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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 hermontheica*) 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 *Aeschynomenes 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. gaurii* 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° 51'N and longitude 6° 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*TZCOMP3DT/WhiteDTSTRSYN) C2”, “(TZEOMPC7/TZCOMP3DTC2) 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*TZCOMP3DT/WhiteDTSTRSYN) C2”, “(TZEOMPC7/TZCOMP3DTC2) 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 COMLI-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 COMLI-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 COMLI-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 COMLI-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

Genotype	Disease incidence (%)		Disease severity	
	6 WAS	8 WAS	6 WAS	8 WAS
((TZL COMLI-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 ^{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

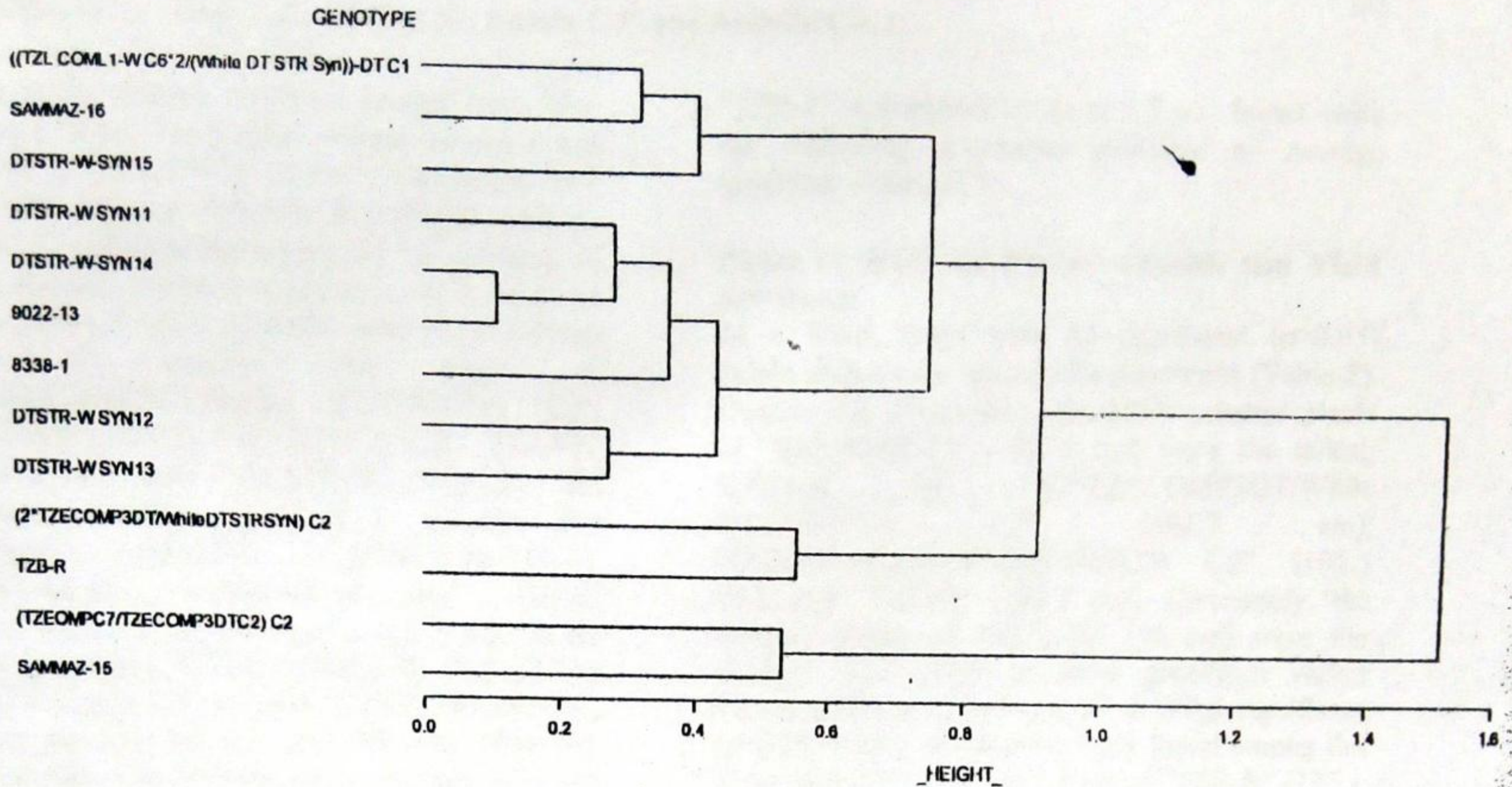


Figure 1: Dendrogram of the relationship for growth and yield characters of the maize genotypes infected with *Maize streak virus* differences in number of days to tasseling among

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

Genotype	Plant height (cm)		Number of leaves per plant		Number of days to tasseling
	6 WAS	8 WAS	6 WAS	8 WAS	
((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 COMLI-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 COMLI-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 COMLI-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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