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Evaluation of Maize (*Zea mays L.*) Genotypes for High Grain Yield and Resistance to Maize Streak Virus Infections under Diverse Agro-Ecological Zones

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Abstract

Background: Maize streak disease (MSD), caused by maize streak virus (MSV) is the most serious biotic constraint to maize (*Zea mays L.*) production in sub-Saharan Africa, threatening food security and incomes of farmers in the region. Under field conditions, the disease can cause up to 100% yield loss, depending on maize genotype and plant age at the time of infection.

Materials and methods: Field trials were established at Ohawu, Kpeve and Nkwanta representing coastal savannah, forest and forest-savannah transition agro-ecological zones (AEZs) respectively of the Volta region of Ghana during 2015 minor season to evaluate 16 maize genotypes for high yielding and resistance to maize streak virus (MSV) infection. The fields were laid out in a Randomised Complete Block Design (RCBD) with four replocations. The plants were scored for disease severity at 10 weeks after planting (WAP) based on a 1-5 visual scale (1=no infection and 5=very severe infection). Both disease and agronomic data were subjected to analysis of variance (ANOVA) using GenStat Release version 12 statistical package.

Results: The study revealed significant varietal, locational and genotype x location interaction effect (p<0.05) on mean MSD severity scores and grain yields. Mean MSD severity scores were highest at Nkwanta, followed by Kpeve and the lowest at Ohawu. The improved varieties Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa, PAN 12, and the breeding lines CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006 displayed mild MSD symptoms and also had higher yields compared to Dzinu-Eve (a local cultivar). However, the study revealed significant genotype x location interaction effect (p<0.05), with Akposoe, Etubi, Honampa and PAN 12 showing higher MSD symptom severity scores at Kpeve than at Nkwanta and Ohawu, whereas the other 12 maize genotypes had higher mean MSD severity scores at Nkwanta than Kpeve and Ohawu.

Conclusion: The maize genotype and locations have significant influence on the level of disease severity and grain yields. Therefore, maize genotypes that showed mild symptoms of MSD and also gave high grain yields should be further evaluated and released as varieties for the locations where they performed better.

Keywords: Maize; Maize streak disease; Maize streak virus; Disease resistance; Yield loss; Agro-ecological zones

Abbreviations:

MSD: Maize Streak Disease; MSV: Maize Streak Virus; AEZ: Agroecological Zone; ANOVA: Analysis of Variance.

Introduction

Maize (*Zea mays L.*) is the world's third most important cereal food crop after wheat and rice Tefera et al. [1] that is widely grown in the tropics [2]. It provides food and income to over 300 million households in Sub-Saharan Africa (SSA). In Ghana, it is the first among the cereal crops grown. The crop is cultivated throughout the ecological zones of Ghana, mainly by small-scale farmers for food, income and as a source of livelihood. Maize is also vital for livestock and poultry feed preparation [3].

In spite of the immense benefits maize offers, its production in SSA is hindered by several constraints such as pests and diseases, poor soil fertility, unfavourable climatic conditions leading to low yields that fail to meet demand. Maize production in Ghana is estimated at around 1.79 MT per annum from an area of approximately 992,000 ha with yield estimates of about 1.7 t ha-1 in farmers' fields [4,5].

This is generally low compared to the global average of 4-5 t ha^{-1} and over 8 t ha^{-1} in the United States of America (USA) [6]. Maize streak disease (MSD) caused by maize streak virus (MSV; genus Mastrevirus, family Geminiviridae) is the most damaging and destructive disease of maize in SSA [7] and the neighbouring Indian Ocean islands of Reunion, Mauritius, Madagascar, Sao Tome and principe [8,9]. MSV is transmitted by as many as six species of leafhopper of the genus Cicadulina, (Homoptera: Cicadelidae) in a persistent manner [10], but mainly by *C. mbila* and *C. storey* [11]. Under field conditions, MSV can cause up to 100% yield loss, depending on maize genotype and plant age at the time of infection [12,13].

Maize streak disease currently threatens food security and livelihoods of the affected communities in the Volta region where maize is their staple food. Oppong et al. [14] reported an overall MSD incidence of 20.28% in the transition and 18.03% in the forest zones of Brong-Ahafo, Ashanti, Eastern and Central regions of Ghana.

However, field surveys recently conducted by Asare-Bediako et al. [15] revealed overall mean MSD incidence of 81.87% in the transition zone and 68.70% in the forest zones of the Volta region, an indication of MSD epidemic in the region. There is therefore the need to identify effective management strategies against the MSD in order to improve yields, incomes, food security and livelihoods of people in the affected communities. Methods so far employed to manage MSD include the use of host plant resistance, insecticidal control of leafhopper vector, herbicidal control of weeds as alternative hosts and cultural practices such as altering planting date to avoid peak infestation of leafhopper vector, deep burial of residue through tillage operations, crop rotation, irrigation, plant density manipulation [10,11,16].

Other agronomic practices that have been recommended for reducing MSV incidence include timely planting, seed treatment with systemic insecticides, and removal of infected plants [17]. However, insecticidal spray or seed treatment to control the leafhopper vector is not affordable by these subsistence farmers, and pesticides abuse by the farmers can lead to environmental and health effects [13]. The land tenure system does not support crop rotation and the unreliable climatic condition does not encourage either early sowing or late sowing to avoid vector infestation. Tillage practices destroy the soil structure and expose the soil to erosion especially in high rainfall areas [13].

Developing and planting of high yielding MSV-resistant maize varieties is the most viable and environmentally friendly option to minimizing yield losses in maize. Preliminary maize screening work revealed a total of 15 maize genotypes that were high yielding and resistant/tolerant to MSV [18,19]. The performance of these maize genotypes in the Volta region is however not known. The study was therefore conducted to assess the performance of these maize genotypes in three different AEZs of the Volta region.

Materials and Methods

Study area

Field trials were established at Nkwanta Agricultural Station in the Nkwanta South district, Kpeve Research Station in the South Dayi district and Ohawu Agricultural College in the Ketu North district of the Volta region during 2015 minor season (September-December, 2015). These sites represent transition, forest and coastal savannah AEZs of the region. The region is located at latitudes 3°45' and longitude 8 45° North and 0 10° and 0 45° East. The rainfall is bimodal; the first from March to July, and the second from the mid-August to October, with annual rainfall ranging between 513.9 mm and 1099.88 mm. The average number of rain days is 86 with extreme annual rainfalls ranging between 922 mm to 1874 mm. The mean annual maximum temperatures range between 24°C to 39°C, while the mean annual minimum temperatures were between 11°C to 26°C. The soil types range from heavy clay to sandy loam [20,21].

Plant materials

Sixteen maize genotypes were evaluated in the three different AEZs for high grain yields and tolerance to MSV infection. These comprised of nine (9) improved maize genotypes (Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa, and PAN 12) that were found to be high yielding and tolerant to MSV during screening experiments in 2016 [19] and six (6) breeding lines (CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006) that were high yielding and tolerant to MSV [18] and 'Dzinu-Eve' a local susceptible check.

Experimental design and field layout

The sixteen (16) maize genotypes were planted in a Randomized Complete Block Design (RCBD) with four replications at each of the three locations. A total land area of 2000 m^2 (80 m x 25 m) was ploughed and harrowed at each of the three experimental sites. It was then divided into four blocks and each block was further divided into 16 plots, with each plot measuring 5 m x 4 m. An alley of 1.5 m was left between the blocks and 1 m between the plots. The maize genotypes were sown directly at two seeds per hill at a planting distance of 0.8 m x 0.8 m and a planting depth of about 0.5 cm. Agronomic practices such as weed control was also done at eight weeks after germination with a hoe and machete. Fertilizer (NPK) was applied at a rate of 250 kg ha^{-1} at three weeks after germination and top-dressed with urea at six weeks after germination. The experiments were carried out under rain fed conditions.

Data collection

Data on disease incidence and severity, plant height (cm), cob weight (g), 100-seed weight (g) and yield (t ha^{-1}) were collected during the study. In each case data was collected from ten plants per plot and the means determined.

The maize genotypes were evaluated for disease incidence and severity at 10 weeks after planting (WAP) based on disease symptoms described [17,22]. Disease incidence (DI) per plot was estimated as the percentage of plants on a plot displaying MSD symptoms as described [14]. MSD symptom severity was assessed for each plot based on a 1-5 scale adopted from Oppong et al. [4] which is essentially the 1-5 scale developed by Kyetere et al. [22], with a modification of 0.5 increments; where 1-represents no infection; 2-mild infection; 3-moderate infection; 4-severe infection; and 5-very severe infection.

Mean plant height (cm) was taken at tasselling and mean seed yield (t ha^{-1}), mean cob weight (g) and mean 100-seed weight (g) were collected at harvest.

Statistical analysis

Mean incidence data was tested for homogeneity of variance before analysis using Levene's test [23]. The test statistic, W, is equivalent to the F statistic that would be produced by such an ANOVA, and is defined as follows:

Where:

k is the number of different groups to which the sampled cases belong,

Ni is the number of cases in the *i*th group,

N is the total number of cases in all groups,

Yij is the value of the measured variable for the jth case from the ith group,

The incidence data was then arc-sine transformed [24], in order to homogenise variances. Other quantitative data including disease severity, plant height, cob weight, 100-seed weight, seed yield were subjected to ANOVA and the Least Significant Difference (LSD) test at 5% level of probability used to separate means when significant differences were observed. Pearson's correlation coefficients were calculated to find the relationships between MSD incidence and severity and grains yield parameters. The GenStat Release version 12 (VSN International) statistical package was employed in the analyses of the data.

Results

Mean MSD incidence

The mean MSD incidence recorded for the 16 maize genotypes in the three AEZs are shown in **Table 1**. ANOVA showed highly significant differences among the sixteen maize genotypes sown at Ohawu (F15,45=4.92; p<0.001), Kpeve (F15,45=2.78; p<0.004) and Nkwanta (F15,45=3.34; p<0.001). At Ohawu, disease incidence ranged from 43.4% for Akposoe to 75.6% for CRI003. MSD incidence at Kpeve also ranged from 70.5% for CRI004 to 90% each for CRI006, Dzinu-Eve, Etubi, Honampa and Obatanpa. The mean MSD incidence at Nkwanta ranged from 73.8% for CRI004 to 90% each for Aburohemaa, CRI001, CRI002, CRI003, CRI005, CRIOO6, Dorke, Dzinu-Eve, Etubi, Honampa, Obatanpa and Omankwa, indicating that the rate of infection was higher in Nkwanta than Kpeve and Ohawu.

A two-way ANOVA of the mean MSD incidence revealed highly significant differences among the three locations (F2,141=329.28; *p*<0.001) **(Table 2)**. Nkwanta had the highest overall mean incidence of 87.9% which was not significantly different from that of Kpeve (83.3%), but significantly higher than that of Ohawu (53.1%). **Table 3** also shows a highly significant genotype x location interaction effects (F30,141=4.16; p<0.001).

Table 1: Mean incidence of maize streak disease on sixteen (16) maize genotypes in three different locations at 10 weeks after planting (WAP).

Genotype	Ohawu	Kpeve	Nkwanta
	Mean MSD incidence (%)	Mean MSD incidence (%)	Mean MSD incidence (%)
Abontem	63.9*	79.8*	85.8*
Aburohemaa	46.6	85.8	90.0
Akposoe	43.4	85.8	85.8
CRI001	54.9	66.6	90.0
CRI002	52.5	85.8	90.0
CRI003	75.6	85.8	90.0
CRI004	33.5	70.5	73.8
CRI005	53.1	78.3	90.0

CRI006	38.4	90.0	90.0
Dorke	45.1	79.8	90.0
Dzinu-Eve	71.0	90.0	90.0
Etubi	64.9	90.0	90.0
Honampa	58.7	90.0	90.0
Obatampa	53.2	90.0	90.0
Omankwa	46.7	85.8	90.0
PAN 12	48.2	81.6	81.6
Mean	53.1	83.8	87.9
l.s.d	14.76	12.1	6.984
p-value	<0.001	0.004	<0.001
CV(%)	19.5	10.2	5.6

*Figures were arc sine-transformed.

Mean MSD severity scores

Mean MSD severity scores for the 16 maize genotypes at 10 WAP in the three locations are shown in **Table 2**. There were significant differences in mean severity scores among the 16 maize genotypes at Ohawu (F15,45=11.87; *p*=0.027), Kpeve (F15,45=10.17; *p*<0.002) and Nkwanta (F15,45=15.73; *p*<0.001).

At Ohawu, CRI004 had the lowest mean severity score of 1.248, whilst Dzinu-Eve had the highest severity score of 2.583. Similarly, at Kpeve, CRI004 had the lowest mean MSD severity score of 1.667 whilst Dzinu-Eve had the highest severity score of 3.41. Further, at Nkwanta field trials, CRI004 had the lowest mean MSD severity score of 1.92 whilst Dzinu-Eve had the highest severity score of 3.72 **(Table 2)**. A two-way ANOVA showed highly significant difference among the locations in respect of the overall mean MSD severity scores (F2,141=257.02; p<0.001) **(Table 3)**.

The overall mean MSD severity score recorded at Nkwanta (2.44) was not significantly different from that of Kpeve (2.319) but it was significantly higher than that of Ohawu (1.64) as shown in **Table 2**. Genotype x location interaction effects on mean MSD severity score was highly significant (F30,141=2.74; p<0.001) as indicated in **Table 3**.

Mean symptom severity scores for Akposoe, Etubi, Honampa and PAN 12 at Kpeve were higher than at Nkwanta, whilst the symptom severity scores for the other 12 genotypes were higher at Nkwanta than at Kpeve **(Table 2)**.

Table 2: Mean maize streak disease (MSD) severity scores for sixteen (16) maize genotypes in three locations at ten weeks after planting (WAP).

Genotype	**Mean MSD severity scores**		
	Ohawu	Kpeve	Nkwanta
Abontem	1.71	2.20	2.28
Aburohemaa	1.42	2.40	2.38
Akposoe	1.28	2.44	2.08
CRI001	1.46	1.81	2.22
CRI002	1.34	2.31	2.56
CRI003	1.95	2.23	2.60
CRI004	1.25	1.67	1.92
CRI005	1.56	1.91	2.21
CRI006	1.33	2.32	2.49
Dorke	1.61	2.23	2.54
Dzinu-Eve	2.58	3.41	3.72
Etubi	2.10	2.77	2.47
Honampa	1.70	2.35	2.19
Obatanpa	1.84	2.40	2.49
Omankwa	1.42	2.30	2.52
PAN 12	1.66	2.39	2.35
Mean	1.64	2.32	2.44
l.s.d	0.291	0.35	0.282
p-value	<0.001	0.002	<0.001
CV (%)	12.5	10.6	8.1

Symptom severity scores (SSS): 1=no symptom; 2=mild symptom; 3=moderate symptom; 4=severe symptom; 5=very severe symptom

Table 3: Mean sum of squares of the effect of locations and genotype x location interaction effects on overall mean maize streak disease (MSD) incidence and severity scores.

Source	**Degree of freedom**	**Final incidence**	**Final severity score**
Genotype	15	560.6**	1.47169**

Location	2	27134.51**	11.95758**
Genotype x Location	30	342.43**	0.12748**
Residual	141	82.41	0.04652

**Highly significant (p<0.01), *Significant (p<0.05)

Mean plant height

The mean plant height recorded for the 16 maize genotypes at Ohawu, Kpeve and Nkwanta are shown in **Table 4**. Results showed highly significant differences among the 16 maize genotypes in respect of mean plant height at the three locations (F15, 717=21.67; p<0.001). At Ohawu, CRI003 had the highest mean plant height of 211.75 cm whilst Honampa had the lowest (153.50 cm). CRI006 had the lowest mean plant height (166.67 cm) at Kpeve whilst Obatanpa had the highest (228.25 cm). At Nkwanta, Obatanpa had the highest mean plant height (152.88 cm) whilst CRI006 had the lowest mean plant height of 117.12 cm.

Two-way ANOVA also showed highly significant differences among the three locations (F2, 717=689.32; p<0.001) as shown in **Table 5**. The highest mean plant height was recorded at Ohawu (186.85 cm), followed by Kpeve (182.25 cm) whereas Nkwanta had the lowest (130.78 cm). The result also showed significant genotypes x locations interaction effects (F30, 717=3.54; p<0.001) **(Table 6)**. For instance, Honampa had the lowest plant height in Ohawu but had higher plant heights at Kpeve and Nkwanta **(Table 4)**.

Table 4: Mean plant heights at tasseling recorded for 16 maize genotypes at three locations (Ohawu, Kpeve and Nkwanta).

Genotype	**Plant height (cm)**		
	Ohawu	Kpeve	Nkwanta
Abontem	191.33	198.17	136.38
Aburohemaa	175.17	169.25	124.00
Akposoe	197.50	197.67	133.81
CRI001	211.58	191.17	130.53
CRI002	192.08	179.50	141.44
CRI003	211.75	180.58	145.75
CRI004	170.92	167.67	125.63
CRI005	180.83	169.92	123.56
CRI006	163.25	166.67	117.19
Dorke	198.92	186.42	131.50
Dzinu-Eve	185.25	173.00	125.50
Etubi	175.33	172.83	120.69
Honampa	153.50	177.67	135.06
Obatanpa	209.92	228.25	152.88
Omankwa	191.17	188.67	130.06
PAN 12	181.08	169.75	118.44
Mean	186.85	182.32	130.78
l.s.d.	9.61	15.58	16.49
p-value	>0.001	>0.001	>0.001
CV%	7.35	8.54	8.83

Mean seed weight per plot, mean cob weight and 100-seed weight

Mean seed weight per plot, mean cob weight and mean 100-seed weight recorded for 16 maize genotypes during field trials at the three AEZs are shown in **Table 5**. ANOVA showed highly significant differences in the mean seed weight per plot among the maize genotypes sown at Ohawu (F15, 45=10.31; p<0.001), Kpeve (F15, 45=3.08; p=0.002) and Nkwanta (p<0.001). At Ohawu pAN 12 had the highest mean seed weight of 1.911 kg, and Dzinu-Eve had the lowest seed weight of 0.093 kg. Similarly, at Kpeve, pAN 12 had the highest mean seed weight (1.703 kg) and Dzinu-Eve had the lowest seed weight of 0.80 kg. At Nkwanta, pAN 12 had the highest mean seed weight of 1.543 kg, and Dzinu-Eve had the lowest seed weight of 0.725 kg.

A two-way ANOVA showed a highly significant difference (p<0.001) between the locations in respect of mean seed weight per plot. Nkwanta had the highest mean seed weight (1.361 kg), followed by Ohawu (1.345 kg) whereas Kpeve had the lowest (1.227 kg) as shown in **Table 5**. Genotype x location interaction effect on mean seed weight was however not significant (p>0.05) **(Table 6)**.

With respect to their mean cob weight, ANOVA showed highly significant differences among the maize genotypes evaluated at Ohawu (F15, 45=12.41; p<0.001), Kpeve (F15, 45=3.60; p<0.001) and Nkwanta (p<0.001). At all the three locations, pAN 12 had the highest mean cob weight whilst Dzinu-Eve had the lowest **(Table 5)**.

The two-way ANOVA showed highly significant differences among the three experimental sites in terms of the mean cob weight (p<0.01) **(Table 6)**. The highest mean cob weight was obtained at Ohawu (1.582 kg), followed by Kpeve (1.483 kg) whereas Nkwanta had the lowest (1.361 kg).

There were also significant differences in 100-seed weight among the 16 maize genotypes evaluated at Ohawu (F15, 45=13.37; p<0.001), Kpeve (F15, 45=2.84; p=0.003) and Nkwanta (p<0.001). At Ohawu, pAN 12 had the highest 100-seed weight of 39.56 g, whilst CRI006 had the lowest 100-seed weight of 19.17 g. However, at Kpeve and Nkwanta, pAN 12 had the highest 100-seed weight whilst Dzinu-Eve had the lowest.

The highest overall mean 100-seed weight was recorded at Ohawu (26.99 g), followed by Kpeve (24.24 g) whilst Nkwanta had the lowest (21.57 g) as shown in **Table 5**. A two-way ANOVA however did not show significant differences (p>0.05) in mean 100-seed weight among the three locations **(Table 6)**.

Genotype x location interaction effects on mean 100-seed weight was also not significant ($p>0.05$).

Table 5: Mean seed weight (kg), mean cob weight (kg) and mean 100-seed weight (g) recorded for 16 maize genotypes in three locations in the Volta region.

Genotype	**Mean seed weight (kg)**			**Mean cob weight (kg)**			**100-seed weight (g)**		
	Ohawu	Kpeve	Nkwanta	Ohawu	Kpeve	Nkwanta	Ohawu	Kpeve	Nkwanta
Abontem	1.208	0.996	0.902	1.354	1.483	1.043	25.80	20.37	18.13
Aburohemaa	1.266	1.107	1.003	1.463	1.137	1.247	25.99	21.81	19.42
Akposoe	1.136	1.170	1.061	1.362	1.359	1.283	24.09	22.24	19.8
CRI001	1.774	1.317	1.193	2.008	1.398	1.409	33.49	28.24	25.13
CRI002	1.623	1.486	1.347	1.958	1.535	1.687	31.61	28.57	25.43
CRI003	1.592	1.248	1.131	1.807	1.838	1.396	28.04	22.72	20.22
CRI004	1.448	1.397	1.266	1.572	1.798	1.65	28.19	27.37	24.36
CRI005	1.300	1.276	1.156	1.426	1.467	1.347	23.01	23.27	20.71
CRI006	0.983	1.134	1.027	1.321	1.472	1.351	19.71	21.17	18.83
Dorke	1.486	1.452	1.316	1.695	1.773	1.627	29.11	27.35	24.34
Dzinu-Eve	0.193	0.800	0.725	1.169	0.876	0.804	21.19	18.98	16.9
Etubi	1.180	1.210	1.096	1.343	1.587	1.467	23.26	24.02	21.38
Honampa	1.239	1.170	1.060	1.357	1.389	1.275	25.18	23.65	25.05
Obatampa	1.238	1.037	0.940	1.507	1.220	1.120	26.10	22.93	20.41
Omankwa	1.217	1.132	1.025	1.439	1.365	1.253	27.45	22.96	20.44
PAN 12	1.911	1.703	1.543	2.537	1.995	1.831	39.56	32.16	28.62
Mean	1.345	1.227	1.112	1.582	1.483	1.361	26.99	24.24	21.57
l.s.d	0.245	0.349	0.316	0.281	0.423	0.388	3.818	5.947	5.297
p-value	<0.001	0.002	<0.002	<0.001	<0.001	<0.001	<0.001	0.003	0.003

Table 6: Mean sum of squares for plant height, mean cob weight, 100-seed weight, and mean seed weight per plot for 16 maize genotypes evaluated at three different locations.

Source	**d.f.**	**Plant height**	**Cob weight**	**100-seed weight**	**Mean seed weight**
Genotypes	15	7808.7**	1033897**	199.72**	669249
Location	2	248400.1**	157182	120.85**	216686
Genotype x Location	30	1276.4**	55458^{ns}	6.23ns	22277ns
Residual	141	360.4	53215	10.12	36882
**Highly significant ($p<0.001$); ns=Not significant ($p>0.05$)					

Correlations between maize streak disease and yield parameters

Table 7 shows the correlations between MSD and yield parameters, pooling all the data from the three locations together. There was significant negative correlation between average MSD incidence and average 100-seed weight ($r=-0.36$, $p<0.05$), average seed weight ($r=-0.31$; $p<0.05$) but weakly negatively correlated with average cob weight ($r=-0.28$; $p<0.05$).

Table 7: Correlations between maize streak disease (MSD) and yield parameters.

Variable	**Mean MSD incidence**	**Mean MSD Severity**	**Mean 100-seed weight**	**Mean Cob weight**
Mean MSD incidence	1.00			
Mean MSD Severity	0.89**	1.00		
Mean 100-seed weight	-0.36*	-0.38*	1.00	
Mean Cob weight	-0.28	-0.32*	0.86**	1.00
Mean seed weight	-0.31*	-0.36*	0.90**	

*Significant ($p<0.05$) **Significant ($p<0.01$)

Similarly, there was significant negative correlation between average MSD severity score and average 100-seed weight (r=-0.38; p<0.05), average cob weight (r=-0.32; p<0.05) and average seed weight (r=-0.36; p<0.05) but positively correlated with average MSD incidence (r=0.89; p<0.01).

Discussion

All the 16 maize genotypes evaluated exhibited varying symptoms of MSV infection at all the three locations representing the three different AEZs of the Volta region. This suggests that MSV is common in the Volta region. This finding thus corroborates the reports of Martin and shepherd, [16]; Oppong et al., [14]; Asare-Bediako et al. [15] that MSD is a major viral disease of maize in Ghana, including Volta region.

Severity of MSD ranged from mild infection (mean SSS of 1.248) to moderate infection (mean SSS of 2.56) among the improved varieties tested across the three locations. It however ranged between moderate (mean SSS of 2.583) to severe infection (mean SSS of 3.72) for the local check (Dzinu-Eve) across the three locations **(Table 2)**. This finding is consistent with the results of the previous varietal screening experiment at Nkwanta [19], indicating that the MSV tolerance/resistance identified in genotypes Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa and pAN 12 was stable at different locations (AEZs) in the Volta region. Apart from pan 12, which is a known MSD tolerant maize variety from PANNAR seed (South Africa), the other eight genotypes were earlier released as improved maize variety with tolerance/resistance to MSV [25,26]. Similarly, the maize genotypes CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006, which are MSV-resistance maize breeding lines [18] were also stable in all the three locations. This suggests that these fifteen maize genotypes possess partial resistance which is stable under varying environmental conditions, indicating a steady state pathogen-host-environment interplay, as reported by Anneke et al. [27]. The differences in the resistance levels among these 15 maize genotypes may be attributed to different number of genes conferring resistance or to the influence of their genetic background [17].

The results of the study revealed that MSD incidence and symptom severity score (SSS) were generally highest at Nkwanta (transition AEZ), followed by Kpeve (forest AEZ) and then Ohawu (coastal savannah AEZ) **(Tables 1 and 2)**. This finding agrees with Asare-Bediako et al. [15] who reported higher MSD incidence and severity scores in the transition ecozone than the forest and the coastal savannah ecozones. This significant locational effect on MSD epidemiology could be due to interplay between the viral pathogen, host (the maize genotypes) and environment, as have been earlier reported [27]. The significant differences in the MSD incidence and severity amongst the three locations could be due to differences in population density of wild grasses that are reservoirs of both MSV and leafhopper vectors [28], the presence within leafhopper populations of a high percentage MSV transmitters; and environmental factors that drive the long distance movement of leafhoppers [29]. This suggests that factors that drive epidemiology of MSV is more favourable at Nkwanta, than Kpeve and less favourable at Ohawu, indicating that maize farmers in the transition AEZ could suffer greater yield losses due to MSV infection than those in the forest and coastal savannah AEZs. It has also been reported that the final major influence on MSD epidemiology is the strain composition of MSV population within leafhoppers and plant host species [16]. The MSV-A strain has been further split into five strain variants (MSV-A1, MSV-A2, MSV-A3, MSV-A4 and MSV-A6) each of which has a different geographical range [16,30]. MSV-A1 is by far the most widely distributed, occurring in every part of Sub-Saharan Africa where MSV-A viruses have been sampled. Oluwafemi et al. [31] observed variations of 30 MSV-A isolates from different parts of Nigeria. It is therefore possible that MSV-A variants occurring in the three AEZs differ, and that more severe strains could occur in the transition zone, hence the higher incidence and severity of MSD at Nkwanta than Kpeve and Ohawu.

The study detected a significant genotype x environment interaction effect in respect of MSD symptom severity scores **(Table 3)**. For instance, the mean symptom severity scores for Akposoe, Etubi, Honampa and PAN 12 were higher at Kpeve than at Nkwanta and Ohawu, whereas the Mean SSS for the other 12 genotypes were all higher at Nkwanta than Kpeve and Ohawu. This indicates that it is not advisable to grow these four maize genotypes (Akposoe, Etubi, Honampa and PAN 12) at Kpeve due to severe MSV infection. However, these genotypes could be planted at Nkwanta, where MSD epidermic has been reported [15]. Contrary to the results of the present work, Welz et al. [32] reported a detectable genotype x location interaction for scores taken at 21 days after inoculation (DAI) but negligible at 83 DAI. They argued that as disease peaks disease symptoms stabilize and location differences become negligible.

The study also revealed significant differences in seed yield amongst the maize genotypes at the various locations, and this could be due to differences in genetic background of the maize genotypes and host-virus interaction effects [25]. At all three locations Dzinu Eve, a local cultivar (included as a check), which exhibited severe symptoms, had the lowest yield, indicating that MSD can cause significant yield losses. This observation is supported by significant negative correlation between MSD incidence and severity and grain yields observed in this study **(Table 7)**, which is also consistent with the report of Bosquez-Perez et al. [33] which states that MSD negatively correlates with plant height and dry weight, grain weight per plot, and 1000-grain weight. This negative relationship between MSD severity and grain yields agrees with Magenya et al. [13] and Martin and Shepherd [16] who reported that MSD is a major maize disease in sub-Saharan Africa. It has also been reported that MSD is a major threat to maize crops among smallholder farmers in Sub-Saharan Africa causing up to US$ 480 million losses.

Interestingly, the improved varieties namely Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa, PAN 12, and the breeding lines CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006 which exhibited mild symptoms had high yields **(Tables 2 and 5)**. Cultivating these improved varieties that are tolerant to MSV infection would therefore reduce the effect of MSV in the region. The MSV-tolerant breeding lines (CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006) could be released as varieties following farmers' field trials within the various AEZs of the Volta region. Through several maize breeding programmes, to date several MSV-tolerant cultivars have been released. It is difficult to breed maize genotypes with high degree of resistance especially through conventional breeding [11]. This is so at least, partly because the resistance genes are scattered among different chromosomes, and this makes it difficult to transfer these genes into breeding lines because of linkage drag [16].

Conclusion

The study revealed that all the 16 maize genotypes evaluated at the three different AEZs showed varying degrees of MSD symptom severities. Both the improved varieties (Abontem, Aburohemaa, Akposoe, Dorke, Etubi, Honampa, Omankwa, Obatanpa and PAN 12) and the breeding lines CRI001, CRI002, CRI003, CRI004, CRI005 and CRI006, exhibited mild to moderate symptoms whereas the local cultivar (Dzinu-Eve) showed severe symptoms across the three AEZs. These MSV-resistant maize genotypes also gave significantly higher seed yields than the local cultivar Dzinu-Eve. MSD incidence and symptom severity score (SSS) were generally highest at Nkwanta (transition ecozone), followed by Kpeve (forest ecozone) and then Ohawu (coastal savannah ecozone), indicating that locations have significant effect on the degree of symptom expression in the maize genotypes. The mean symptom severity scores for Akposoe, Etubi, Honampa and PAN 12 were higher at Kpeve than at Nkwanta and Ohawu, whereas the Mean SSS for the other 12 genotypes were all higher at Nkwanta than Kpeve and Ohawu. This indicates a significant genotype x location interaction effect. It is therefore recommended that genotypes that showed mild symptoms of MSD and also gave high grain yields should be further evaluated and released as varieties for the locations where they performed better.

Conflicts of Interest

The authors declare that no conflicts of interest exist.

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Availability of Data and Materials

All data generated or analysed during this study are included in this published article

Ethics Approval and Consent to Participate

Not applicable.

Competing Interest

The authors declare that no conflicts of interest exist.

Authors Contribution

All authors performed the experiment. Author EAB developed the concept, wrote the protocol and the first draft of the manuscript. Authors EAB, GVP and KJT designed the study. Authors EAB and GA managed the analyses of the study. Author AAK and SAB managed the literature searches. All authors read and approved the final manuscript.

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