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BIOLOGICAL TRANSMISSION AND SEVERITY OF BLACKEYE COWPEA MOSAIC VIRUS IN SOYBEAN (*Glycine max* L. Merr.) LINES

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SUMMARY

Experiment was conducted under screenhouse conditions to evaluate the effect of *Blackeye cowpea mosaic virus* (BlCMV) infected seeds on the growth and seed weight of selected soybean lines. Seeds harvested from ten soybean lines infected with BlCMV were evaluated using Completely Randomised Design with five replications. Seeds from confirmed healthy soybean plants were used as control. Disease incidence, disease severity, growth and seed weight per plant were recorded and infection was confirmed using Antigen Coated Plate-Enzyme-Linked Immunosorbent Assay (ACP-ELISA). Data were subjected to Analysis of Variance at $p \leqslant 0.05$. At 4 weeks after sowing (WAS), 100 % disease incidence was observed among the BlCMV infected plants. TGX 1990 - 46F showed the lowest height reduction (4.8 %). Reduction in number of branches (22.2 %) and seed weight (86.7 %) was mildest in TGX 1951 - 3F. Based on most of the parameters evaluated, TGX 1951 - 3F and TGX 1990 - 46F were the least affected in seed-transmitted BlCMV – host plant pathosystem. These lines are candidates for further research in the effort to achieve sustainable strategy for reducing virus spread and improving soybean productivity in BlCMV endemic areas..

Keywords: BlCMV; disease severity; disease incidence; resistant genes; soybean

SOYBEAN (*Glycine max* L. Merr.) is an important crop in the tropical and subtropical regions of the world (7). Hitherto, its production was concentrated in the savanna agro-ecology of the country but more States (Benue, Kaduna, Kogi, Kwara, Oyo, Ondo, Adamawa, Taraba and Plateau) are now involved in large scale production (2). Soybean is an excellent source of food for human consumption and contributes substantially to the development of livestock industry. Soybean seed contains 34 to 36 % protein and is rich in vitamins such as thiamine, niacin, riboflavin, vitamin E and vitamin K, for normal body growth and development (3). In addition soybean has tremendous industrial applications such as pharmaceuticals, manufacture of oil, vanishes, printing inks and cosmetics (9). It is an important companion crop in traditional farming systems because of its ability to fix atmospheric nitrogen into the soil (1).

Inspite of its numerous uses, soybean production is limited by several abiotic and biotic factors. These factors individually or in combination directly reduce soybean seed yields. Such factors include unpredictable weather, insect pest attack, diseases, weed infestations and variable soil quality. Legume productivity is constrained by several viruses including *Blackeye cowpea mosaic virus* (BlCMV) (14). BlCMV, a potyvirus, was first observed in Florida, U.S.A (6). However, it has since spread to other regions of the world. The virus induces both local and systemic symptoms in susceptible

genotypes but symptoms and susceptibility depend on the cultivar and the virus strain. BICMV is mostly transmitted non-persistently by aphids. It is also seed-borne and seed-transmitted. It is also readily transmissible by sap inoculation.

Seed has been described as the most important productive material and more than 90 % of all food crops in the world are propagated by seed (12). In developing countries including Nigeria, farmers usually rely on seeds from the previous harvest for crop establishment at the beginning of the new season. Studies have shown that seed-borne and seed transmitted viruses may prove catastrophic if used for crop regeneration (4). Seed-borne viruses are difficult to control because infected seeds serve as means of long distance transmission and may initiate disease epidemics. Seed companies may suffer huge financial losses and their germplasm may be outrightly rejected at the international markets. Effective management of seed-transmitted viruses partly depends on cultivation of virus-free seeds. The objective of this study was to evaluate the effect of BICMV-infected seeds on the growth and seed weight of selected soybean lines.

MATERIALS AND METHODS

Study Location

The experiment was carried out under screenhouse conditions (temperature: 36 – 40 °C; relative humidity: 55 %) at the Teaching and Research Farm, Federal University of Technology (FUT), Minna (9°51'N, 6°44'E and 212 m above sea level), Niger State. Nigeria. Minna is located in the Southern Guinea Savanna with annual mean rainfall of 1200 mm. The rainfall is distributed between April and early October with peak around September. The relative humidity is between 40 and 80 %.

Source of Seeds

Soybean (TGX 1951 - 3F, TGX 1990 - 46F, TGX 1990 - 57F, TGX 2005 - 1F, TGX 2007 - 1F, TGX 2007 - 3F, TGX2009 - 1F, TGX 2009 - 9F, TGX 2012 - 1F and TGX 2013 - 1F) seeds harvested from the BICMV infected and confirmed healthy plants were obtained from the stock in the Department of Crop Production, Federal University of Technology, Minna. The seeds were stored for six months in paper bags at room temperature before the experiment.

Treatments, Experimental Design and Sowing

The ten selected soybean lines (TGX 1951 - 3F, TGX 1990 - 46F, TGX 1990 - 57F, TGX 2005 - 1F, TGX 2007 - 1F, TGX 2007 - 3F, TGX2009 - 1F, TGX 2009 - 9F, TGX 2012 - 1F and TGX 2013 - 1F) constituted the treatments. The experiment was arranged in Completely Randomised Design (CRD) with five replications. Five seeds of each soybean lines were sown in plastic pots (30 cm in diameter and 30 cm high). Seedlings were thinned to three plants per pot after emergence and the plants were maintained under screenhouse conditions (32 – 40 °C). Seeds from confirmed healthy soybean plants were used as control.

Data Collection and Virus Detection

Plants were assessed at 2, 3 and 4 weeks after sowing (WAS) for disease incidence and severity. BICMV severity was rated on a scale of 1 to 5 as described by Arif and Hassan (5). On the scale: 1 = absence of foliar symptoms; 2 = slight leaf mosaic; 3 = moderate leaf mosaic; 4 = severe leaf, leaf distortion and stunting; 5 = severe leaf mosaic with marked stunting and death of plants. Plant height, leaf diameter, and number of branches per plant were determined at 2, 3, 4 WAS while seed weight per plant was taken at harvest. At harvest, leaves were collected from

infected and control plants and subjected to Antigen Coated Plate-Enzyme-Linked Immunosorbent Assay (ACP-ELISA) to confirm infection (8). The leaves were ground (1:10; w/v) in coating buffer at pH 7.4 using mortars and pestles. One hundred microlitres of the leaf extract from each soybean line was tested in duplicate wells of the microtitre plate. Extracts of leaves from BICMV infected soybean and healthy soybean plants were used as positive and negative control, respectively. Absorbance values were accepted to be positive when the mean of the duplicate wells exceeded two times the negative control.

Statistical Analysis

Data on growth and yield characters were subjected to Analysis of Variance (ANOVA) and where significant ($p \leqslant 0.05$), means were separated using the Least Significant Difference (LSD). Statistical analysis was carried out using Statistical Analysis System (11).

RESULTS

Symptom of BICMV disease was sighted on the plants of virus infected seeds at 12 days after sowing. However, the leaves of the plants from healthy soybean seeds were apparently healthy. At 2 and 3 WAS, 100 % disease incidence was observed except in TGX 2012 - 1F, TGX 1951 - 3F and TGX 2005 - 1F where disease incidence averaged 80, 85 and 87.5 %, respectively (Table 1). However, the differences in disease incidence among the infected plants were not significant ($p>0.05$). At 4WAS after sowing, 100 % disease incidence occurred regardless of the soybean line. The infected soybean plants responded differently to infection but the differences in severity scores were not significant throughout the period of assessment. Disease severity generally varied between low (score = 2) and moderate (score = 3) level at 2 WAS among the infected plants (Table 1). The same trend was maintained at 3 WAS except in diseased TGX 2007 - 3F which exhibited a mean severity score of 4. At 4 WAS, disease severity ranged from 3 to 4, with TGX 2007 - 3F exhibiting the highest severity value. All the leaves of infected plants tested positive for BICMV whereas the healthy plants showed negative reaction (Table 2). Virus concentration in infected leaves varied from 0.25 to 1.2. The lowest titre (0.25) was found in TGX 1951 - 3F and TGX 1990 - 46F while TGX 2007 - 3F contained the highest (1.2).

Control plants were generally taller than the BICMV infected plants and at 2 WAS the difference was significant ($p<0.05$) in TGX 1990 - 57F, TGX 2007 - 1F and TGX 2013 - 1F (Fig. 1). TGX 2012 - 1F exhibited the lowest height reduction (6.3 %), followed by TGX 1951 - 3F (9.7 %). Height reduction was also relatively low in TGX 1990 - 46F (10.7 %) and TGX2009 - 1F (15 %) whereas the infected plants of TGX 2013 - 1F suffered the highest height reduction (78.3 %). At 3WAS, height difference between infected and healthy plants became more evident in 60 % of the soybean lines. The lowest height reduction was found in TGX 2007 - 3F (12.5 %), followed by 13.5 % reduction observed in infected plants of TGX 1990 - 46F. TGX 2013 - 1F exhibited the highest height reduction (77 %) while a range of 17.4 to 68.3 % was observed in the remaining genotypes. At 4 WAS, however, the infected plants of TGX 1990 - 46F showed the lowest height reduction (4.8 %), closely followed by TGX 1951 - 3F which exhibited 5.8 % height reduction. In TGX 2012 - 1F, 13.7 % height reduction was found. As observed in the previous weeks, TGX 2013 - 1F suffered the highest height reduction (75.6 %) while the remaining

genotypes exhibited a range of 15.6 to 53.8 %.

At 2 WAS, leaf diameter of infected plants was comparable to control plants in TGX 1951 - 3F, TGX 2007 - 3F and TGX2009 - 1F (Fig. 2). There was no reduction in leaf diameter of TGX2009 - 1F while 16.7 % reduction was found in TGX 2007 - 3F. Leaf diameter reductions among the remaining soybean lines varied between 42.3 and 81.8 %, with the highest value obtained in TGX 2007 - 1F. At 3WAS, TGX2009 - 1F showed the lowest 17.6 % leaf diameter reduction. In the remaining soybean lines, leaf diameter decreased by 30 to 78.4 %, with TGX 2009 - 9F being the most adversely affected. Again, there was no reduction in leaf diameter of TGX2009 - 1F at 4WAS. A range of 29.2 to 76 % reductions was found in the remaining soybean lines, with TGX 2013 - 1F being the most vulnerable.

Table 1: Disease incidence and severity from *Blackeye mosaic virus* infected soybean seeds at different weeks after sowing (WAS) in a screenhouse

	Disease incidence (%)			Disease severity		
Soybean line	2 WAS	3 WAS	4 WAS	2 WAS	3 WAS	4 WAS
TGX 1951 - 3F	85.0	85.0	100.0	2.0	3.0	3.0
TGX 1990 - 46F	100.0	100.0	100.0	2.0	3.0	3.0
TGX 1990 - 57F	100.0	100.0	100.0	2.5	3.0	3.0
TGX 2005 - 1F	87.5	87.5	100.0	3.0	3.0	3.0
TGX 2007 - 1F	100.0	100.0	100.0	2.5	2.5	3.0
TGX 2007 - 3F	100.0	100.0	100.0	3.0	4.0	4.0
TGX2009 - 1F	85.0	85.0	100.0	2.0	2.0	3.0
TGX 2009 - 9F	100.0	100.0	100.0	3.0	3.0	3.5
TGX 2012 - 1F	80.0	80.0	100.0	2.5	2.5	3.5
TGX 2013 - 1F	100.0	100.0	100.0	3.0	3.0	3.0
±SEM	10.0	7.8	4.7	0.5	0.9	0.6

Table 2. Virus concentrations from the leaves of *Blackeye mosaic virus* infected and healthy (control) soybean seeds based on Enzyme-Linked Immunosorbent Assay (ELISA)

	Absorbance (405_{nm})		Absorbance (405_{nm})	
Soybean line	Infected	Remark	Control	Remark
TGX 1951 - 3F	0.25	+	0.10	–
TGX 1990 - 46F	0.25	+	0.11	–
TGX 1990 - 57F	0.41	++	0.12	–
TGX 2005 - 1F	0.42	++	0.11	–
TGX 2007 - 1F	0.39	++	0.10	–
TGX 2007 - 3F	1.20	+++	0.11	–
TGX2009 - 1F	0.41	++	0.11	–
TGX 2009 - 9F	0.90	+++	0.11	–
TGX 2012 - 1F	0.80	+++	0.10	–
TGX 2013 - 1F	0.41	++	0.10	–
Positive control	1.40			
Negative control	0.12			

– = negative; + = positive (absorbance of the negative control × 2); ++ = positive (absorbance of the negative control × 3); +++ = positive (absorbance of the negative control × 4 and above)

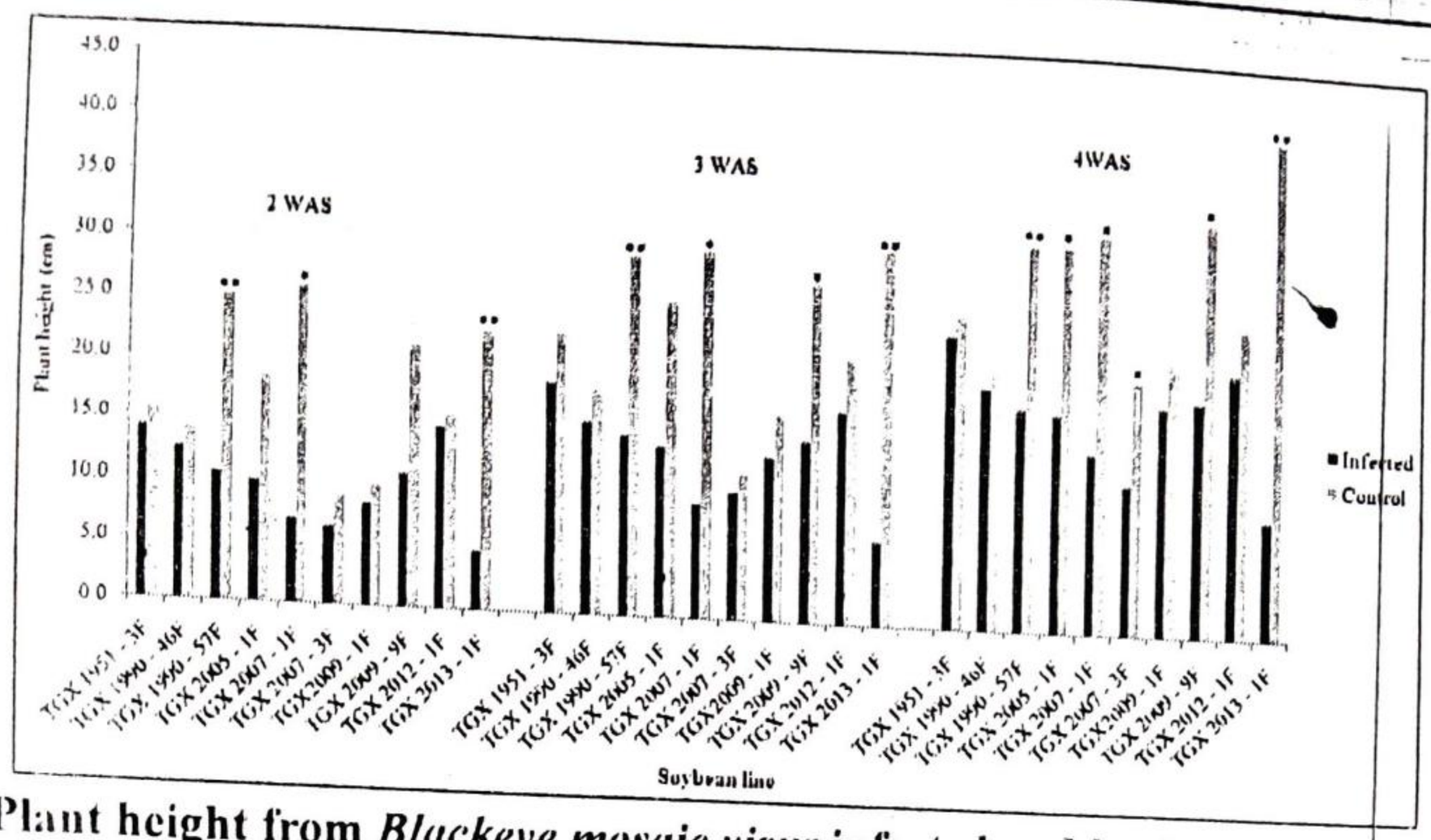

Fig. 1: Plant height from *Blackeye mosaic virus* infected and healthy (control) soybean seeds at different weeks after sowing (WAS) in a screenhouse *Significant at $p \leqslant 0.05$; **Significant at $p \leqslant 0.01$

The effect of BICMV on number of branches was not as dramatic as in other parameters. At 2 and 3 WAS, the difference in number of branches per plant between infected and non-infected plants was significant only in TGX 2007 - 1F and TGX 2013 - 1F as shown in Fig. 3. A similar result was obtained in these two soybean lines as well as in TGX 1990 - 57F and TGX 2012 - 1F at 4WAS. At 2 WAS, there was no reduction in the number of branches of TGX 1951 - 3F, TGX 2007 - 3F and TGX2009 - 1F. In the remaining soybean lines, branches were reduced by 20 to 80 %, with TGX 2013 – 1 exhibiting the highest. At 3 WAS, reduction in number of branches was relatively low in TGX 1990 - 46F (14.3 %), TGX 1951 - 3F (16.7 %) and TGX2009 - 1F (20 %). In the remaining soybean lines, branches were reduced by 33.3 to 83.3 % and the highest reduction was found in TGX 2013 - 1F. At 4 WAS, the lowest reduction in number of branches was found in TGX 1951 - 3F (22.2 %) whereas TGX 2013 - 1F was the most vulnerable (75 %). Number of branches decreased by 25 % in TGX 1990 - 46F and TGX 2005 - 1F while TGX2009 - 1F suffered 28.6 % reduction. In the remaining soybean lines, relatively high reductions (37.5 to 54.5 %) were encountered.

Seed weight was significantly reduced by BICMV infection in all the soybean lines (Fig. 4). Reductions in seed weight varied between 86.7 and 94.5 % with the two extreme values encountered in TGX 1951 - 3F and TGX 2013 - 1F, respectively.

DISCUSSION

The data on disease incidence revealed similar genetic background among the evaluated soybean lines. Although not all the plants from infected seeds elicited symptoms of BICMV at 2 and 3 WAS, the fact that complete infection was found at 4 WAS indicated that the virus could survive in the seed of infected soybean plant for up to six months after harvest. Survival in the seed of infected plants is therefore, an effective medium for BICMV transmission which may result in disease epidemic. There is no doubt that viruses can be found in different parts of the seed such as embryo, endosperm and even on the seed

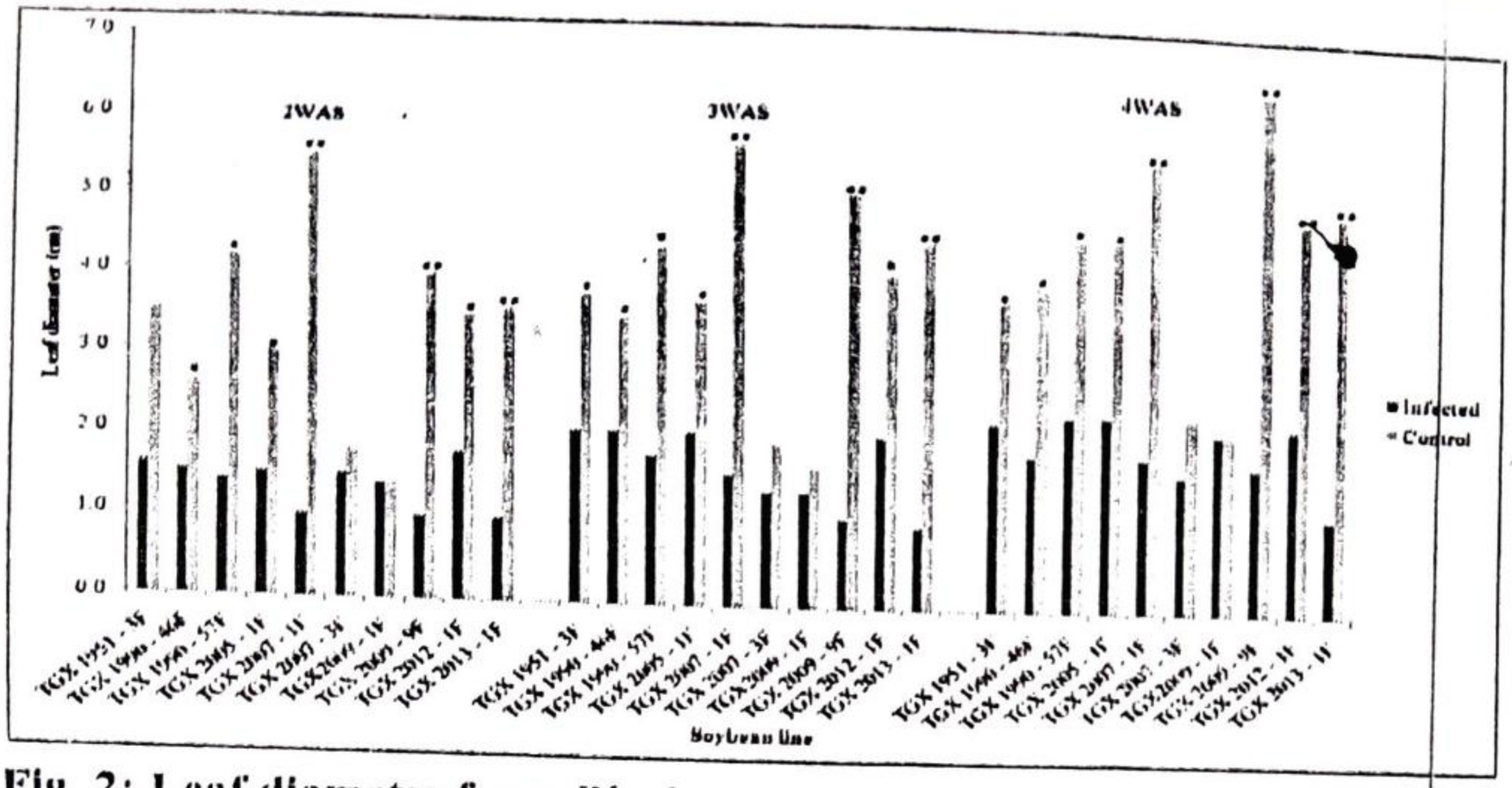

Fig. 2: Leaf diameter from *Blackeye mosaic virus* infected and healthy (control) soybean seeds at different weeks after sowing (WAS) in a screenhouse *Significant at $p \leq 0.05$; **Significant at $p \leq 0.01$

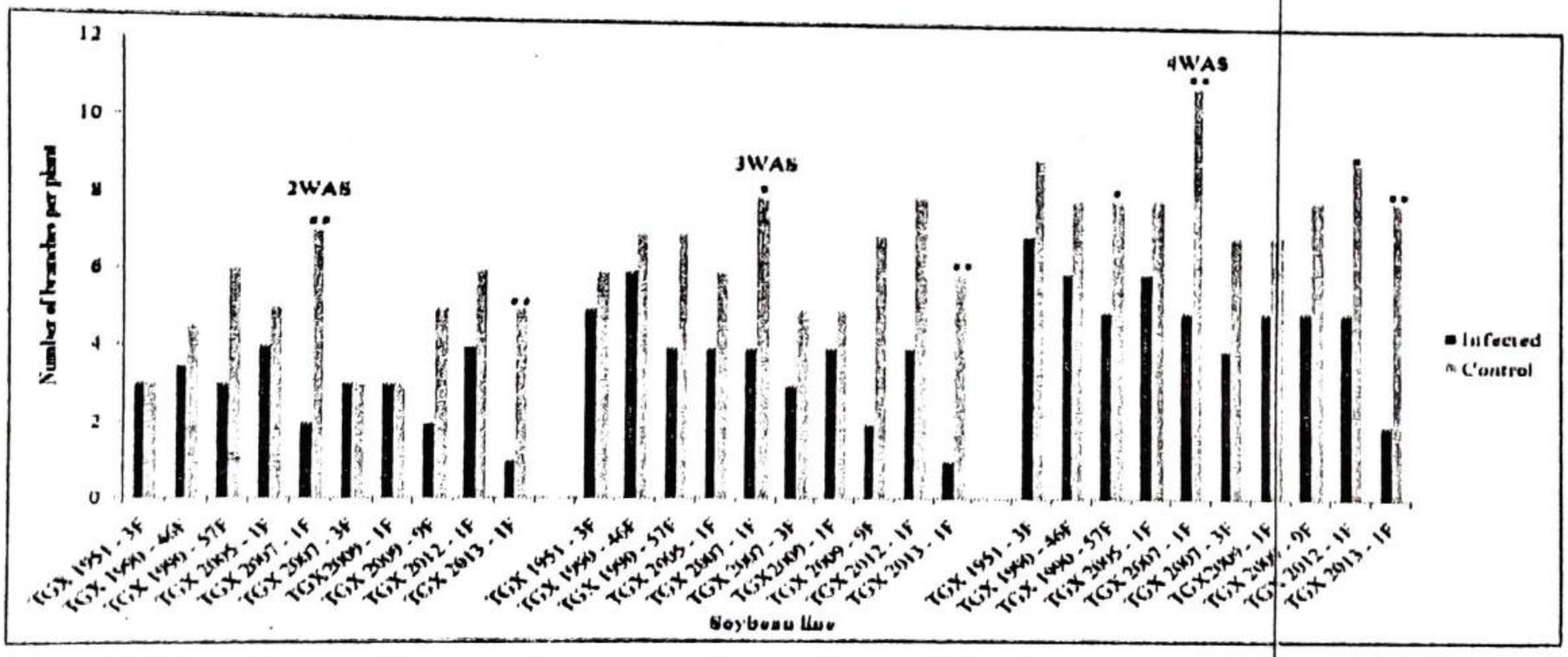

Fig. 3: Number of branches per plant from *Blackeye mosaic virus* infected and healthy (control) soybean seeds at different weeks after sowing (WAS) in a screenhouse *Significant at $p \leq 0.05$; **Significant at $p \leq 0.01$

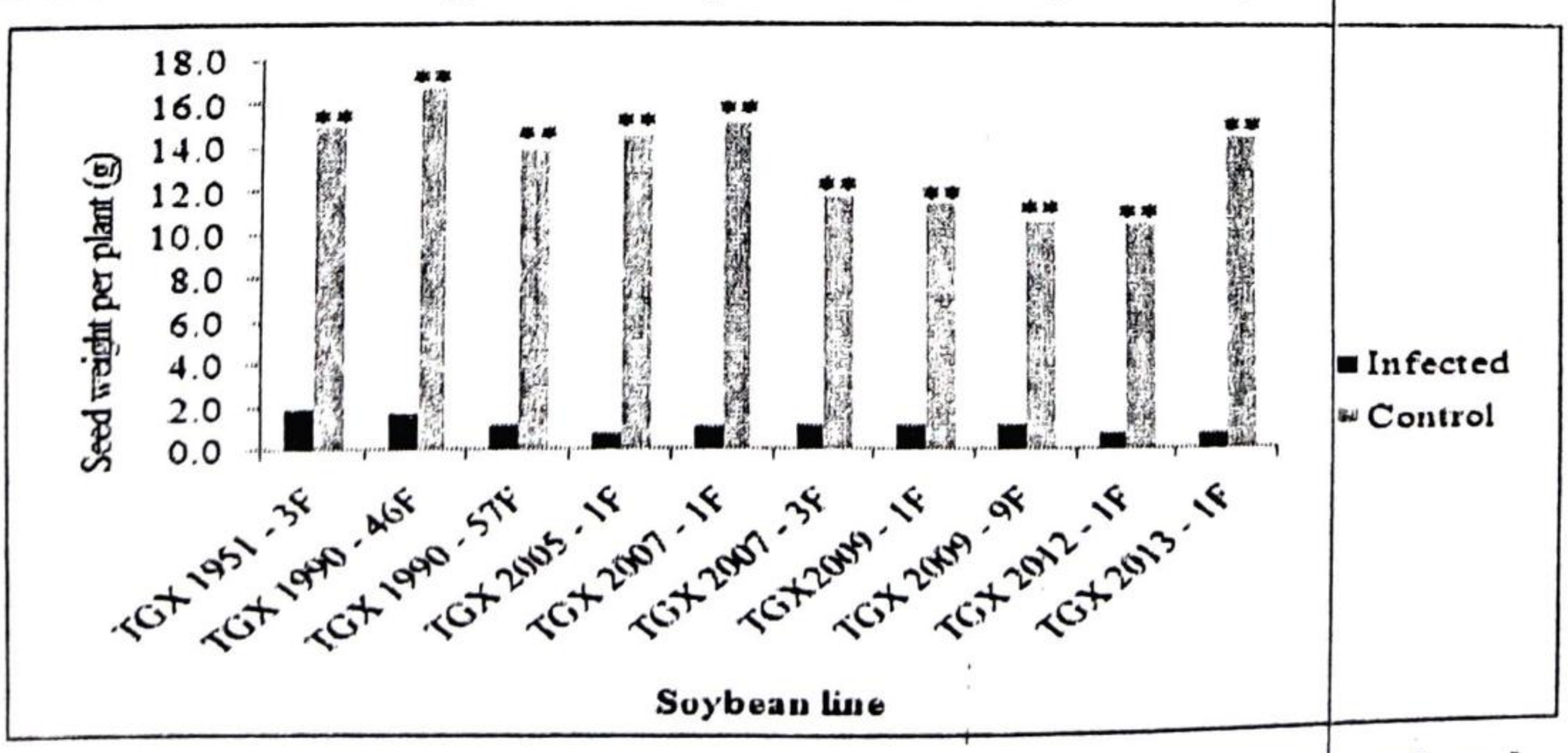

Fig. 4: Seed weight per plant from *Blackeye mosaic virus* infected and healthy (control) soybean seeds in a screenhouse **Significant at $p \leq 0.01$

coat. However, most transmission occurs when the embryo is infected. Transmission of BlCMV by infected seeds corroborated the findings of Udayashankar *et al.* (15) in an experiment involving cowpea seeds infected with BlCMV. Complete infection was not detected in TGX 2012 - 1F, TGX 1951 - 3F and TGX 2005 - 1F at the early growth stage, probably because they contained resistant gene(s). However, the fact that all the plants showed symptoms of infection afterward implied that there was no inhibition to virus survival in the seeds of infected plants. The differences in the reactions of evaluated soybean lines revealed their genetic variation. Disease severity was consistently high in TGX 2007 - 3F probably because of its susceptibility to the virus. It could be argued that virus concentration was highest in the leaves of infected plants of TGX 2007 - 3F due to the highest diseases severity. This implied a positive correlation between symptom scoring and serological test.

Virus-infected plants were generally shorter than the healthy plants due to the deleterious impact of the virus. Studies have shown that viruses are capable of reducing metabolic activity in infected plant which in turn exerts negative effect on its growth and development (17). Some infected plants elicited severe height reductions, indicating that genetic background of the evaluated plants played a significant role in the level of resistance observed among the soybean lines. The same reason possibly accounted for the variation observed in leaf diameter. The observed growth reductions were consequences of poor physiological and photosynthetic activities induced by virus particles. These results agreed with the findings of Ryslava *et al.* (10). In some soybean lines, growth characters were mildly reduced owing to low virus concentration in infected seeds. Varma *et al.* (16) observed that 100 ng of *Blackgram mottle virus* (BMoV) was required in the embryo of blackgram seed for the resulting seedling to become systemically infected. Although BMoV is not a potyvirus, it is possible to encounter a similar phenomenon with BlCMV in soybean seed. Since most of the infected plants produced number of branches similar to the healthy plants, it revealed that this character was not adversely affected in seed-transmitted BlCMV disease.

Reduction in seed weight was high irrespective of the soybean line owing to the aggregate effects of reductions in plant height, leaf diameter and number of branches. Therefore, the fitness and productivity of virus-infected plants was lower than the healthy plants due to physiological stress with low photosynthetic rate of the symptomatic leaves (13).

CONCLUSION AND RECOMMENDATION

Based on most of the parameters evaluated, TGX 1951 - 3F and TGX 1990 - 46F were the least affected in seed-transmitted BlCMV – host plant pathosystem. These lines are candidates for further research in the effort to achieve sustainable strategy for reducing virus spread and improving soybean productivity in BlCMV endemic areas.

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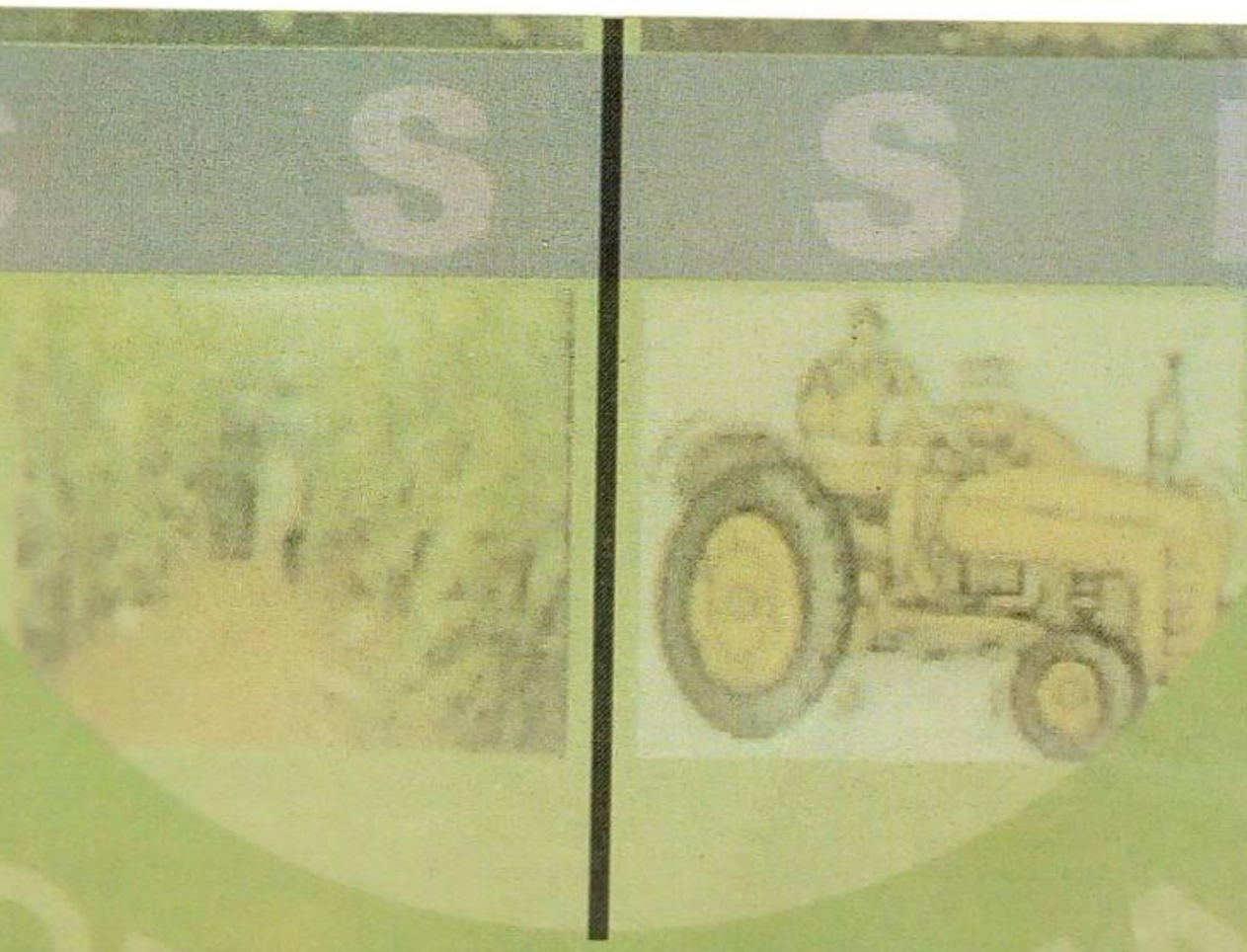

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GROWTH AND YIELD OF STRIGA-TOLERANT MAIZE GENOTYPES UNDER MAIZE STREAK VIRUS INFECTION IN MINNA, NORTHERN NIGERIA

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ABSTRACT

Striga infestation and Maize streak virus (MSV) disease constitute serious limitations to maize productivity in sub-Saharan Africa. Adoption of resistant maize varieties remains the most effective and sustainable control measure against both biotic stresses. Thirteen maize genotypes with differential Striga resistance background were evaluated against MSV infection in Minna, Nigeria during the 2017 wet season. Maize seeds were planted in July 2017 and seedlings were observed for MSV disease incidence, disease severity, growth and yield characters. The data were subjected to cluster and analysis of variance. The lowest (20 %) incidence of MSV disease was found in "9022-13". The genotypes "(2*TZECOMP3DT/White DTSTRSYN) C2", "(TZEOMPC7/TZECOMP3DTC2) C2" and "9022-13" exhibited the lowest disease severity (symptom score = 2.0). Cob (92.3 g) and grain (70.7 g) weights per plant were highest in "SAMMAZ-15". The Striga-tolerant maize genotype "SAMMAZ 15" was the best for cob and grain weight under MSV infection and "(TZEOMPC7/TZECOMP3DTC2) C2" was identified as the most genetically related to "SAMMAZ 15". Therefore, both genotypes are recommended for cultivation in areas that are prone to Striga and MSV disease.

Key words: cob weight, disease incidence, grain weight, *maize streak virus*, symptom severity

INTRODUCTION

Maize (*Zea mays* L.) is a staple food for millions of people in sub-Saharan Africa. It is also processed into various forms for domestic and industrial purposes (Gwirtz and Garcia-Casal, 2014). Maize is commonly intercropped with legume crops such as cowpea, groundnut and soyabean (Alabi and Esobhawan, 2006) for various purposes, including control of insect pests and diseases. It is believed to have originated in Central America, particularly in Mexico (Matsuoka, 2005) from its wild relative teosinte (*Zea mays* L. subsp. *parviglumis*). The crop was probably introduced to West Africa in the 16th century from Arab countries or from West Indies and Central and South America to the Gold Coast (now Ghana) through Sao Tome. It thrives well in all the agro-ecological zones of Nigeria but cultivation is highly concentrated in the Savanna belt. Globally, the United States of America is the largest producer of maize, with more than 50 % of the total production (FAO, 2016). In 2016, maize production in Nigeria was about 10.4 million tonnes (FAO, 2016). This estimate comes mainly from the resource-poor smallholder farmers. It has been predicted that the global demand for maize in 2020 would increase to 852 million Metric tonnes (MT) compared with 760 million MT for wheat and 503 million MT for rice (James, 2003), indicating that maize productivity must rise appreciably beyond the present 1 t/ha in most African countries. Maize productivity is low in developing countries because production is at subsistence level. In addition, witch weed (*Striga hermontheca*) infestation causes severe yield losses (Badu-Apraku *et al.*, 2008). Several strategies have been proposed for ameliorating the *Striga* menace with the goal of reducing yield losses below economic threshold. These include increased nitrogen fertilizer application, interplanting with

legumes such as cowpea, groundnut, and *Aeschnomenes histrix*. However, cultivation of resistant varieties remains the most effective strategy. *Maize streak virus* has been observed in Nigeria since 1970s as a serious setback to maize productivity. Its outbreak is capable of causing 100 % yield loss in susceptible varieties (Caravina, 2014). *Maize streak virus* belongs to the genus *Mastrevirus* of the family *Geminiviridae*. Susceptible plants exhibit whitish or yellowish short broken streaks along the leaf veins. The virus is transmitted persistently by the leafhoppers (*Cicadulina* spp) (Olaoye, 2009). Leafhoppers can acquire the virus within a short period of feeding on infected plants. Of the 22 known leafhoppers, only eight species are efficient transmitters of MSV: *Cicadulina arachidis* China, *C. bipunctata* Melichar, *C. ghaurii* Dabrowski, *C. latens* Fennah, *C. mbila* Naudé, *C. parazeae* Ghauri, *C. similis* China, and *C. storeyi* China (= *C. triangula* Ruppel) (Fajemisin, 2001). In a study, Alegbejo and Banwo (2005) reported a positive correlation between leafhopper population and MSV disease incidence in Nigeria. In northern Nigeria, leafhopper population is usually high towards the end of rainfall, between September and October. Adoption of resistant cultivars is the most effective strategy against MSV disease. Therefore, efforts are continually geared towards identification of sources of resistant genes. Maize varieties that are tolerant to *Striga* infestation are available in the country, just as the MSV-resistant varieties. However, there is scarcity of information on the varieties that combine both attributes. Identification of *Striga* and MSV-tolerant maize varieties would serve as an insurance against total crop loss and a reliable strategy for encouraging food security. Therefore, this study was conducted to identify high-yielding *Striga*-tolerant maize genotypes under MSV disease pressure.

MATERIALS AND METHODS

Description of the Study Site

The experiment was conducted at the Teaching and Research Farm, Federal University of Technology, Minna. It is located at latitude 9^0 51′N and longitude 6^0 44′E, and is 212 metres above sea level. Minna is situated in the Southern Guinea agro-ecology of Nigeria with distinct rainy and dry seasons. The rainy season normally spans between April and October. The relative humidity of Minna ranges from 40 to 80 %. The site has been used for the cultivation of maize, guinea corn millet, cowpea, soyabean and groundnut in the last five years.

Land Preparation and Planting Material

The site was cleared of plant debris, ploughed and ridged on 14th July, 2017. Ridges were 5 m long, and maize seeds were sown at inter- and intra-row spacing of 75 cm × 50 cm, respectively. Thirteen *Striga*-tolerant maize genotypes were obtained from the Maize Breeding Unit, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. They were "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1", "(2*TZECOMP3DT/WhiteDTSTRSYN) C2", "(TZEOMPC7/TZECOMP3DTC2) C2", "8338-1 (*Striga* susceptible hybrid)", "9022-13 (*Striga* resistant hybrid)", "DTSTR-W-SYN11", "DTSTR-W-SYN12", "DTSTR-W SYN13", "DTSTR-W-SYN14", "DTSTR-W-SYN15", "SAMMAZ-15", "SAMMAZ-16", "TZB-R (*Striga* susceptible) ".

Experimental Design and Agronomic Practices

The treatments consisted of the 13 *Striga*-tolerant maize varieties listed above. The treatments were laid out using randomised complete block design (RCBD) with three replications. Three maize seeds were sown in their respective plots on 15th July, 2017 and the seedlings were thinned to one plant per stand at 1 week after sowing (WAS). Manual weeding was carried out at 3 and 6 WAS.

Data Collection

Incidence of MSV disease was determined at 6 and 8 WAS, based on percentage of the total plants eliciting foliar streaking symptom. A 5-point scale was used for assessing the disease severity (Salaudeen, 2012) as follows :1 = no foliar symptoms; 2 = very few streaks on 11 – 25 % of leaf surface; 3 = moderate streaking of 26 – 50 % on leaf surface; 4 = severe streaking on 51 – 75 % of leaf surface; 5 = very severe streaking on >75 % of leaf surface. The growth (plant height and number of leaves per plant) and yield (number of days to tasselling, number of days to silking, ear height, number of cobs per plant, cob weight per plant, and grain weight per plant) parameters were also recorded.

Statistical Analysis

The data collected were subjected to analysis of variance using PROC GLM option of the Statistical Analysis System (SAS, 2008) and significance was determined at 5 % probability level. The treatment means were separated using the Student-Newman-Keuls (SNK) test. The growth and yield data were further subjected to cluster analysis, using the average linkage method (Everitt *et al.*, 2011).

RESULTS

Incidence and severity of MSV infection

At 6 WAS, none of the plants of the maize genotypes (2*TZECOMP3DT/WhiteDTSTRSYN) C2", "(TZEOMPC7/TZECOMP3DTC2) C2, "DTSTR-W-SYN11" and "DTSTR-W-SYN12" was infected by the virus. In the remaining genotypes, MSV disease incidence varied significantly ($p<0.05$) between 20 and 60 % (Table

1). Similarly, disease incidence ranged from 20 – 60 % at 8 WAS. The highest disease incidence was found in "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1" and "DTSTR-W SYN13", whereas "9022-13" exhibited the lowest (20 %) incidence of MSV disease. White short streaks were observed on the leaves of MSV infected plants but at varying levels of severity. The plants of "(2*TZECOMP3DT/White DTSTRSYN) C2", "(TZEOMPC7/TZECOMP3DTC2) C2", "DTSTR-W SYN11" and "DTSTR-W SYN12" had symptom severity score of 1 whereas five genotypes (8338-1, DTSTR-W-SYN15, SAMMAZ-15, SAMMAZ-16 and TZB-R) exhibited a symptom rating of 2 at 6 WAS. In the maize genotypes "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1" and "DTSTR-W-SYN14", disease severity of 2.7 and 3.7 was observed, respectively. The highest symptom score of 4 was found in "9022-13" and "DTSTR-W SYN13". At 8 WAS, all the asymptomatic plants elicited typical symptoms of MSV disease. Disease severity ratings varied between 2 and 3 but the differences were not significant (p>0.05). Disease severity decreased in the plants of "9022-13" and"DTSTR-W SYN13" from 4 to 2 and 3, respectively. In addition to "9022-13", the genotypes 2*TZECOMP3DT/White DTSTRSYN) C2" and "(TZEOMPC7/TZECOMP3DTC2) C2" exhibited the lowest disease severity (symptom score = 2). Similarly, the maize genotypes "DTSTR-W-SYN11" and "DTSTR-W-SYN15" had same disease severity rating (symptom score =2.3). In "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1", "8338-1", "DTSTR-W-SYN12" and "TZB-R" a symptom score of 2.7 was found while the remaining genotypes exhibited an average symptom rating of 3.

Effect of MSV on Plants' Growth and Yield Attributes

At 6 WAS, there were no significant (p>0.05) height differences among the genotypes (Table 2). Despite this observation, the MSV infected plants of "SAMMAZ-15" (103.8 cm) were the tallest, followed by "(2*TZECOMP3DT/White DTSTRSYN) C2" (101.7 cm), "(TZEOMPC7/TZECOMP3DTC2) C2" (100.5 cm), and "TZB-R" (100.3 cm). Conversely, the infected plants of "9022-13" (78 cm) were the shortest. The height of other genotypes varied between 79.3 and 94.7 cm. At 8 WAS significant (p<0.05) height differences were found among the genotypes (Table 2). The plants of "TZB-R" (136.1 cm) were the tallest but its mean height was not significantly (p>0.05) different from those of "SAMMAZ-15" (133.7 cm), "TZEOMPC7/TZECOMP3DTC2) C2" (131.4 cm), "(2*TZECOMP3DT/White DTSTRSYN) C2" (130.6 cm), "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1" (121.3 cm), "8338-1" (119.6 cm) and "DTSTR-W-SYN15" (119.5 cm). Although the shortest plants were observed in "DTSTR-W-SYN12" (104.4 cm), the value obtained was statistically similar to those of "DTSTR-W-SYN11" (114.0 cm), "SAMMAZ-16" (112.9 cm), "9022-13" (111.3 cm), "DTSTR-W-SYN14" (108.7 cm) and "DTSTR-W SYN13" (104.8 cm).

Table 1: Incidence and severity ratings of the maize plants infected with *Maize streak virus* disease in Minna, Northern Nigeria

	Disease incidence (%)		Disease severity	
Genotype	6 WAS	8 WAS	6 WAS	8 WAS
((TZL COML1-W C6*2/(White DT STR Syn))-DT C1	26.7±11.5^{c}	60±0^{a}	2.7±0.6^{b}	2.7±0.6^{a}
(2*TZECOMP3DT/WhiteDTSTRSYN) C2	0±0^{d}	46.7±11.5^{ab}	1.0±0^{c}	2.0±0^{a}
(TZEOMPC7/TZECOMP3DTC2) C2	0±0^{d}	40±0^{ab}	1.0±0^{c}	2.0±0^{a}
8338-1	46.7±23.6^{ab}	40±11.5^{ab}	2.0±0^{bc}	2.7±0.6^{a}
9022-13	20.0.0±0^{cd}	20±0^{ab}	4.0±0^{a}	2.0±0^{a}
DTSTR-W-SYN11	0±0^{d}	40±0^{ab}	1.0±0^{c}	2.3±0.6^{a}
DTSTR-W-SYN12	0±0^{d}	26.7±11.5^{b}	1.0±0^{c}	2.7±0.6^{a}
DTSTR-W-SYN13	60.0±0^{a}	60.0±0^{a}	4.0±0^{a}	3.0±0^{a}
DTSTR-W-SYN14	26.7±11.5^{c}	26.7±11.5^{b}	3.7±1.2^{a}	3.0±1.7^{a}
DTSTR-W-SYN15	20.0±0^{cd}	26.7±11.5^{b}	2.0±0^{bc}	2.3±0.6^{a}
SAMMAZ-15	20.0±0^{cd}	26.7±11.5^{b}	2.0±0^{bc}	3.0±0^{a}
SAMMAZ-16	26.7±11.5^{c}	33.3±11.5^{ab}	2.0±0^{bc}	3.0±0^{a}
TZB-R	20.0±0^{cd}	33.3±11.5^{ab}	2.0±0^{bc}	2.7±0.6^{a}
±SEM	4.7	6	0.2	0.3

Means with similar superscript letter (s) within the column do not differ significantly (p>0.05) based on Student-Newman-Keuls test

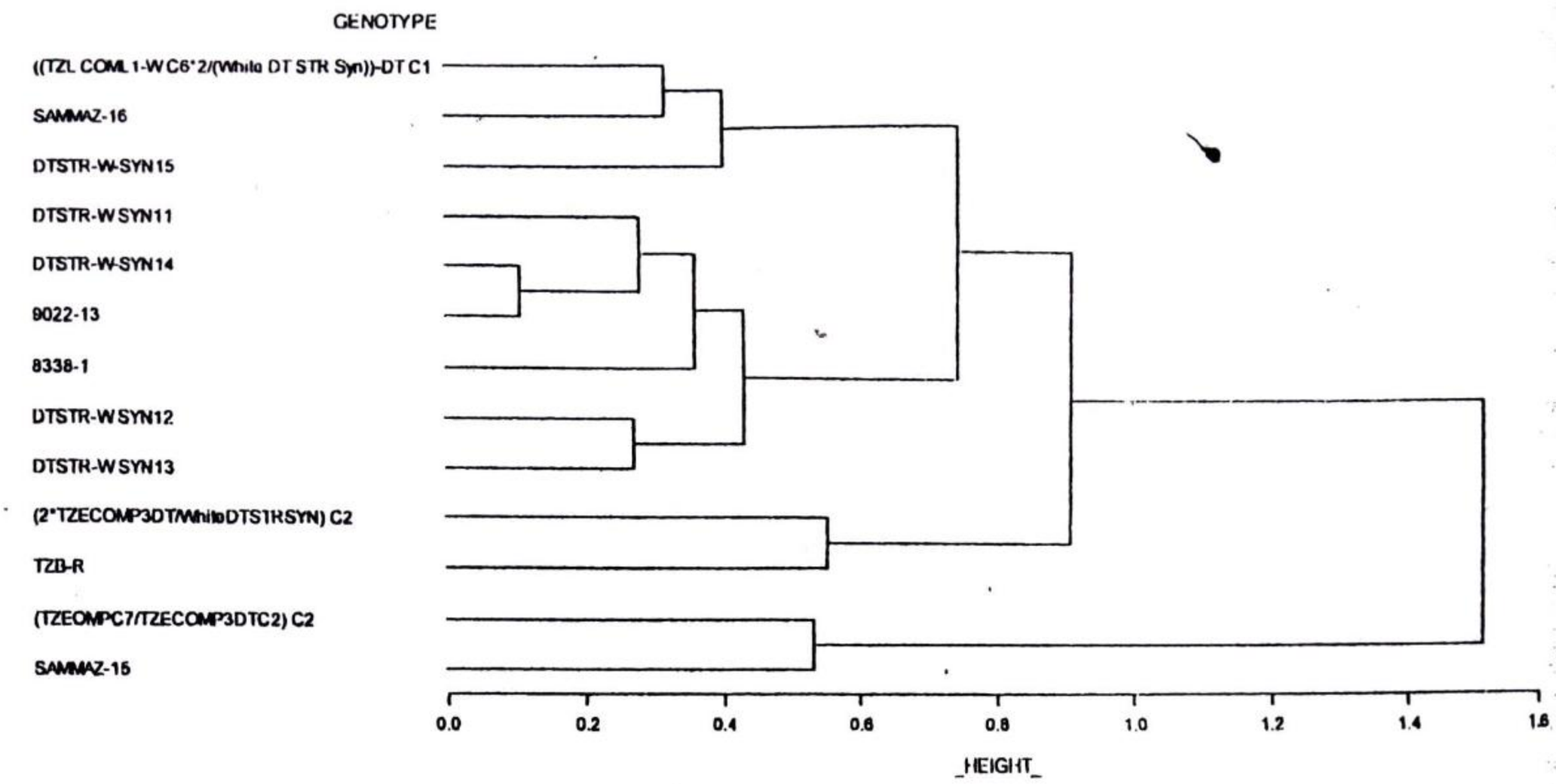

Figure 1: Dendogram of the relationship for growth and yield characters of the maize genotypes infected with *Maize streak virus*

differences in number of days to tasseling among

Table 2: Growth parameters of the maize plants infected with *Maize streak virus* disease in Minna, Northern Nigeria

Genotype	Plant height (cm) 6 WAS	Plant height (cm) 8 WAS	Number of leaves per plant 6 WAS	Number of leaves per plant 8 WAS	Number of days to tasseling
((TZL COML1-W C6*2/(White DT STR Syn))-DT C1	86.6±11.3^{a}	121.3±4.4^{ab}	8±0.6^{ab}	10±0.7^{a}	60±4.0^{a}
(2*TZECOMP3DT/WhiteDTSTRSYN) C2	101.7±4.6^{a}	130.6±8.3^{ab}	9±0.6^{a}	10±1.0^{a}	58±3.2^{a}
(TZEOMPC7/TZECOMP3DTC2) C2	100.5±6.6^{a}	131.4±16.2^{ab}	9±0^{a}	10±0.6^{a}	59±3.2^{a}
8338-1	91.2±9.4^{a}	119.6±7.8^{ab}	7±0.6^{b}	9±0.6^{a}	62±1.0^{a}
9022-13	78.0±15.8^{a}	111.3±7.5^{b}	7±0.6^{b}	9±0.6^{a}	62±1.0^{a}
DTSTR-W-SYN11	89.3±14.1^{a}	114.0±15.1^{b}	8±0.6^{ab}	9±0^{a}	63±3.2^{a}
DTSTR-W-SYN12	84.6±5.8^{a}	104.4±5.7^{b}	7±0.6^{b}	9±0.6^{a}	63±0^{a}
DTSTR-W-SYN13	81.8±16.6^{a}	104.8±13.9^{b}	8±1.0^{ab}	9±1.0^{a}	61±1.5^{a}
DTSTR-W-SYN14	79.3±10.4^{a}	108.7±4.2^{b}	9±1.2^{a}	10±0.6^{a}	62±1.2^{a}
DTSTR-W-SYN15	94.7±10.8^{a}	119.5±10.8^{ab}	9±0.6^{a}	10±1.0^{a}	60±1.5^{a}
SAMMAZ-15	103.8±1.2^{a}	133.7±6.6^{ab}	8±0.6^{ab}	10±0.6^{a}	61±1.0^{a}
SAMMAZ-16	89.3±9.8^{a}	112.9±12.1^{b}	8±0.6^{ab}	10±0.6^{a}	58±5.9^{a}
TZB-R	100.3±12.6^{a}	136.1±13.9^{a}	8±0.6^{ab}	9±0.6^{a}	60±2.9^{a}
±SEM	6.2	5.9	0.4	0.3	1.6

Means with similar superscript letter (s) within the column do not differ significantly (p>0.05) based on Student-Newman-Keuls test

Significant ($p < 0.05$) differences were also found for number of leaves per plant (Table 2). A range of 7 (8338-1, 9022-13 and DTSTR-W-SYN12) to 9 [(2*TZECOMP3DT/White DTSTRSYN) C2, TZEOMPC7/TZECOMP3DTC2) C2, DTSTR-W-SYN14 and DTSTR-W-SYN15] leaves per plant was observed at 6 WAS. The remaining genotypes produced an average of 8 leaves per plant. At 8 WAS, number of leaves varied but not significantly ($p > 0.05$) between 9 and 10 per plant. The lowest number of leaves per plant was found in "8338-1", "9022-13" "DTSTR-W- SYN11", "DTSTR-W-SYN12", "DTSTR-W SYN13" and "TZB-R". The other genotypes produced an average of 10 leaves per plant. There were no significant (p>0.05) the maize genotypes (Table 2). In spite of this, tassel formation was earliest in "SAMMAZ-16" and "(2*TZECOMP3DT/White DTSTRSYN) C2" (58 days after sowing) while tasseling was observed at 63 days after sowing (DAS) in "DTSTR-W- SYN11" and "DTSTR-W - SYN12" (Table 3). In the remaining genotypes tasseling was observed between 60 and 62 DAS. As reported for days to tasseling, there were no significant (p>0.05) differences in number of days to silking among the maize genotypes but values ranged between 63 (DTSTR-W-SYN15) and 70 (8338-1, DTSTR-W-SYN11, DTSTR-W SYN13) DAS. Ear height was significantly ($p < 0.05$) highest in "TZB-R" (86.5 cm), whereas the differences in ear height among the other genotypes (51.3 – 69.1 cm) were not significant (p>0.05) (Table 3). There were no

significant ($p > 0.05$) differences in number of cobs per plant among the genotypes. Apart from "(TZEOMPC7/TZECOMP3DTC2) C2", "DTSTR-W SYN13", "DTSTR-W-SYN15" and "SAMMAZ-15" which produced two cobs other genotypes had one cob per plant. The evaluated genotypes exhibited significant ($p < 0.05$) variation in cob weight per plant (Table 3). The highest cob weight per plant was found in "SAMMAZ-15" (92.3 g). Next was that of "(TZEOMPC7/TZECOMP3DTC2) C2" (79.4 g), which was statistically similar to those of "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1" (64.4 g) and "SAMMAZ-16" (63.1 g). The lowest cob weight per plant was found in "DTSTR-W-SYN12" (38.8 g) but was statistically comparable to the cob weights of the remaining genotypes (42.2 – 53.7 g per plant). The trend of grain weight per plant was as observed for cob weight per plant (Table 3). The highest grain weight was found in "SAMMAZ-15" (70.7 g), followed by "(TZEOMPC7/TZECOMP3DTC2) C2" which had grain weight of 58.4 g per plant. The lowest grain weight per plant was observed in "DTSTR-W SYN12" (27.1 g) which was not significantly ($p>0.05$) different from grain weights of the remaining genotypes. Cluster analysis revealed that "SAMMAZ 15" and "(TZEOMPC7/TZECOMP3DTC2) C2" belonged to the same group (cluster 1). Conversely, "(2*TZECOMP3DT/White DTSTRSYN) C2" and "TZB-R" were members of the same group (cluster 2), whereas the remaining genotypes formed cluster 3 (Figure 1).

DISCUSSION

Maize streak disease affected the growth and yield parameters of the evaluated genotypes relative to their genetic background. At 6 WAS some of the evaluated plants did not elicit disease symptoms. Those plants could be termed as "escapes". The observation that the "escape" plants eventually exhibited MSV disease symptoms at 8 WAS confirmed that they were not immune to the pathogen. Such plants ultimately elicited disease symptoms owing to the persistent nature of MSV transmission by the leafhopper vectors (Magenya *et al.*, 2008). There was no total infection at 8 WAS because leafhoppers normally feed on young plants but as the plants mature their cells and tissues become lignified. This discourages further feeding and disease transmission under field conditions. Twenty two species of the leafhoppers have been found globally and 18 are in Africa (Magenya *et al.*,2008). Of these, only eight species are efficient transmitters of MSV. Even within the leafhoppers that transmit the pathogen, marked variability occurs for virus acquisition and transmission efficiency time; some are able to acquire the virus within few seconds whereas others require up to 24 hours. Moderate level of infection was observed because leafhopper population was low at the time of evaluation (wet season). Thus studies on leafhopper dynamics have shown that the population of the vector is usually high towards the end of rainy season (Alegbejo and Banwo, 2005). Therefore, all these probably accounted for the observed variation in the MSV disease incidence. The severity of MSV disease rose gradually from minute streaks to elongated form which eventually covered the entire leaf surface as a consequence of the virus' replication and multiplication in the host plants. This agreed with the findings of Bosque-Pérez *et al.* (2000). The formation of streaks on leaf surface was due to inhibition of the activity of chloroplasts (Bosque-Pérez *et al.*, 1998). Generally, viruses recruit their host structures for self multiplication and establishment. Therefore, disease severity declined as the plants matured because of the progressive lignification of cells and tissues of the host plants. The data on disease severity revealed a moderate level of infection. Symptom severity was slightly higher at 8 WAS than 6 WAS in some genotypes as a result of continuous multiplication of the virus in such plants. Those plants which exhibited a slight decrease in symptom severity at 8 WAS probably contained MSV resistant genes. This is in agreement with the findings of Bosque-Pérez *et al.* (1998) who reported that plant infection at the early growth stage resulted in severe symptom expression while late infection was characterized by development of few streaks. The data on most of the evaluated parameters indicated that the impact of MSV disease was similar among the maize genotypes. The differences in growth and yield parameters of the maize genotypes could be attributed to their inherent genetic background and partly due to deleterious effects of MSV infection. This is in tandem with the result obtained by Mawere *et al.* (2006) when some inbred maize lines were infected with MSV. Cob and grain weights are important characters in maize breeding and the differences exhibited among the genotypes for these traits were significant. This implied that selection would favour some genotypes for maize improvement program. Therefore, the *Striga*-tolerant maize genotype "SAMMAZ 15" was the most productive under MSV infection. However, "TZEOMPC7/TZECOMP3DTC2) C2", "((TZL COML1-W C6*2/(White DT STR Syn))- DT C1" and "SAMMAZ 16" which also exhibited high cob and grain weights could serve as alternative promising candidates under MSV disease pressure.

Table 3: Yield and yield related attributes of the maize plants infected with *Maize streak virus* disease in Minna. Northern Nigeria

Genotype	Number of days to silking	Ear height (cm)	Number of cobs per plant	Cob weight per plant (g)	Grain weight per plant (g)
((TZL COML1-W C6*2/(White DT STR Syn))-DT C1	68±0.6 [a]	68.2±4.2 [b]	1±0 [a]	64.4±10.6 [ab]	44.9±10.7 [ab]
(2*TZECOMP3DT/WhiteDTSTRSYN) C2	66±2.1 [a]	68.6±3.4 [b]	1±0 [a]	47.6±10.1 [b]	34.7±3.9 [b]
(TZEOMPC7/TZECOMP3DTC2) C2	66±3.6 [a]	65.6±4.1 [b]	2±0.6 [a]	79.4±17.0 [ab]	58.4±10.5 [ab]
8338-1	70±1.0 [a]	56.2±0.3 [b]	1±0 [a]	42.2±16.9 [b]	31.8±12.9 [b]
9022-13	68±1.5 [a]	60.6±2.2 [b]	1±0 [a]	48.2±17.1 [b]	32.1±14.3 [b]
DTSTR-W-SYN11	70±4.0 [a]	67.7±4.6 [b]	1±0 [a]	44.9±23.5 [b]	33.0±21.6 [b]
DTSTR-W-SYN12	68±3.2 [a]	55.1±5.8 [b]	1±0.6 [a]	38.8±13.3 [b]	27.1±7.2 [b]
DTSTR-W- SYN13	70±2.6 [a]	51.3±8.0 [b]	2±0.6 [a]	45.9±25.8 [b]	31.5±17.7 [b]
DTSTR-W-SYN14	67±1.2 [a]	59.3±15.4 [b]	1±0.6 [a]	46.7±5.6 [b]	33.4±1.7 [b]
DTSTR-W-SYN15	63±1.5 [a]	62.8±2.8 [b]	2±0.6 [a]	53.7±16.7 [b]	41.6±13.8 [ab]
SAMMAZ-15	68±0.6 [a]	69.1±5.0 [b]	2±0.6 [a]	92.3±12.3 [a]	70.7±20.8 [a]
SAMMAZ-16	69±3.2 [a]	62.6±13.8 [b]	1±0.6 [a]	63.1±20.6 [ab]	47.7±16.7 [ab]
TZB-R	68±1.2 [a]	86.5±1.1 [a]	1±0.6 [a]	50.4±10.9 [b]	34.7±6.7 [b]
±SEM	1.3	3.9	0.3	9	7.2

Means with similar superscript letter (s) within the column do not differ significantly ($p>0.05$) based on Student-Newman-Keuls test

The result of cluster analysis showed that "(TZEOMPC7/TZECOMP3DTC2) C2" belonged to the same group with "SAMMAZ 15" revealed that they were the most genetically related. Additionally, the data on number of leaves per plant implied that the two genotypes possessed additional advantage of being good sources of fodder for livestock feeding. This is premised on the fact that maize is mostly cultivated by peasant farmers that practice mixed farming in sub-Saharan Africa. Therefore, genotypes having multipurpose values would gain wider acceptability and adoption.

CONCLUSION AND RECOMMENDATION

This study revealed that MSV disease incidence and severity were genotype dependent. The *Striga*-tolerant maize genotypes "SAMMAZ 15" was the best for cob and grain weight under MSV infection while "(TZEOMPC7/TZECOMP3DTC2) C2" was identified as the most genetically related to "SAMMAZ 15". Further studies should be conducted to ascertain the validity of the results obtained from this experiment.

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