved, the varieties in Mozambique are still highly susceptible to many diseases. The disease pressure is high on QPM varieties because the varieties were presumably developed from germplasn with little resistance to prevalent pathogens in Mozambique. Downy mildew is one of the most serious diseases that compromise yield. Downy mildew, which is caused by

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Peronosclerospora sorghi reduces grain yield when it attacks the maize crop during the early growth stages and development (Denic *et al.,* 2001). In Africa, this disease is prevalent in East Africa (Weston and Uppal, 1932), southern Nigeria in West Africa, Abedon and Tracy (1988) and Mozambique in Southern Africa (Plumb-Dhindsa and Mondjane, 1984; Denic, 1994). Rana et al. (1982) reported that Indian inbred maize lines were resistant to DM pathogens (*Peronosclerospora sorghi* (*SDM) and Perenosclerospora heteropogoni; (RDM*). They also reported that resistance was polygenically inherited and that resistance was dominant over susceptibility in that germplasm. In a later study, Nair et al. (2004) found that resistance was partially dominant when lines were subjected to SDM infection, but was complete in lines infected with RDM. However, they concluded that additive genetic variance was more important than the non-additive genetic variance in controlling resistance to SDM and RDM, (Nair *et al.,* 2004), suggesting that resistance could be improved by selection. In Mozambique, the SDM is the predominant pathogen that has been associated with DM in maize.

Recurrent selection (RS) methods have been widely used to improve yield and agronomic performance of maize populations (Ceballos *et al.,* 1991). During recurrent selection it is desired to improve mean performance for the desirable attributes without compromising the genetic variation which is required to ensure continued selection gains. Thus the RS which has been proven to be efficient in exploiting additive effects (Moll and Smith, 1981) would be used to improve three QPM populations for resistance to DM in Mozambique. A survey of available literature showed that very little RS, if any, has been conducted to improve QPM especially for DM resistance. However, some progress on DM resistance has been reported in normal maize (CIMMYT, 2001), especially when S1 selection was used in combination with full-sib selection (Ajala, 1992). The QPM populations under cultivation in Mozambique have not been studied for genetic variability for DM resistance and their response to selection for DM resistance. This study was, therefore, based on the premise that DM resistance is polygenically controlled by predominantly additive gene action, and can be improved by recurrent selection.

Objectives and Research hypothesis

The specific objectives of the study were:
a) To study the response to recurrent selection for DM resistance and other important traits using selfed progenies (S1) in combination with full-sib evaluation of three QPM populations,
b) To determine correlated responses of the three populations for yield, ASI, grain texture, grain moisture and other important agronomic characteristics after two cycles of recurrent selection.

The hypothesis tested was:
a) Resistance to DM in QPM populations can be improved by using recurrent selection, and genetic variability for DM and other important traits remains high after cycles of recurrent selection.

MATERIALS AND METHODS

Location of the study

The experiment was conducted at Umbeluzi Research Station, which is located 30 km south of Maputo, with a mean altitude of 15m above sea level (a.s.l). The research station area is located in the Boane district in the Maputo province, Mozambique, between the latitude 26°02' – 26°04' south and the longitude 32°17' – 32°19' west. The climate is subtropical, with a monomodal rainfall pattern. The average rainfall per annum is 678 mm. January is the wettest month and August the driest month of the year. The rainy season runs from October to April and the dry season from May to September. The annual average temperature is 22.9°C. The highest average temperature is in January (25.6°C) and the lowest in July (17.8°C). The relative humidity does not vary markedly during the year with values ranging between 65% during August/September to 72% in March/April.

Germplasm

The three quality protein maize populations Sussuma (S_2 generation), ZM521Q, and Pop62SRQ (Table 1) used in this study were obtained from . They are high grain yielding but highly susceptible to downy mildew. 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) Mexico and Harare. All the populations are adapted to tropical environments in East and Southern Africa. They were converted to QPM at Instituto de Investigação Agrária de Moçambique (IIAM), in Mozambique. The characteristics of these populations are summarized in Table 1.

Establishment of screening nurseries and artificial inoculation of spreader rows for downy mildew

Downy mildew nurseries were established three seasons to screen the progenies at Umbeluzi Research Station, (URS) in December 2003, November 2004, and November 2005. Selected ears from selfed (S1) seeds of each population were planted for screening for DM resistance. The population size of about 5,316 plants for each population was established. 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

Table 1: Characteristics of three QPM populations subjected to recurrent selection for downy mildew resistance in Mozambique
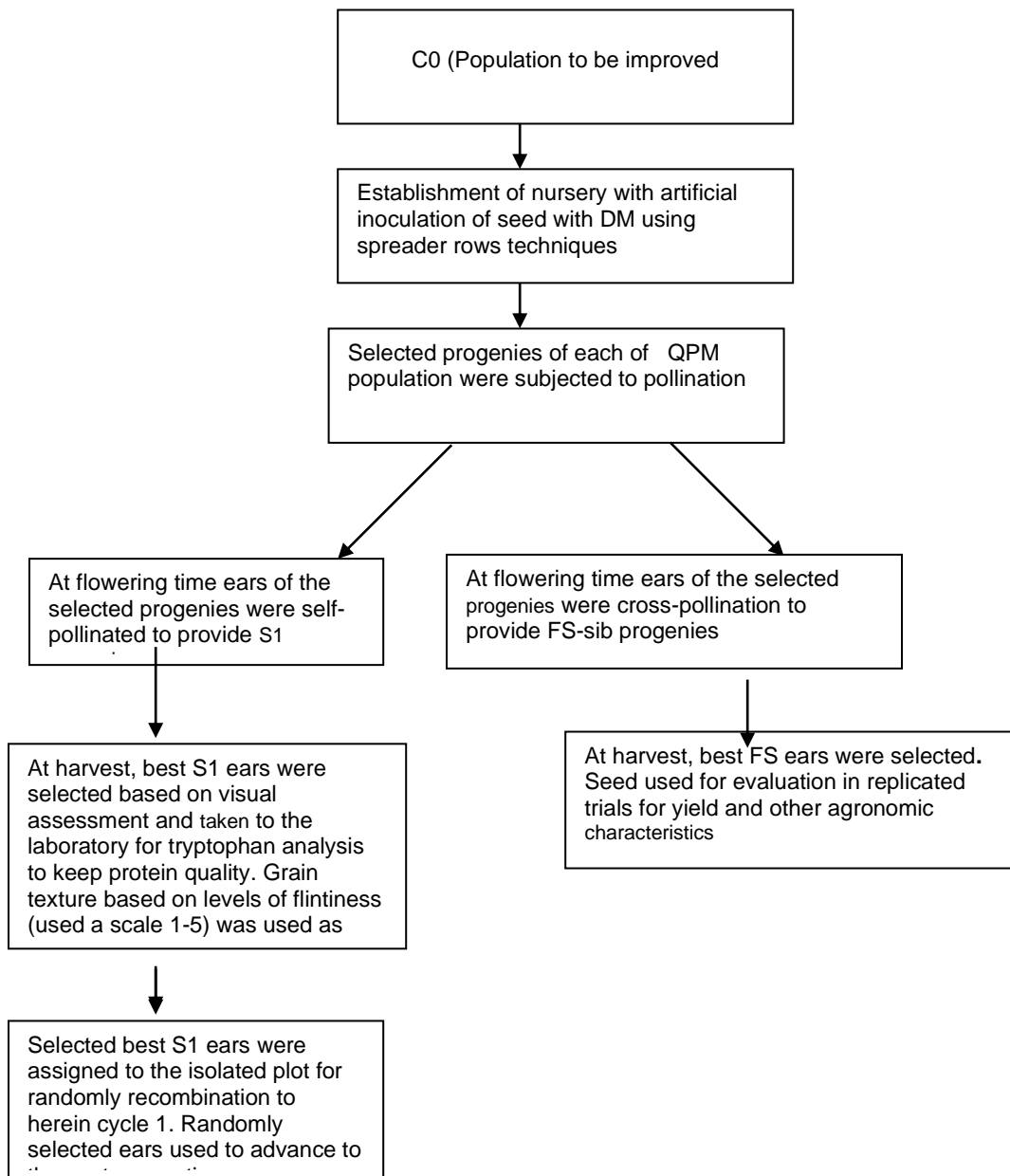
Designate Name	Source Population	Characteristics
ZM 521Q	[ZM521/SW8075DMR//QSRDMR] F2	● Intermediate to late maturing; high-yielding white grain, flint grain type. Improved for quality protein Adapted to tropical environments. Recommended for medium and high altitude (15-1500 m.a.s.l) areas.
SUSSUMA	Sussuma S2	● Has Obatanpa GH background, derived from Pop63SR, originated from CIMMYT, Mexico. Intermediate to Late maturing; high-yielding white grain; semi- dent grain type. Improved for high quality maize protein, grain texture and drought tolerance at ex-INIA, IIAM. Adapted to tropical environments. Recommended for medium and high altitudes (15-1200 m.a.s.l) areas.
POP 62 SRQ	Pop 62 SR	● QPM early maturing; high-yielding white grain, flint grain type. Adapted to tropical environment. Recommended for medium to high altitude (15-1200 m.a.s.l) areas

rows. Field layout involved planting four rows of spreaders (susceptible checks) at the beginning of each block, followed by five rows of the population to be screened, and at the end of the block. The progenies of the selected plants from the selfed generation (S1) were planted in an ear-to-row method in which progenies of each plant were planted in one 5 m long row only. Agronomic practices included fertilizer application at planting with NPK (12:24:12) and that 375 kg ha^{-1} of the compound at planting and 150 kg ha^{-1} of urea 46% N at top dressing, herbicide application with glyphosate before planting followed by weeding and top dressing with urea (46% N) during the vegetative stage. Stalk borer control was done by spraying with insecticide Decis (pyrethroid) at regular intervals to reduce crop loss. A combination of night-time infection techniques developed in Thailand (Caldwell *et al.,* 1997), and a modified inoculation procedure (Caldwell *et al.,* 1997) were used to inoculate trials. Seeds of a susceptible variety were selected, and treated with 5% savlon (desinfectant) for 1 min, and then washed with tap water, and left to pre-germinate for 72 hrs. Downy mildew diseased leaves were harvested late afternoon and used to make a layer in a plastic box. The layer of seedlings was placed over the layer of diseased leaves and left to sporulate over night, in a controlled chamber at 20 °C. The infected seedlings were then planted in the field as spreader rows and the S1 progeny

rows were planted 14 days later. The pathogen was already sporulating on the spreader plants by the time the test materials were planted.

Formation of the cycles

During the test period, all selected plants had their ear shoots covered with cellophane bags at flowering time. The ears of the selected progenies were self-pollinated to provide S1 seed. Pollen from selfed plants was used to pollinate ears from other randomly selected plants to form full-sib seed. Full-sib families formed in C1 were harvested and evaluated and the results used as base to select the S1 progenies on visual assessment. Selfed progenies based on the best FS progenies were selected for quality protein content using light tables (Pixley and Bjarnason, 2002). To confirm the results of light table selection, enzyme-linked immunosorbent assay (Elisa) test was conducted in the laboratory for selected grain, and only those that met QPM protein requirement levels were selected. The selected S1 seeds were planted in an isolated plot to allow them to inter-mate and then the seed was bulked to form cycle 2. 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% (2658 plants), 25% (665 plants) and 25% (166 plants) for the populations Sussuma, ZM521Q

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┌─────────────────────────────────────┐
│  C0 (Population to be improved       │
└─────────────────────────────────────┘
                  │
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┌─────────────────────────────────────┐
│  Establishment of nursery with       │
│  artificial inoculation of seed      │
│  with DM using spreader rows          │
│  techniques                           │
└─────────────────────────────────────┘
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┌─────────────────────────────────────┐
│  Selected progenies of each of QPM   │
│  population were subjected to         │
│  pollination                          │
└─────────────────────────────────────┘
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At flowering time ears of the selected progenies were self-pollinated to provide S1	At flowering time ears of the selected progenies were cross-pollination to provide FS-sib progenies

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At harvest, best S1 ears were selected based on visual assessment and taken to the laboratory for tryptophan analysis to keep protein quality. Grain texture based on levels of flintiness (used a scale 1-5) was used as	At harvest, best FS ears were selected. Seed used for evaluation in replicated trials for yield and other agronomic characteristics

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Selected best S1 ears were assigned to the isolated plot for randomly recombination to herein cycle 1. Randomly selected ears used to advance to

Figure 1 Formation of cycle using S1 and full-sib families in QPM populations

and Pop62SRQ, respectively. The rational of choosing this selection intensity was to maintain the variability within populations for future selections. These were plants with adequate FS seed with resistance to DM used to form the base population referred to herein as a cycle 1.

In 2005/06, a trial was planted for evaluation of the two cycles of each population. A simple lattice 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 5 m length, 80 cm between and 25 cm within rows. The hills were over planted and thinned to one plant per hill. Additional variables, such as days to 50% anthesis, 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. 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 blocks means and were equal to or below the average grain moisture at harvest and with desirable quality protein content were selected. Selfed

(S1) progenies based on superior FS families were advanced to the next generation.

Selection method

The selection method for DM was based on single plant selection. This was done just before flowering stage (because of the need for cross and self pollination). The best rows were selected and in each row the best five plants were selected. The best plants were those that showed resistance to downy mildew. The selected plants were hand self-pollinated to generate selfed progenies, and cross pollination was carried out for full-sib progenies formation using the same selected plants. 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, based on DM disease severity scores. Plants with zero (0) severities scores were not selected because they could not be separated from escapes. Only plants that showed symptoms with severity scores of 2 and 3 indicating high resistance were selected. About 10% (510/5,316) of the plants with scores of 2 to 3 (rating scale 0 to 5) were selected, equivalent to 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 final analysis of tryptophan content to keep the protein quality of the selected progenies for the next generation of selection. Selected progenies with resistance to DM were also selected on the basis of grain texture. Selection for grain texture was based on levels of flintiness of the grain, and was done after harvest. In each population best ears were selected for flintiness using the scale of 1 (flint) to 5 (completely dent). Only plants showing grain texture scores between 1.9 and 2.8 indicating high levels of flintiness were selected and advanced to the next cycle of selection. An open pollinated Quality Protein Maize (QPM) variety (Longe 5) was used as the source population from which S1 families and cycles C1 and C2 were derived.To start an S1 line (first selfed generation) recurrent selection, the source population was planted in isolation during the second rains of 2010 (2010B). During the first season of 2011 (2011A), 400 selfed progenies were evaluated ear-to-row. The progenies were of 2-row plots of 5m long each with spacing of 0.75m between rows, replicated twice. The recurrent S1 selection was conducted under artificial inoculation for turcicum leaf blight. Ten plants with desirable traits in each family were inoculated with turcicum infested sorghum seeds at V6-7 stage. The same cultural practices were followed for the S1 evaluation as discussed earlier. Half the seed was stored for recombination of selected S1 lines to make a source population for the next cycle as described by Hallauer and Martison. The recombination phase was carried out during the second rain season of 2011 (2011B) at

NaCCRI. This reconstituted a new population which was C1 of Longe 5. Individuals in subsequent cycles were not selfed due to time constraint instead in 2012A season, 200 families of isolation seed (C1 seed) were planted in isolation. Data was recorded on Days to silking (DTS), Days to Anthesis (DTA), Plant Height (PH), Ear Height (EH), Ear Aspect (EA), Disease severity and grain yield (GY).

Experimental layout of yield trial

For yield evaluation and other agronomic characteristics, full-sib families were formed by cross pollinating and the selected plants were used. Trials were laid out as a randomized complete block design with three replications. Each entry was planted in two rows. 5m long with spacing of 80cm between rows and 25cm between hills within rows.

Data collection

Disease development was monitored throughout the growth cycle, and the data was recorded. Downy mildew disease incidence and severity were scored twice after planting as infection takes place about three weeks after planting, based on visual assessment of the whole plot. Disease incidence was scored by recording the number of plants in each population showing DM symptoms and expressing that as a percentage of total plant population. Disease severity was scored on the whole plant as a proportion of total leaf area diseased using a rating scale of 1 to 5 where 1= no disease on leaves, 2 = lesions on lower leaves and no lesions on leaves above the ear, 3 = disease on most leaves and some lower leaves dead, 4 = dead lower leaves and many lesions on all leaves and ear, and 5 = nearly all the leaves are dead (CIMMYT, 2001).

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: $Y_{ijk} = \mu + \beta_i + g_j + e_{ijk}$, where μ is the general mean, β_i the effect of ith blocks, g_j the effect of jth genotype and e_{ij} the error associated with particular measurement.
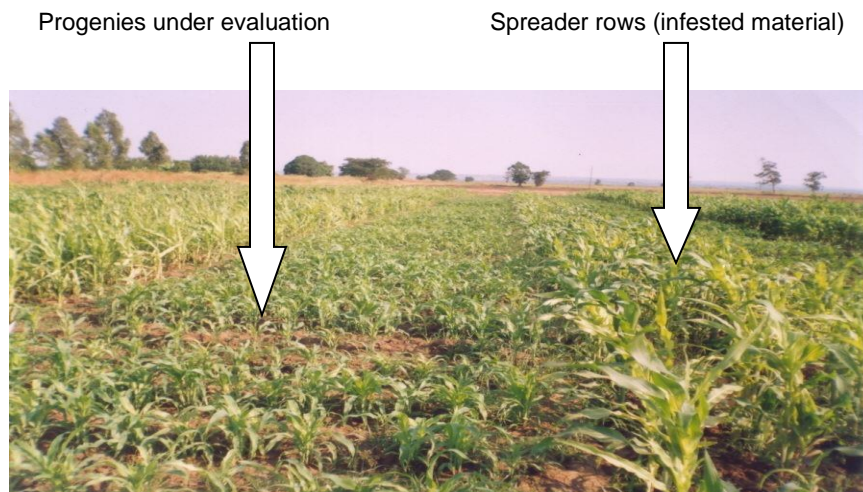
Figure 2 Downy mildew nursery planted at Umbeluzi ResearchStation in December 2005

Table 2 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	$\Sigma^2 e + \sigma^2 g$
Within genotypes	(r-1)(g-1)	$\Sigma(yij-yi.)^2$	M2	$\Sigma^2 e$
Total	(rg-1)			

Response to selection was determined using the following formula: $R = iH^2\sigma^2_P$ (Falconer, 1961), where i = selection intensity of 50 and 25%; H^2 = broad sense heritability; and σ^2_P = phenotypic variance.

Response to selection per cycle^{-1} was also calculated as the difference between cycles where appropriate (C2-C1).

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

Responses to selection per cycle^{-1} in C1 and C2 for all three QPM populations are presented in Table 3 as the difference between two cycles (C2-C1. Variances associated with differences among FS families in three QPM populations were highly significant (4, 5, and 6). Seed availability of C0 was not enough, but although C0 was evaluated it was necessary to be included to show the base population of the original study.

Downy Mildew

Downy mildew ratings for resistance showed a reduction in disease severity of 0.35 in Sussuma, 0.45 in ZM521Q, and 0.55 in Pop62SRQ per cycle (Table 3). The change from C1 to C2 had reduced the infection rate from 4.60 to 3.90 in Sussuma, from 3.00 to 2.10 in ZM521Q, and from 4.40 to 3.30 in Pop62SRQ (Table 3). Mean squares for downy mildew rating revealed highly significant variation (P≤0.01) among full-sib families in all QPM populations (Appendices 1, 2, and 3). Genetic variances for DM resistance increased from C1 to C2 from 0.069 to 0.119 in Sussuma; from 0.054 to 0.1442 in ZM521Q; and from 0.097 to 0.313 in Pop62SRQ (Tables 3.4, 3.5 and 3.6). Comparatively, higher heritability estimates were observed for DM resistance in C1 in Pop62SRQ (0.70) than Sussuma population (0.63) and ZM521Q (0.60) (Tables 3.4, 3.5 and 3.6).

In C2, higher heritability estimates for DM resistance were observed in Sussuma (0.76), followed by Pop 62SRQ (0.71), and ZM521Q (0.63) (Tables 4, 5, and 6). Genetic coefficients of variation (GCV) for DM resi-

Table 3 Means and response to selection for DM rating, yield and agronomic traits of different cycles of selection in three QPM populations

	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}	*LSD*
DM rating (1-5)	4.60	4.25	3.9	-0.35	1.2	3.0	2.75	2.30	-0.45	0.7	4.40	3.50	2.95	-0.55	*0.6*
Yield (t ha^{-1})	3.36	3.49	3.67	0.18	1.08	3.05	3.15	3.30	0.15	1.80	1.65	1.89	2.0	0.18	*0.67*
Plant height (cm)	147.2	145.6	145.1	-0.50	34.0	165.3	164.7	163.9	-0.70	44.7	152.1	150.9	150	-0.9	*22.0*
Ear height (cm)	64.3	63.7	62.8	-0.90	0.15	82.6	81.5	80.8	-0.70	0.44	76.2	75.4	74.9	-0.50	*0.29*
Days to 50% silking	64.6	62.2	60.3	-2.15	0.11	66.0	63.7	61.2	-2.50	0.13	71.0	68.8	65.8	-3.0	*0.17*
Days to 50% pollenshed	61.5	59.6	58.1	-1.5	0.09	62.5	60.6	59.7	-0.9	1.2	67.3	65.4	63.3	-2.1	*0.12*
Anth-Silk Interval (ASI)	3.1	2.6	2.2	-0.40	1.3	3.5	3.1	2.1	-1.0	2.0	3.7	3.4	2.5	-0.90	*1.6*
Ear per plant	1.07	1.11	1.15	0.04	1.1	0.88	0.93	1.06	0.13	0.9	1.06	1.08	1.16	0.08	*1.3.*
Grain moisture (%)	15.60	17.40	14.90	-2.50	1.4	15.20	17.30	14.90	-2.40	5.9	15.50	15.70	14.87	-0.83	*1.5*
Grain Texture (1-5)	*2.7*	*2.1*	*1.4*	*-0.70*	*0.8*	*2.9*	*2.1*	*1.8*	*-0.30*	*0.8*	*2.5*	*2.1*	*1.7*	*-0.40*	*0.5*

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

Table 4 Estimated variance components of the SUSSUMA population 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
Downy Mildew	0.069	0.046	0.63	0.119	0.051	0.76
Yield	0.561	0.131	0.69	0.667	0.135	0.72
Plant height	206.9	30.10	0.91	361.8	31.30	0.94
Ant-silking Interv (ASI)	0.443	0.054	0.72	0.559	0.260	0.85
Grain moisture	1.965	0.876	0.60	3.504	1.250	0.86

Table 5 Estimated variance components of the ZM 521 Q populations 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
Downy Mildew	0.054	0.032	0.60	0.1442	0.1019	0.63
Yield	0.337	0.179	0.78	1.790	0.184	0.90
Plant height	96.73	34.70	0.79	176.1	36.93	0.84
Ant-silking Interv (ASI)	0.158	0.118	0.66	0.561	0.090	0.89
Grain moisture	2.210	1.480	0.71	2.258	3.140	0.79

stance changed less in Sussuma than in Pop62SRQ with advances in selection. The increase in genetic covariance (Covg (FS-S1) for yield from C1 to C2 was more pronounced in ZM521Q and Pop 62SRQ (Table 7).

Grain yield

The gain per cycle was 180 kg in Sussuma, 150 kg in ZM521Q and 180 kg in Pop62SRQ (Table 3). Mean squares for grain yield among full-sib families was highly significant (P≤0.01) in C2 of all populations (Appendices 1, 2, and 3). Similarly heritability estimates were highest in ZM521Q (0.90) in C1, and lowest in Sussuma (0.72) (Table 4, 5 and). Genetic variances for grain yield increased from 0.561 to 0.667 in Sussuma; from 0.337 to 1.790 in ZM521Q; and from 0.944 to 2.699 in Pop62SRQ (Tables 4, 5, and 6) with selection. Genetic coefficients

of variation (GCV) for yield changed very little from C1 to C2 in Sussuma whereas in Pop62SRQ GCV were approximately four times higher in C2 compared to values in C1 (Tables 7). More pronounced increase in genetic covariance (Covg (FS-S1) for yield was found in ZM521Q and Pop62SRQ from C1 to C2 (Table 7). Using a selection of intensity of 50 % in C1 and 25 % in C2 the response to selection was 0.50 in C1 and 0.88 in C2 for Sussuma, 0.41 in C1 and 1.61 in ZM521Q and 0.64 in C1 and 1.87 in C2 for Pop62SRQ population (Table 8).

Plant height

The gains per cycle were negligible in all their populations, Sussuma, ZM521Q and in Pop62SRQ (Table 3). Mean squares (Appendices 1, 2 and 3) were

Table 6 Estimated variance components of the Pop 62 SRQ population related to the different agronomic traits in cycles C1 and C2

| | Pop 62 SRQ | | | | | |
| | C1 | | | | C2 | |
Traits	σ^2_g	Se	H^2	σ^2_g	Se	H^2
Downy Mildew	0.097	0.135	0.70	0.313	0.046	0.71
Yield	0.944	0.618	0.68	2.699	0.610	0.81
Plant height	185.6	55.00	0.74	581.3	89.80	0.92
Ant-silking Interv (ASI)	2.120	1.040	0.55	2.466	0.407	0.69
Grain moisture	0.725	0.537	0.65	5.986	0.731	0.76

Table 7 Genetic parameter estimates for FS families of the three QPM populations on cycles C1 and C2

	YIELD					
	SUSSUMA		ZM521Q		Pop62SRQ	
	C1	C2	C1	C2	C1	C2
Parameter	FS	FS	FS	FS	FS	FS
GCV	21.46	22.25	18.43	40.54	52.51	82.14
σ^2_G	0.561	0.667	0.337	1.79	0.944	2.699
Covg(FS-S1)	34.89	38.43	15.88	59.45	60.36	116.2
H^2	0.69	0.72	0.78	0.9	0.68	0.81

significant (P≤0.01) for plant height in all three QPM populations.. Mean square for C2 was significant (P≤0.01) in ZM521Q but not significant in Sussuma and Pop62SRQ (Appendices 1, 2 and 3. Heritability estimates were 0.91 in C1 and 0.94 in C2 for Sussuma, 0.74 in C1 and 0.92 in C2 for Pop62SRQ, and 0.79 in C1 and 0.89 in C2 in ZM521Q. Genetic variances for plant height showed an increase from C1 to C2 from 206.9 to 361.8 in Sussuma, from 96.37 to 176.1 in ZM521Q, and from 185.6 to 581.3 in Pop62SRQ (Tables 4, 5 and 6).

GCV = Genetic coefient of variation; Covg = genetic covariance; σ 2G = genetic variance; H2 = broad-sense heritability;

Anthesis-Silking Interval (ASI)

The gain per cycle for ASI reduced by 3.5% in Sussuma 3.0% in ZM521Q and 3.4% in Pop62SRQ (Table 3). Mean square among full-sib families for ASI was significant in Sussuma but not in ZM521Q and Pop62SRQ (Appendices 1, 2, and 3). Heritability estimate for Sussuma were 0.72 in C1 and 0.85 in C2, 0.66 in C1 and 0.89 in C2 in ZM521Q, and 0.55 in C1 and 0.69 in Pop62SRQ (Tables 4, 5, and 6). The invcreas in genetic variances for ASI was small in Sussuma but was large in ZM521Q (Tables 4, 5, and 6).

Grain Moisture

Selection reduced grain moisture by 4.78 % in Sussuma, 4.90 % in ZM521Q and 4.79 % in Pop62SRQ (Table 3). Mean squares for grain moisture among full-sib families was significant in all populations (Appendices 1, 2 and 3). Heritability estimates were 0.60 in C1 and 0.86 in C2 for Sussuma, 0.71 in C1 and 0.79 in C2 for ZM521Q, and 0.65 in C1 and 0.76 for C2 Pop62SRQ (Tables 4, 5 and 6). Genetic variances for grain moisture increased from 1.965 in C1 to 3.504 in C2 for Sussuma, from 2.210 in C1 to 2.258 in C2 for ZM521Q; and from 0.725 in C1 to 5.986 in C2 for Pop62SRQ (Tables 4, 5 and 6).

Table 8 Response to selection for yield in three QPM populations in C1 and C2

	Yield					
	Sussuma		ZM521Q		Pop62SRQ	
	C1	C2	C1	C2	C1	C2
I	0.798	1.271	0.798	1.271	0.798	1.271
H^2	0.69	0.72	0.78	0.90	0.68	0.81
σ_P	0.9018	0.9638	0.6555	1.4071	1.1778	1.8209
RS	0.50	0.88	0.41	1.61	0.64	1.87

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

Table 9 Genetic parameter estimates for FS families of the three QPM populations

	Downy Mildew					
	SUSSUMA		ZM 521 Q		Pop 62 SRQ	
	C1	C2	C1	C2	C1	C2
Parameter	FS	FS	FS	FS	FS	FS
GCV	6.21	8.83	8.78	16.51	8.55	16.96
σ^2_G	0.069	0.118	0.054	0.144	0.097	0.313
Covg(FS-S1)	5.26	5.96	4.36	10.9	5.64	18.81
H^2	0.63	0.76	0.6	0.63	0.7	0.71

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

Table 10 Response to selection in Downy Mildew on three QPM populations in C1 and C2

	Downy Mildew					
	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	0.63	0.76	0.6	0.63	0.7	0.71
σ_P	0.334	0.394	0.299	0.48	0.37	0.668
RS	0.17	0.38	0.14	0.38	0.21	0.6

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

Correlation Coefficients

In Sussuma significant correlation were observed between DM and ASI, and grain yield with ears per plant and grain moisture. Plant height was also significantly correlated with ears per plant and grain moisture. Grain texture exhibited high correlation with grain moisture (Table 11). In ZM521Q correlations were shown between DM with ear per plant and plant height with grain yield (Table 3.12). In Pop62SRQ, DM exhibited high correlation with ASI, and grain texture was correlated with

Table 3.11 Correlations coefficients among measured parameters of Sussuma population in C2

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	0.357*						
Ear per Plant	-0.06	0.043					
Grain Moisture	0.113	-0.295	0.229*				
Grain Texture	0.099	0.015	-0.113	0.1730*			
Grain Yield	-0.19	-0.533	0.287*	0.4380**	-0.196		
Plant Height	0.068	0.209	0.222*	0.2510*	-0.157	0.181	

Table 12 Correlations coefficients among measured parameters of ZM521Q population in C 2

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	-0.1100						
Ear per Plant	-0.0800	0.2020*					
Grain Moisture	0.0180	-0.1210	-0.2440				
Grain Texture	0.0550	0.2610*	-0.0350	-0.0180			
Grain Yield	0.0690	-0.1640	-0.1200	-0.0420	0.0740		
Plant Height	0.1000*	-0.1440	0.0460	0.0350	0.0090	0.3440*	

Table 13 Correlations coefficients among measured parameters of Pop62SR1Q population in C 2

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	0.275*						
Ear per Plant	-0.060	-0.143					
Grain Moisture	0.186	-0.145	-0.0100				
Grain Texture	0.026	-0.304	-0.0230	0.2810*			
Grain Yield	0.102	-0.491	0.1540	0.1230	0.2330*		
Plant Height	0.003	-0.014	0.0650	0.0250	0.1000	-0.0130	

grain moisture. Grain yield showed high correlation with grain texture (Table 3.13).

DISCUSSION

Sussuma

Analyses of variance of FS in Sussuma population indicated highly significant variations among progenies.These variations could be useful for effective selection against DM resistance. A survey of the literature indicates that there are few previous studies of recurrent selection for DM resistance in QPM, most of the previous studies were conducted with normal maize. In the current study, two cycles of recurrent selection for DM resistance significantly reduced the infection rates from 4.6 to 3.9 (1.0 to 5.0 scale) in Sussuma. Moderate temperature (15-32°C) and high humidity favour infection of DM (Denic *et al.,* 2001). The incidence of this disease is always high in southern part of Mozambique where such conditions areprevalent (Denic, 1994). An increase in genetic variance and heritability estimates for DM from C1 to C2 were observed in this population. This was probably due to the large number of S1 progenies advanced to the next cycle. The more 500 S1s advanced for inter-mating could have maximized panmixis. This is consistent with the finding of Denic et al. (1997) who observed that DM was highly heritable and not very complex to score. These authors concluded that screening of advanced lines

should be sufficient to identify DM resistance in a maize breeding programme. Previously, Ajala (1992) found additive gene action being important in controlling resistance against DM.. Nair et al. (2004) also reported that DM resistance is multi-genic and controlled by many partially dominant genes.

Data on disease spread indicated that after two cycles of recurrent selection, the reduction in disease severity per cycle was 4.24 % in Sussuma. These findings are in conformity with those reported by De Leon et al. (1993), who observed reduction in the severity of downy mildew infection in advanced cycles of recurrent selection in maize populations. He also documented significant progress in levels of downy mildew resistance (-1.1.0 %) with correspondent increase in grain yield (507 kg ha^{-1}) in four maize populations after conducting three cycles of S1 recurrent selection.

Mean square values for grain yield were highly significant (P≤ 0.01) for cycles and high correlation was observed between DM and number of ears per plant. It could be argued that improvement in grain yield was related with increased resistance to DM. Ceballos et al. (1991) reported similar relationship between disease resistance and higher grain yield. Heritability estimates for grain yield were high indicating that an improvement would be achieved from field selection for grain yield. These results were similar to those of Abedon and Tracy (1998), who reported very close correspondence of expected and observed responses (446 vs. 421 kg ha^{-1}) after two cycles of S1 recurrent selection in a high yielding maize synthetic variety. Recurrent selection significantly (P≤ 0.01) increased grain yield in Sussuma from 3.49 to 3.67 t ha^{-1}. This response of Sussuma population could be a possible manifestation of its increased resistance to DM as observed in the present study.

Grain yield increased by 180 kg ha^{-1} (4.73 %) per cycle in Sussuma. Highly significant increase in grain yield (507 kg cycle^{-1}) in four populations was revealed by De Leon et al. (1993), after three cycles of S1 recurrent selection for downy mildew resistance. Ceballos et al. (1991) reported 19 % gain cycle^{-1} in early and 7 % gain cycle^{-1} in intermediate populations for grain yield under disease pressure. Similarly, Weyhrich et al. (1998) experienced significant increase in grain yield in the BS 11 maize population. They reported selection of intensity 110 and 220 kg ha^{-1} gains cycle^{-1} after out four cycles of progeny selection with 10 % and 30 % respectively.

Analysis of variance of full-sib progenies indicated the presence of highly significant (P≤0.01) genetic variation in Sussuma for days to tasseling, silking and pollen shedding. These results suggested that despite high genetic variability among S1 lines, they were indeed highly consistent in performance over the two cycles of S1 line recurrent selection. These results are in agreement with those of De Leon et al. (1993), who reported significant differences for maturity in four tropical

maize populations implementing S1-S2 line recurrent selection for downy mildew resistance. Abedon and Tracy (1998), observed significant variations for mid-silking and mid-pollen shedding using recurrent selection for rust resistance in three sweet corn populations. Using full-sib recurrent selection for northern corn leaf blight disease resistance in subtropical maize populations, Ceballos et al. (1991) reported a significant decrease in maturity parameters.

The reduction in days to silking and pollen shed per cycles in Sussuma were 3.1 to 2.2. Johnson et al. (1986) reported early flowering with a 4.4% increase in grain yield cycle^{-1} after conducting 15 cycles of full-sib recurrent selection in one lowland tropical maize population, Tuxpeno Crema1.

ZM521Q and Pop62SRQ

Populations ZM521Q and Pop62SRQ showed similar responses as Sussuma population. Populations ZM521Q and Pop62SRQ showed highly significant variations among progenies. Downy mildew (DM) resistance rating was significantly reduced from 3.0 to 2.1 after two cycles of recurrent selection, while in Pop62SRQ the DM infection rate was reduced from 4.40 to 3.30. In both populations increases in genetic variances and heritability estimates were observed for DM from C1 to C2.

These findings are in conformity with those reported by Ajala (1992). The reduction in disease severity per cycle was 3.5 % in ZM521Q, and 3.75 %, in Pop62SRQ after two cycles. De Leon et al. (1993) also observed reduction in the severity of downy mildew infection in advanced cycles of recurrent selection in maize populations.

Highly significant correlations coefficients between grain yield and grain moisture; grain yield and ASI were observed in Pop62SRQ, while in ZM521Q highly significant correlations were detected among DM and plant height. These findings are in conformity with those reported by Ceballos et al. (1991) who observed similar association between disease resistance and higher grain yield. The grain yield increase after two cycles of recurrent selection was from 3.05 to 3.30 t ha^{-1} for ZM521Q, and from 1.65 to 2.0 t ha^{-1}. The increase in yield cycle^{-1} was 150 kg ha^{-1} in ZM521Q and 180 kg ha^{-1} in Pop62SRQ. Ceballos et al. (1991) reported 19 % gain cycle^{-1} in early and 7 % gain cycle^{-1} under intermediate disease pressure trials for grain yield in maize populations.

Days for ASI reduced per cycles in ZM521Q and in Pop62SRQ. For silking and pollen shedding in Pop62SRQ the days reduced from 3.7 to 2.5, while in ZM521Q days reduced from 3.5 to 2.1. Johnson et al. (1986) reported early flowering with a 4.4% increase in grain yield cycle^{-1} after conducting 15 cycles of full-sib recurrent selection in one lowland tropical maize population, Tuxpeno Crema1.

CONCLUSIONS

Two cycles of S1 recurrent selection significantly improved DM 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 DM resistance and other important characteristics generally increased or remained unchanged which was important for future continued selection within these populations. The objective of the Mozambican maize programme is to improve the nutritionally enhanced populations for DM resistance and other desirable characteristics. The germplasm generated so far in this work lays a firm foundation to achieve this objective.

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Appendix 1 Means of DM, grain yield and secondary traits of Full-Sib families of Sussuma population in cycle two

Entry Sussuma C 2	Downy Midew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
	(1-5)	t ha^{-1}	Rank	D	Cm	#	%
		Bottom Ten					
15	2.3	1.70	30	3.4	130.4	1.11	14.3
6	3.4	2.70	29	2.4	130.1	1.01	14.0
9	1.5	2.83	28	3.3	125.2	1.07	14.3
14	2.3	3.03	27	4.3	132.0	1.05	16.2
27	3.8	3.13	26	2.7	129.7	1.03	13.8
26	3.1	3.15	25	2.9	156.6	1.02	17.1
8	1.1	3.16	24	2.6	130.3	1.00	14.0
22	2.6	3.20	23	2.9	119.7	1.01	13.6
22	1.8	3.20	23	2.9	119.7	1.01	13.6
2	3.2	3.27	22	2.6	147.6	1.01	15.0
		Top Ten					
17	2.8	5.07	1	2.1	174.7	1.06	15.4
4	1.9	4.78	2	3.9	155.5	1.14	14.0
12	2.1	4.75	3	4.2	148.8	0.96	14.0
19	2.0	4.58	4	2.6	151.1	0.97	14.6
3	1.8	4.57	5	2.9	172.8	1.12	13.7
13	2.1	4.33	6	2.0	155.6	1.10	14.6
25	3.8	4.30	7	3.7	145.8	1.05	13.6
30	1.5	4.28	8	2.9	150.0	1.04	15.3
29	3.0	4.02	9	3.4	141.2	1.07	14.7
28	1.7	3.80	10	2.7	159.3	0.86	14.7
Mean	3.9	**3.67**		**2.2**	**145.1**	**1.15**	**14.9**
LSD (0.05)	3.3	**1.08**		**1.3**		**0.15**	**1.4**
Mse	4.3	**0.58**		**0.7**	**195.3**	**0.01**	**0.8**
CV	3.6	**20.75**		**27.2**	**9.6**	**8.94**	**6**
P	3.2	**0**		**0.045**		**0.17**	**0**
P	2.9	***		*	Ns	Ns	***
Min	2.5	**1.7**	**1**	**2**	**119.7**	**0.86**	**13.4**
Max	2.9	**5.07**	**30**	**4.3**	**174.7**	**1.14**	**17.1**
StandardError	0.6	0.53		0.7	9.6	0.07	0.7

Appendix 2 Means of DM, grain yield and secondary traits of full-sib families of ZM521Q population in cycle two

Entry	Downy Mildew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
ZM 521 Q C 2							
	(1-5)	t ha⁻¹	Rank	d	Cm	#	%
		Botton ten					
12	4.1	1.55	142	1.9	163.0	0.48	23.2
30	3.8	1.58	141	2.0	150.2	0.93	21.7
38	3.6	1.13	145	2.8	127.4	0.54	22.7
44	3.5	0.80	146	1.5	154.5	1.45	23.1
49	3.4	1.72	139	2.6	165.4	0.79	25.4
83	3.4	1.25	144	2.1	160.8	0.86	18.7
102	3.3	1.79	138	3.0	159.5	1.16	17.6
121	3.2	1.66	140	2.5	153.0	0.86	26.7
122	3.1	1.52	143	2.7	133.5	0.81	21.1
2	3.0	1.81	136	2.5	186.3	0.73	20.6
		Top ten					
32	2.3	5.05	5	3.1	177.3	1.07	20.9
123	2.4	5.16	4	2.5	174.6	1.17	22.8
133	2.4	5.34	3	2.4	156.5	0.88	23.7
134	2.5	4.98	7	3.5	161.5	0.98	27.1
135	2.5	5.03	6	2.5	199.6	0.91	25.6
136	2.6	4.90	10	2.0	182.3	0.91	23.0
138	2.7	4.95	8	2.0	142.2	0.95	24.7
142	2.8	5.37	2	3.0	141.3	0.93	26.9
145	2.9	4.91	9	1.3	186.6	0.99	21.6
148	2.9	6.05	1	2.0	120.2	0.94	19.6
Mean	**2.30**	**3.30**	**73**	**2.1**	**153.9**	**1.06**	**14.90**
LSD (0.05)	**0.7**	**1.80**	**42**	**2.0**	**44.7**	**0.44**	**5.9**
Mse	**0.2**	**0.83**		**1.1**	**557.2**	**0.05**	**8.6**
CV	**14.6**	**27.63**		**42.9**	**14.4**	**23.08**	**12.9**
P	**0.005**	**0.000**		**0.883**	**0.013**	**0.303**	**0.015**
P	******	*******		ns	*****	Ns	*****
Min	**2.3**	**0.80**	**1**	**-2.0**	**120.2**	**0.48**	**15.0**
Max	**4.1**	**6.05**	**146**	**4.0**	**210.5**	**1.45**	**28.6**
StandardError	0.3	0.91		1.0	22.6	0.22	3.0

Appendix 3 Means of DM, grain yield and secondary traits of full-sib families of Pop62SRQ population in cycle two

Entry	Downy Mildew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
Pop 62SRC 2							
	(1-5)	t ha^{-1}	Rank	D	Cm	#	%
		Bottom Ten					
15	2.7	1.10	30	3.7	154.0	1.30	25.8
21	3.2	1.31	29	2.2	142.9	1.06	20.7
30	3.5	1.34	28	3.3	141.9	0.99	24.9
17	4.0	1.45	27	1.4	142.5	1.19	25.2
6	4.2	1.57	26	3.4	145.9	1.15	20.4
2	2.9	1.75	25	3.0	146.5	1.14	23.1
10	3.3	1.76	24	2.0	143.6	1.31	23.3
24	4.6	1.76	23	2.4	159.4	0.98	27.4
9	3.2	1.78	22	2.0	156.5	1.37	22.6
12	3.7	1.91	21	2.6	160.7	1.10	26.2
		Top Ten					
22	0.7	2.77	1	2.3	164.1	1.23	21.3
29	1.7	2.72	2	1.7	161.7	1.44	20.4
14	1.9	2.70	3	3.3	151.3	1.07	27.5
18	1.6	2.49	4	2.4	162.6	0.96	26.3
16	2.2	2.40	5	2.3	148.6	1.15	28.1
11	1.8	2.33	6	2.3	126.4	1.03	25.8
8	2.3	2.28	7	2.0	145.2	1.10	23.1
7	2.1	2.28	8	2.3	153.9	0.93	20.3
27	1.8	2.28	9	2.7	143.1	1.29	23.2
23	1.9	2.20	10	2.3	156.9	1.21	25.6
Mean	**2.95**	**2.00**		**2.5**	**150.0**	**1.16**	**14.87**
LSD (0.05)	**0.6**	**0.67**	**9**	**1.6**	**22.0**	**0.29**	
MSe	**0.1**	**0.25**		**0.9**	**273.6**	**0.03**	**5.7**
CV	**13.5**	**25.05**		**38.4**	**11.0**	**15.64**	**9.9**
P	**0.000**	**0.000**		**0.329**	**0.067**	**0.084**	
P	*****	*****		**Ns**	**+**	**+**	**Ns**
Min	**0.7**	**1.10**	**1**	**1.4**	**126.4**	**0.93**	**20.3**
Max	**4.6**	**2.77**	**30**	**3.7**	**164.1**	**1.44**	**28.1**
StandardError	0.3	0.33		0.8	10.7	0.14	2.0

Appendix 4 Means of DM, grain yield and secondary traits of Full-Sib families of Sussuma population in cycle one

Entry	Downy Mildew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
SUSSUMA C1							
	(1-5)	t ha^{-1}	Rank	d	Cm	#	%
		Botton ten					
12	4.8	1.97	18	2.6	150.7	1.07	18.5
30	4..6	2.37	25	3.2	158.3	1.08	18.3
38	4.5	2.46	22	3.6	156.4	1.00	18.3
44	4.0	2.66	13	2.0	155.5	1.01	17.9
49	4.4	2.73	19	2.2	157.3	1.00	17.8
83	4.2	2.74	10	2.3	158.8	1.19	17.6
102	4.3	2.76	27	2.7	153.9	1.07	17.3
121	4.5	2.77	21	2.4	161.4	1.00	17.1
122	4.1	3.05	11	3.6	156.5	1.00	17.0
2	4.3	3.07	24	3.0	161.5	1.05	16.9
		Top Ten					
32	3.8	3.35	15	1.9	161.5	1.09	17.5
123	3.6	3.37	14	3.0	153.5	1.00	17.6
133	3.7	3.48	7	2.2	155.1	1.10	17.8
134	3.7	3.49	26	2.8	153.0	1.08	17.6
135	3.8	3.52	29	1.2	148.2	1.00	17.5
136	3.6	3.60	17	1.5	156.3	1.11	16.9
138	3.8	3.62	28	3.3	151.3	1.00	16.8
142	3.7	3.66	23	2.8	160.5	1.04	17.0
145	3.6	3.77	8	3.4	162.9	1.03	16.9
148	3.7	4.17	30	1.9	156.9	1.01	17.2
Mean	4.25	**3.49**		2.6	**145.6**	1.11	17.40
LSD (0.05)	3.3	**1.00**		2.9	**16.0**	0.14	27.2
Mse	4.3	**0.45**		3.8	**150.4**	1.00	24.3
CV	22.5	**21.27**	6	3.2	**7.9**	1.05	24.7
P	3.2	**0.005**	12	2.1	**0.449**	1.22	29.2
P	2.9	**	2	3.5	ns	1.01	26.7
Min	3.6	**1.97**	4	2.0	**144.0**		24.1
Max	4.9	**4.17**	3	1.9	**164.1**	1.05	
StandardError		**3.14**			155.6	0.14	24.9

Appendix 5 Means of DM, grain yield and secondary traits of Full-Sib families of ZM521Q population in cycle one

Entry ZM521Q C1	Downy Mildew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
	(1-5)	t ha^{-1}	Rank	d	Cm	#	%
		Botton ten					
12	3.8	0.97	30	2.6		1.01	16.1
28	3.5	1.01	29	2.1	145.9	1.12	17.5
38	3.5	1.01	28	1.7	145.9	1.03	17.8
39	3.4	1.12	27	3.0	140.2	0.97	17.8
42	3.3	1.16	26	2.3	153.0	1.01	18.6
57	3.3	1.23	25	2.4	158.8	1.01	16.5
88	2.9	1.29	24	1.8	147.8	0.97	17.1
123	2.8	1.39	23	2.0	160.2	1.05	18.7
135	2.7	1.42	22	1.5	152.8	1.00	18.6
144	2.6	1.58	21	2.7	160.0	1.03	18.9
32	2.8	2.47	1	1.7	147.5	0.94	18.6
96	2.9	2.46	2	2.3	160.8	1.13	16.8
113	2.5	2.19	3	1.8	154.5	1.08	16.3
124	2.3	2.15	4	1.6	155.0	1.10	19.1
129	2.5	2.15	5	2.6	166.6	1.03	18.5
135	2.4	2.08	6	2.7	152.9	0.98	21.4
138	2,5	2.02	7	2.4	163.7	0.98	17.2
141	2.6	2.01	8	2.1	164.3	1.08	16.9
143	2.3	1.89	9	2.4	166.7	1.30	16.5
145	2.7	1.87	10	2.2	148.4	1.17	17.0
Mean	**2.75**	**3.15**	**37**	**3.1**	**146..7**	**0.93**	**17.30**
LSD (0.05)	**3.0**	**0.78**	**38**	**2.7**	**2.3**	**1.03**	**15.7**
Mse	**3.1**	**0.25**	**42**	**2.9**	**2.0**	**1.03**	**16.5**
CV	**2.8**	**28.82**	**41**	**2.3**	**60.2**	**1.11**	**16.5**
P	**2.9**	**0.003**	**30**	**2.5**	**0.716**	**0.97**	**19.0**
P	**2.7**	******	**22**	******	**ns**	**0.99**	**18.6**
Min	**2.3**	**0.97**	**31**	**0.97**	**0.7**	**0.99**	**20.0**
Max	**3.0**	**2.47**	**36**	**2.47**	**3.8**	**0.96**	**24.2**
StandardError	3.0	**1.73**	14	**1.73**	**2.4**	1.20	17.0

Appendix 6 Means of DM, grain yield and secondary traits of Full-Sib families of Pop62SRQ population in cycle one

Entry	Downy Mildew	Grain Yield	Rank	ASI	Plant Height	Ears/ Plant	Grain Moist
Pop62SRQC1							
	(1-5)	t ha^{-1}	Rank	d	Cm	#	%
		Botton ten					
15	4.7	1.10	30	3.7	154.5	1.00	17.1
21	4.6	1.31	29	2.2	160.8	1.18	16.0
30	4.3	1.34	28	3.3	166.0	0.87	17.4
17	4.3	1.45	27	1.4	147.5	1.02	16.9
6	4.1	1.57	26	3.4	152.9	1.00	18.1
2	4.0	1.75	25	3.0	154.5	0.97	16.8
10	4.0	1.76	24	2.0	151.9	1.31	14.4
24	4.0	1.76	23	2.4	156.1	1.12	18.1
9	3.8	1.78	22	2.0	152.8	1.14	16.2
12	3.6	1.91	21	2.6	149.1	1.22	15.0
22	2.5	2.77	1	2.3	159.7	1.20	15.5
29	2.6	2.72	2	1.7	155.0	0.97	15.8
14	2.8	2.70	3	3.3		0.93	14.8
18	2.9	2.49	4	2.4	164.3	1.31	15.1
16	3.0	2.40	5	2.3	157.6	1.21	19.6
11	3.0	2.33	6	2.3	161.1	0.93	17.4
8	3.1	2.28	7	2.0	149.8	1.08	15.1
7	3.2	2.28	8	2.3	153.0	1.12	14.0
27	3.3	2.28	9	2.7	148.4	0.95	15.0
23	3.5	2.20	10	2.3	163.7	1.38	15.4
Mean	3.50	1.89	16	3.4	150.9	1.08	15.70
LSD (0.05)	1.3	0.67	9	2.3	13.1	0.42	4.5
Mse	0.6	0.25		2.0	68.6	0.06	8.2
CV	33.5	25.05		60.2	5.3	22.86	10.6
P	0.118	0.000		0.716	0.000	0.273	0.153
P	ns	***		ns	***	ns	Ns
Min	1.1	1.10	1	0.7	136.6	0.87	24.0
Max	3.5	2.77	30	3.8	166.7	1.49	29.8
StandardError		2.00		2.4	2.5		

Appendix 7 Correlations coefficients among measured parameters of Sussuma population in C 1

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	-0.1200						
Ear per Plant	-0.0700	-0.0220					
Grain Moisture	0.0380	-0.1280	-0.4330				
Grain Texture	0.0430	0.02860	-0.2350	0.2800*			
Grain Yield	0.0690	-0.1454	0.1200*	-0.4200	0.0540		
Plant Height	0.0750	-0.1360	0.0460	0.3500	0.0190	0.0440	

Appendix 8 Correlations coefficients among measured parameters of ZM521Q population in C 1

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	0.247*						
Ear per Plant	-0.08	-0.436					
Grain Moisture	0.031	-0.159	0.122*				
Grain Texture	0.056	0.067	-0.213	-0.1300			
Grain Yield	-0.39	-0.853	0.187*	0.2380*	-0.167		
Plant Height	0.058	0.0210	0.067	-0.2510	-0.159	0.0198	

Appendix 9 Correlations coefficients among measured parameters of Pop62SR1Q population in C 1

	ASI	Downy Mildew	Ear per Plant	Grain Moisture	Grain Texture	Grain Yield	Plant Height
ASI							
Downy Mildew	-0.0285						
Ear per Plant	-0.060	-0.234					
Grain Moisture	0.0186	0.0154	-0.0100				
Grain Texture	0.026	-0.340	-0.0230	0.1320*			
Grain Yield	0.0102	0.091	0.1540	0.02810	0.3240*		
Plant Height	0.003	-0.136	0.0650	0.0520	0.1000	-0.0230	