

PERFORMANCE OF THREE-WAY CROSS HYBRIDS FOR AGRONOMIC TRAITS AND RESISTANCE TO MAIZE STREAK VIRUS DISEASE IN KENYA

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ABSTRACT

Maize Streak virus (MSV) disease is a major disease in many parts of Africa, and is the most important viral pathogen of maize in Kenya. A study was conducted in 2004 to evaluate the agronomic performance and maize streak virus (MSV) resistance of maize (*Zea mays* L.) three-way crosses developed in Kenya. Twenty hybrids and one check were grown under normal conditions in a randomised complete block design, in two replications at Embu, 1540 masl; and Muguga, 2093 masl). In a parallel trial in Muguga, hybrids were also evaluated in two replications under artificial inoculation with MSV. The analyses of variance combined across environments showed significant differences ($P < 0.05$) among genotypes for grain yield, days to 50% pollen shed, days to mid-silk and ear height. Genotype x environment interaction was significant ($P < 0.01$) for grain yield and days to mid-silk, indicating some hybrids were more adapted in some environments. Grain yield for MU03-025 (10.04 t ha⁻¹) was significantly better ($P < 0.05$) than the check, H513 (7.53 t ha⁻¹). In the disease inoculated experiment, the best hybrids for disease resistance were MU03-012 and MU03-006 (score of 1.75), while H513 had a mean score of >3.0. The highest yielding hybrid under disease inoculation, MU03-026 showed yield gain of 5.2 t ha⁻¹ above that of H513. The results indicate adoption of disease resistant hybrids would result in a higher maize yields in the mid-altitude areas of Kenya.

Key Words: Genotype x environment, mid-altitude, *Zea mays*

RÉSUMÉ

La maladie à virus du maïs strié (MSV) est une affection importante dans plusieurs régions africaines et représente le pathogène viral le plus visible pour le maïs au Kenya. Une étude a été conduite en 2004 dans le but d'évaluer la performance agronomique et la résistance au virus du maïs strié (MSV) dans le maïs (*Zea mays* L.) par croisement triple réalisé au Kenya. 20 hybrides et un contrôle étaient plantés sous conditions normales dans une conception de bloc aléatoire complet en deux replications à Embu, 1540 masl ; et Muguga, 2093 masl. Dans une étude parallèle menée à Muguga, des hybrides étaient également évalués en 2 replications sous inoculation artificielle au MSV. L'analyse de variances combinées à travers les environnements a montré des différences significatives ($P < 0,05$) au sein de génotypes quant au rendement en grain, jours à 50% de couverture pollinique, jour à mi-soie et hauteur d'oreilles. L'interaction génotype x environnement était significatif ($P < 0,01$) concernant le rendement de grain et jours à mi-soie, démontrant une adaptation accrue de certains hybrides à certains environnements. Le rendement de grains pour MU03-025 (10,04 t ha⁻¹) était significativement ($P < 0,005$) meilleur que celui du contrôle H513 (7,53 t ha⁻¹). Dans l'expérience par inoculation de la maladie, les meilleurs hybrides pour leur résistance à la maladie étaient MV03-012 & MV03-006 (Score de 1,75) pendant que H513 présentait un score moyen >3,0. L'hybride à plus haut rendement sous inoculation de la maladie MV 03-026, présentait un rendement de grain de 5,2 t ha⁻¹ au dessus de celui de H513. Les résultats indiquent que l'adoption d'hybrides résistants à la maladie se solderait par des rendements élevés de maïs dans les régions de moyenne altitude au Kenya.

Mots Clés: Génotype x environnement, altitude moyenne, *Zea mays*

INTRODUCTION

Maize Streak virus (MSV) disease is a major disease in many parts of Africa, and is the most important viral pathogen of maize in Kenya (Macleod *et al.*, 2001). MSV causes yield losses between 40-100 percent, an equivalent loss of close to 1 million metric tonnes per *annum* for Kenya (ISAAA *Briefs*, No. 16, 1999). This is a distressing loss considering that maize is a staple food for over 90% of the population in Kenya.

There are six major agro-ecological zones (mainly based on temperatures and rainfall patterns) for maize production in Kenya that were defined by a study conducted by the Kenya Agricultural Research Institute (KARI) and the International Maize and Wheat Improvement Centre (CIMMYT) (Hassan, 1998). Maize streak disease epidemics have been frequent in the mid-altitude ecologies of Kenya since 1988 (Njuguna *et al.*, 1990). There is evidence that MSV is prevalent in Central Kenya, which, comprise a large part of the mid-altitude ecology (Louie, 1980). Njuguna (1996) found that incidences MSV disease were highest (54%) in Central Kenya. Moreover, in a recent survey conducted among small-scale farmers in Kenya in 2004 has shown that maize yields are significantly reduced by MSV in mid-altitude areas of Kenya (KARI, 2004). Yet, the incidences show that maize varieties grown by farmers are genetically vulnerable to MSV.

Maize streak disease is characterised by chlorotic stripes on the leaves that contribute to reduction of photosynthetic tissue depending on disease severity. Loss in yield is more serious when infection occurs at seedling stage (Efron *et al.*, 1989). Although MSV can be indirectly controlled by use of chemicals on the vector and by use of cultural practices, developing maize streak disease resistant varieties is the most cost-effective control option affordable by the risk-prone, resource-poor farmers in Kenya (KARI, 1990; Gethi *et al.*, 1997).

Breeding for resistance to MSV has, therefore, been a goal of several breeding programmes in Africa (Goodman, 1981). Resistance to maize streak disease has been identified in various maize germplasm. The International Centre for Maize and Wheat Improvement (CIMMYT) in

Zimbabwe has made use of population ZSR 923 BULK as a source of maize streak resistant genes to develop lines with resistance to MSV (Pixley and Zambezi, 1996). Also, the International Centre for Tropical Agriculture (IITA) has used TZ-Y population (Kim *et al.* 1981, 1989; Ajala, 1999); while CIRAD-France, CVR₃-C₃ population and other sources of resistance have been used in South African breeding programs (Barrow, 1992). Breeding options range from simple selection procedures, backcrossing to pedigree breeding methods to extract new lines. Research at IITA and CIMMYT-Harare has resulted in several lines and populations resistant to MSV (Kim *et al.*, 1987, 1989; Ngwira and Pixley, 1998).

In Kenya, breeding for MSV resistance involves collection, introduction and evaluation of diverse sources of resistance (Ininda *et al.*, 1999; Njuguna, 1999; KARI, 2000), line recycling and pedigree breeding (Ininda *et al.* 2002, Ininda, 2005). At the S₄ stage, selected lines are evaluated for agronomic traits and in various hybrid combinations. Hybrids developed are tested in diverse ecologies for stability and disease expression to identify superior varieties for farmers (KARI, 1995). While substantial progress has been made in breeding maize varieties adapted to the highland ecology (>1800 masl, with one long rain season per year) in Kenya, a major limitation in release of appropriate varieties for the mid-altitude areas (1400-1800 masl, two distinct rainfall seasons per year) has been combining high yield and disease resistance in adapted cultivars. The objective of this study was to test the hypothesis that high yielding, maize streak virus (MSV) resistant hybrids can be obtained through breeding, and that these hybrids suffer less yield loss due to maize streak disease than susceptible hybrids.

MATERIALS AND METHODS

Germplasm. The germplasm used for this trial were three-way cross hybrids developed at Muguga, 2093 masl, in Kenya (Table 1). Inbred lines used were S_{4,5} lines selected in a pedigree breeding programme initiated primarily for line recycling and development of pure-lines at Muguga. At every stage of generation advance, within and between row selections was done for

adaptability and resistance to foliar diseases. Screening inbred lines for MSV resistance was done at the S_1 generation and a final screen at the S_4 generation. Thirteen $S_{4,5}$ lines were finally selected for resistance to MSV (score of <1.5 as described in Table 2) and each line bulked at S_5 generation. Inbred lines were used as parents and crossed differentially to two streak-resistant single-cross testers obtained from CIMMYT. The single cross testers used were (CML312/CML442) and (CML395/CML444). These resultant crosses were twenty different three-way cross hybrids (Table 1).

Field trials. Two separate experiments were planted in 2004 in two mid-altitude ecologies in

Central Kenya; Embu, 1540 masl and Muguga, 2093 masl. Embu and Muguga locations are classified as mid-altitude ecologies based on annual rainfall patterns and mean temperatures. In Experiment A, the twenty hybrids (Table 1) and one check hybrid, H513 were planted in a randomised complete block design in two replications and two locations in Central Kenya. The experimental unit was a two-row plot planted with 11 hills, at a spacing of 75 cm x 30 cm to give an extrapolated plant population of 53,333 plants ha^{-1} . Nitrogen fertiliser was applied at the rate of 60 kg N per ha split in two portions. Hand-weeding was done twice during the trial.

In Experiment B, planted the same season (a planting time difference of two weeks) as

TABLE 1. Three-Way Cross hybrids made between selected lines and two Single-Cross testers

Cross code	Pedigree
MU03-002	{[EM12-210/CML202]-X-26-3-2-1-3}/[CML395XCML444]
MU03-004	{[EM12-210/CML202]-X-26-3-2-2-1}/[CML395XCML444]
MU03-006	{[EM12-210/CML202]-X-26-3-2-2-4}/[CML395XCML444]
MU03-009	{[EM12-210/CML202]-X-68-4-3-3-5}/[CML312XCML442]
MU03-010	{[EM12-210/CML202]-X-68-4-3-3-5}/[CML395XCML444]
MU03-011	{[EM12-210/CML202]-X-68-6-1-1-1}/[CML312XCML442]
MU03-012	{[EM12-210/CML202]-X-68-6-1-1-1}/[CML395XCML444]
MU03-013	{[EM12-210/CML202]-X-68-6-1-1-2}/[CML312XCML442]
MU03-014	{[EM12-210/CML202]-X-68-6-1-1-2}/[CML395XCML444]
MU03-016	{[EM12-210/CML202]-X-68-6-1-1-5}/[CML395XCML444]
MU03-017	{[EM12-210/CML202]-X-71-1-1-2-5}/[CML312XCML442]
MU03-018	{[EM12-210/CML202]-X-71-1-1-2-5}/[CML395XCML444]
MU03-019	{[EM12-210/CML202]-X-71-1-2-1-1}/[CML312XCML442]
MU03-021	{[EM12-210/CML202]-X-71-1-2-1-2}/[CML312XCML442]
MU03-022	{[EM12-210/CML202]-X-71-1-2-1-2}/[CML395XCML444]
MU03-024	{[EM12-210/CML202]-X-71-1-2-1-3}/[CML395XCML444]
MU03-025	{[EM12-210/CML202]-X-71-1-2-1-4}/[CML312XCML442]
MU03-026	{[EM12-210/CML202]-X-71-1-2-1-4}/[CML395XCML444]
MU03-028	{[EM12-210/CML202]-X-71-7-1-5-5}/[CML312XCML442]
MU03-029	{[EM12-210/CML202]-X-71-7-1-5-5}/[CML395XCML444]
H513	Local check

TABLE 2. Maize streak virus (MSV) symptom rating scale (Modified from Mesfin *et al.*, 1992)

Rate	Observed plant symptoms
1	Very few streaks or no symptoms: Symptoms only observed by very close inspection in form of specks with no subsequent development
2	Light streaking: Clearly visible but limited symptoms, spots or streaks developing on several leaves. Young leaves have less symptoms
3	Moderate streaking: Many long streaks homogeneous distribution until plant maturity
4	Severe at least 60% of leaf area uniformly over all leaves and the whole plant.
5	Very severe streaking: 75% of leaf area or more affected with stunting

Experiment A, at Muguga, the twenty hybrids and one check H513 were planted using the same method as Experiment A, except that B was artificially inoculated with the highland isolate of the MSV virus at the 2nd leaf stage.

Disease inoculation. The leafhoppers used for infection were mass reared *Cicadulina mbila* population with 100% transmission rate. Viruliferous leafhoppers were caught in vacuum aspirator, and confined in a glass tube attached to the leaf of the target plant for 48 hr inoculation access period (Leuschner and Buddenhagen, 1980). At the 2-3 leaf stage, plants were artificially infected by attaching a small plastic vial with three viruliferous leaf hoppers enclosed on to distal part of the leaf for 24 hours. Disease rating was a modified score on a scale of 1-5 with half points as described by Mesfin *et al.* (1992), (Table 2). Disease rating was done twice during the growth period. Final scores were taken during grain filling stage.

Data collection. For both Experiments A and B, data were collected for (i) days to 50% pollen shed, (ii) days to mid-silk, (iii) anthesis-silking interval (ASI), (iv) ear height, (v) plant height, (vi) root lodging, (vii) stem lodging, (viii) foliar diseases, (ix) field weight of unshelled ears, and (x) moisture content at harvest. Grain yield was calculated by assuming 80 shelling percentage for all hybrids and adjusting for a 12.5% moisture content for all hybrids. Parameters measured in the inoculated trial, Experiment B were similar to those in Experiment A, except that it included the

mean disease rating for each hybrid. Data were analysed using the SAS General Linear Model Procedure (PROC GLM) and means separated by students t-test.

RESULTS

Field trials under disease free conditions (Experiment A). Results of analysis of the field trial in Embu are shown in Table 3. There was significant variation among the hybrids for grain yield ($P < 0.01$), days to 50 percent pollen shed ($P < 0.001$) and days to mid-silk ($P < 0.001$) at Embu. Table 3 also shows that the experimental means in Embu were 8.89 t ha⁻¹ for grain yield, 83.7 days to pollen shed, 85.1 days to mid-silk and 101.2 cm in plant height.

Results of analysis of the field trial at Muguga are shown in Table 4. There was significant variation between the hybrids for yield ($P < 0.05$), days to mid-silk ($P < 0.001$), and ear height ($P < 0.001$). The experimental means at Muguga were 8.35 t ha⁻¹ for grain yield, 98.5 days to pollen shed, 102.1.1 days to mid-silk and 104.1 cm in plant height.

Across location analysis (Table 5) shows that genotypes differed strongly for grain yield and days to mid-silk ($P < 0.001$). Genotype x Environment interaction was significant for grain yield and days to mid-silk at $P < 0.01$ (Table 5). The means across locations were 8.62 for grain yield, 91.1 days to pollen shed, 93.6 days to mid-silk, and 102.6 cm in plant height (Table 5). The combined analysis shows that genotype x environment interaction was significant for grain

yield and days to 50% mid-silk (Table 5). The range of mean yields across location was between 6.51 and 10.04 t ha⁻¹.

Table 7 shows the best hybrids combined across locations were MU03-025, MU03-024, MU03-011, MU03-022, MU03-004, MU03-014, MU03-028, MU03-016, MU03-006, MU03-029, MU03-

019, MU03-017. These hybrids showed a mean grain yield of above the combined mean of 8.62 t ha⁻¹. The highest yielding hybrid in the disease-free trial, MU03-025 showed 3.98 t ha⁻¹ above the check, while the lowest yielding hybrid, MU03-026 had 1.03 t ha⁻¹ below H513 (Table 8). Only two hybrids, MU03-026 and MU03-021

TABLE 3. Mean squares for genotype source of variation and coefficient of variation (CV) for grain yield and other agronomic traits Embu, 2004

Source of variation	Grain Yield (t ha ⁻¹) [‡]	Pollen	Silk	EH [†]
Genotype	3.6989**	17.3651***	22.7140***	399.4594
Error	0.7634	2.9052	3.5388	263.2169
CV (%)	10.4677	1.9069	2.2107	16.02726
Mean	8.3471	83.6818	85.0909	101.2272

,*, significant at 0.01, and 0.001 probability levels respectively; Pollen=Days to 50% pollen shed; Silk= days to 50% mid-silk; EH[†] measured from the node of top ear attachment; [‡] Yield adjusted at 12.5% moisture content

TABLE 4. Mean squares for genotype source of variation and coefficient of variation (CV) for grain yield and other agronomic traits at Muguga, 2004

Source of variation	Grain Yield (t ha ⁻¹) [‡]	Pollen	Silk	EH [†]
Genotype	2.9819*	197.1780	71.1969***	200.0346***
Error	1.1718	237.3596	2.4426	20.3217
CV (%)	12.1700	15.6447	1.5300	4.3331
Mean	8.895	98.4772	102.0909	104.0340

*, **,***, significant at 0.05, .001, and 0.001 probability levels respectively; Pollen=Days to 50% pollen shed; silk= days to 50% mid-silk; EH[†] measured from the node of top ear attachment; [‡] Yield adjusted at 12.5% moisture content

TABLE 5. Mean squares for genotype source of variation and coefficient of variation (CV) for grain yield and other agronomic traits combined across locations, 2004

Source of variation	Grain Yield (t ha ⁻¹) [‡]	Pollen	Silk	EH [†]
Genotype	3.9579***	87.8232	83.3290***	482.4560
Genotype x location	3.3996**	120.1640	14.120**	133.5583
Error	1.0913	113.0005	4.3979	165.7082
CV%	12.1176	11.6713	2.2407	12.5428
Mean	8.6211	91.0795	93.5909	102.6306

,*, significant at 0.01, and 0.001 probability levels respectively; Pollen=Days to 50% pollen shed; Silk= days to 50% mid-silk; EH[†] measured from the node of top ear attachment; [‡] Yield adjusted at 12.5% moisture content

performed worse than the check in the disease free trial.

Field trials in the inoculated trial (Experiment B). The disease inoculated trial, Experiment B, showed significant ($P < 0.001$) differences among

hybrids for grain yield, days to 50% pollen shed, days to 50% mid-silk, ear height, and disease severity (Table 6). The experimental means were 4.66 t ha⁻¹ for grain yield, 101.1 days to 50% pollen shed, 102.1 days to mid-silk, 95.6 cm in ear height and a mean disease score of 2.13 (Table 6).

TABLE 6. Mean squares for genotype source of variation under disease inoculation for grain yield, days to 50 percent pollen shed, days to mid-silk and ear height for at Muguga, 2004

Source of variation	Grain yield (t ha ⁻¹) [†]	Pollen	Silk	EH [‡]	MSV§
Genotype	5.6129***	43.2022***	37.7897***	276.8780***	0.2491***
Check vs. genotype	9.7540	51.0017	136.0280*	39.2942	4.4197***
Error	0.6958	2.5894	4.2871	64.7453	0.0422
CV (%)	17.8774	1.5918	2.0190	8.4032	9.6629
Mean	4.6660	101.0875	102.5500	95.7542	2.1281

*, **, ***, significant at 0.05, .001, and 0.001 probability levels respectively; Pollen=Days to 50% pollen shed; Silk=days to 50% mid-silk; EH[‡] measured from the node of top ear attachment; [†]Yield adjusted at 12.5% moisture content; §MSV=mean score for maize streak virus disease severity

TABLE 7. Mean yield (t ha⁻¹) under disease-free and inoculated trials in Embu and Muguga

Hybrid	Site				MSV [§]
	Muguga	Embu	Combined	Inoculated [†]	
MU03-025	11.27	8.81	10.04	4.01	2.00
MU03-022	10.37	8.38	9.37	5.86	2.00
MU03-028	10.27	8.65	9.46	4.39	2.40
MU03-010	10.18	5.69	7.94	5.46	1.90
MU03-029	10.05	7.88	8.97	4.73	2.13
MU03-024	9.79	9.90	9.85	5.01	1.90
MU03-017	9.79	7.78	8.79	4.73	2.50
MU03-011	9.71	9.32	9.52	5.25	2.00
MU03-014	9.38	9.15	9.27	5.47	2.13
MU03-006	9.18	8.30	8.74	6.54	1.75
MU03-018	8.76	7.88	8.32	3.41	1.87
MU03-012	8.48	8.01	8.25	6.81	1.75
MU03-016	8.30	9.88	9.09	5.23	2.13
MU03-019	8.30	9.59	8.95	4.18	2.25
MU03-009	8.26	7.04	7.65	1.49	1.90
MU03-004	7.86	10.75	9.30	5.93	1.90
MU03-002	7.83	6.65	7.24	6.37	2.40
MU03-013	7.77	5.27	6.52	4.48	2.40
MU03-026	7.14	8.81	7.98	7.17	1.90
MU03-021	6.25	8.98	7.62	4.09	2.13
H513	8.34	8.89	8.62		
Mean	7.29	7.77	7.53	1.95	3.5
LSD	2.30	1.86	1.50	4.66	1.68

[†]Inoculated trial was planted at Muguga; §MSV mean score on a scale of 1-5

The performance of hybrids under disease inoculation is shown further in Tables 7, 8 and 9. Table 7 shows that all hybrids had lower yields under disease inoculation than in the disease free conditions. Hybrids evaluated under inoculated trial showed a range of grain yield between 7.17 to 1.49 t ha⁻¹, and an experimental mean of 4.66 t ha⁻¹ (Table 7). The highest yielding hybrids under disease conditions were MU03-026, MU03-012, MU03-006, MU03-002, MU03-004, MU03-022

MU03-014, MU03-010, MU03-011 MU03-016 MU03-024 MU03-029 and MU03-017. All these hybrids showed a mean grain yield above the check (Table 7). The lowest yielding hybrid in both locations was MU03-013, which showed an overall grain yield of 6.51 t ha⁻¹.

Table 8 shows the levels by which each hybrid out yielded the check variety H513 in the inoculated trial. MU03-026 out-yielded the check by 5.2 t ha⁻¹ in the inoculated trial ($P < 0.05$). Only

TABLE 8. Mean grain yield differences (t ha⁻¹) in Muguga between three-way cross hybrids compared to local check (H513) in inoculated and disease free conditions

Hybrid	Difference H513 \pm t ha ⁻¹	
	Disease-free	Inoculated
MU03-025	3.98	2.06
MU03-022	3.08	3.90
MU03-028	2.97	2.43
MU03-010	2.89	3.51
MU03-029	2.763	2.77
MU03-024	2.51	3.05
MU03-017	2.50	2.78
MU03-011	2.42	3.30
MU03-014	2.09	3.52
MU03-006	1.89	4.59
MU03-018	1.48	1.46
MU03-012	1.19	4.85
MU03-016	1.01	3.28
MU03-019	1.01	2.23
MU03-009	0.97	-0.46
MU03-004	0.57	3.98
MU03-002	0.54	4.42
MU03-013	0.48	2.53
MU03-026	-0.15	5.22
MU03-021	-1.03	2.14
Mean	1.66	3.08

TABLE 9. Summary classification for twenty hybrids based on mean disease rating in inoculated experiment

MSV ^S score	Classification of hybrid	Hybrid
1.0-1.75	Highly resistant	MU03-006, MU03-012
1.76-2.4	Medium-High resistance	MU03-018, MU03-025, MU03-022, MU03-028, MU03-029, MU03-014, MU03-024, MU03-010 MU03-004 MU03-026, MU03-002, MU03-009
2.5-3.0	Moderate resistant	MU03-017
>3.0	Susceptible	H513

MSV^S scored on scale of 1-5

one hybrid, MU03-009, performed worse than check in grain yield in the inoculated trial (Table 8).

Table 9 shows the mean rating for maize streak for twenty-one hybrids tested under artificial inoculation with maize streak diseases. Most hybrids are classified as resistant to maize streak disease (MSV score <2.4) when compared to the check (MSV score =3.5). The hybrids, MU03-006 and MU03-012, were highly resistant to maize streak disease (MSV score 1.0-1.75); while MU03-018, MU03-025, MU03-022, MU03-028, MU03-029, MU03-014, MU03-010, MU03-004, MU03-026, MU03-002, MU03-009 were medium to high resistant to maize streak disease (MSV score 1.76-2.4); MU03-017 showed moderate resistance (MSV score 2.5-3.0) and the check, H513 was susceptible (MSV score >3.0). The check hybrid, H513, was classified susceptible check with a mean rating of 3.5.

DISCUSSION

The differences among the hybrids for grain yield and other agronomic traits indicate the potential inherent genetic diversity in the hybrids. The results show that the mean yield across sites was higher than the mean of the check. The results further indicate presence of genetic variability for maize streak disease resistance coupled with high grain yields in maize. Thus, there is potential for sustainable improvement of disease resistant and high yielding maize varieties.

The significant Genotype x Environment interaction for grain yield and mid-silk suggest that some hybrids performed better in one of the two sites. For example, MU03-025 was the best hybrid in Embu and Muguga indicating the potential for its suitability across environments. Significant g x e interactions for yield was more pronounced in hybrid MU03-010 where the difference in yield in the two sites was about 4 t ha⁻¹, indicating that this hybrid is more suited for Muguga. Mean grain yields were however lower under the disease-inoculated trial. This is expected because of loss photosynthetic area due to occurrence of disease. The low performance of the hybrid MU03-026 in disease-free experiment was not reflected in the inoculated trial.

The higher yielding hybrids under disease-free

conditions were not necessarily high yielding under disease pressure. This can be explained by the fact that yield related traits segregate independent of MSV resistant genes. This was reflected in hybrids MU03-025, MU03-022 and MU03-028. Table 6 showed the highest yielding hybrid in the inoculated trial was MU03-026 (grain yield=7.12 t ha⁻¹; 5 t ha⁻¹ above the check mean). The yields under disease pressure of MU03-006 and MU03-012 were 6.55 and 6.80 t ha⁻¹, respectively, which were the same as those of best hybrid in inoculated trial based on the t-test.

Mean grain yields in the inoculated trial for all hybrids were better than the check by 3.0 t ha⁻¹ compared to 1.65 t ha⁻¹ under no disease conditions. This indicates potential of these hybrids to replace the currently grown hybrids. Some hybrids showed stability in yield levels under both no disease and high disease pressure. For example, MU03-026 had mean grain yields of 7.1 t ha⁻¹ in Muguga, 8.8 t ha⁻¹ in Embu, and 7.2 t ha⁻¹ under severe disease pressure in Muguga. This represents a yield loss <0.1% due to MSV; indicating MU03-026 can be recommended for MSV prone areas and also areas where MSV is not prevalent. This is important since a commercially viable hybrid, must perform well both in diseased- and disease-free environments. However, the disease trial was only done in one site, hence, more sites are needed to come up with conclusive results of performance of different hybrids under disease pressure.

The data also showed that the average yield loss due to MSV ranged from <7.0% in some varieties such as MU03-026, MU03-002, to as high as 74% in H513. This agrees well with results obtained by other authors. Bosque-Perez *et al.* (1998), found that varieties susceptible to maize streak disease, had a yield reduction of 71% compared to yield loss of 1.5-10% for disease resistant cultivars. Varieties differed significantly for maturity in the two sites (P<0.001). In Embu, with mean pollen shed of 84 days was much earlier than at that Muguga, 99 days. Mid-silk was 85 days at Embu and 102 days at Muguga. In both sites, the hybrids differed significantly for grain yield and days to 50% silking. The mean anthesis-silking interval was small (data not shown), hence, hybrids are adapted for moderately stressed areas.

There is an indication that performance for

disease resistance and grain yield depended on the particular combinations of line x tester used. For example, CML312/CML442 showed superior combinations with four lines, while CML395/CML444 showed superior combinations with three lines. This calls for a Line x Tester analysis to identify lines of good general and specific combining ability. The data will assist in straight identification of superior three-way cross hybrids. The considerable differences noted in grain yield for hybrids rated as either medium or moderate resistance could be explained by the observation by some authors that disease pressure on some hybrids is not always related to yield performance. For example, Barrow (1992) found that MSV resistant hybrids showed considerable range in yield loss despite having a low rating for MSV indicating that resistance may not always be related to symptom rating. For any hybrid to be recommended to farmers, it is necessary that it must have an added advantage over the commonly grown hybrids. Hybrids that show stable yield across disease-free and diseased environments (MU03-012, MU03-022, MU03-024 and MU03-006) are more likely to benefit the farmers. The results thus support the hypothesis that high yielding and maize streak virus (MSV) resistant hybrids can be obtained through breeding, and that these hybrids suffer less yield loss due to maize streak disease than susceptible hybrids. The adoption of MSV resistant hybrids would result in higher maize yields in the mid-altitude areas of Kenya where maize streak disease is a major limiting factor to maize production.

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