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GROWTH AND YIELD RESPONSES OF SELECTED COWPEA (*Vigna unguiculata* L. Walp) GENOTYPES TO CUCUMBER MOSAIC VIRUS DISEASE

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ABSTRACT

Cowpea is a dependable source of protein for human growth and development. The crop is widely cultivated in sub-Saharan Africa including Nigeria. In spite of its numerous uses, infection by *Cucumber mosaic virus* (CMV) disease constitutes a serious problem to cowpea productivity and once plants are infected, there is no remedy as in the case of other pathogens such as bacteria, fungi and nematodes. Cultivation of resistant genotypes is cost effective, ecologically sound and sustainable strategy against the disease. Twenty-three cowpea genotypes with differential yield and resistance background were evaluated against CMV infection in screen house. Cowpea seedlings were inoculated at ten days after sowing. The plants were observed for CMV disease incidence, disease severity, growth and yield parameters. The data collected were subjected to cluster and analysis of variance. The genotype 09 K-480 was observed to have the lowest disease incidence (22.2%). However, the genotypes lID15- 40, 12 K- 261 and 12 K- 809 exhibited the lowest disease severity (score = 2.3). Seed weight (1.5 g) per plant were heaviest in 08 K - 125 - 107. Therefore, the genotype 08 K - 125 - 107 is recommended for cultivation in areas that are prone to CMV disease. Additionally, this genotype probably combines CMV tolerant genes that could be explored for breeding purposes.

Keywords: Breeding, *Cucumber mosaic virus*, Disease incidence, Disease severity, Seed weight.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) is a short-day leguminous crop in the tropics and subtropics. It is a drought tolerant and warm-weather crop. The crop has the ability of fixing atmospheric nitrogen into the soil with the help of bacteria living in its root nodules (Asiwe *et al.*, 2009). This crop can grow well in soil containing above 85 % sand and 0.2 % organic matters and low level of phosphorus.. Cowpea thrives well in agro-ecological zone where the annual rainfall is between 500 mm and 1200 mm. More than 5.4 million metric tonnes of dried cowpea are produced worldwide annually. Nigeria produces 61 % of Africa production share and 58 % worldwide production. Nigeria, Niger, Senegal, Ghana, Mali and Burkina Faso are known to be the key producers of cowpea in West Africa (Food and Agriculture Organization [FAO], 2016). However, Nigeria is the largest producer and consumer of cowpea in the World, and the country production share comes mainly from the Northern region of Nigeria (FAO, 2016).

Cucumber mosaic virus (CMV) has a wide host range and it attacks vegetables, ornamentals, weeds and other crops such as Cowpea (Crescenzy, 2003). This virus has been reported in Argentina, France, United State and some African countries as a major threat to annual crops including cowpea (Nault *et al.*, 2006). It affects yield, quality and quantity of infected crops and severity of infection can be determined by the level of susceptibility of the cultivar. The virus constitutes a serious problem to cowpea productivity and once cowpea is infected, there is no remedy as in the case of other pathogens such as bacteria, fungi and

nematodes. Aliyu *et al.* (2012) reported 100 % yield losses in susceptible cultivars, and farmers in such case abandon their farms. Therefore, this study was conducted to identify sources of resistance to *Cucumber mosaic virus* disease on selected cowpea genotypes in the southern guinea agro-ecological zone of Nigeria.

MATERIALS AND METHODS

Two trials were conducted in the screen house at the Teaching and Research Farm of Department of Crop Production, Federal University of Technology, Minna, Niger State, Nigeria ($9^0$51'N, $6^0$44'E and 212 m above sea level), during 2017 cropping season. Minna is located in the Southern Guinea Savannah agro-ecological zone of Nigeria with a mean annual rainfall of 1200 mm (Adeboye *et al.,* 2011). The rainfall usually begins in April and terminates in the first week of October. The temperature ranges of Minna are between 35 ^{0}C and 37.5 ^{0}C and relative humidity between 40 % and 80 %. The soils of Minna are said to originate from basement complex rocks and are generally classified as Alfisol (Adeboye *et al.,* 2011).

Source of Cowpea Seeds

Twenty-three cowpea genotypes were collected from International Institute of Tropical Agriculture (IITA), Kano Station, Kano State, Nigeria for the study. These genotypes are Ife Brown, TVU 408, 11D-15-40, 04K-267-8, 07K-230-2-9, 07K-291-69, 08K-125-24, 08K-125-107, 08K-193-15, 09K-480, 10K-819-4, 10K-836-3, 12K-261, 12K-515, 12K-809, IT08K-125-100, IT08K-187-5, IT10K-292-10, IT10K-822-7, IT10K-828-3, IT10K-830-9, IT10K-837-1, IT10K-837-1 and IT12K-113. They were chosen due to desirable attributes such as early maturing and high yielding.

Treatments and Experimental Design

The twenty-three genotypes (treatments) were arranged in a Completely Randomised Design (CRD) with three replications.

Source of Inoculum and Multiplication

The CMV isolate used was obtained from the Department of Crop Production, Federal University of Technology, Minna Niger State. *Cucumber mosaic virus* isolate was extracted by grinding 1g/1ml of isolate in extraction buffer containing 0.1M sodium phosphate dibasic, 0.1M potassium phosphate monobasic, 0.0lM ethylene diamine tetra acetic acid and 0.00lM-cystine per litre of distilled water using a pre-cooled sterilized mortar and pestle as described by Kumar (2009). Two microliters of β- Mercapto-ethanol was added to the extract just before used following the Kumar (2009) method. Thereafter, cowpea seedlings were infected with CMV inoculum at 10 days after sowing (DAS) by rubbing the virus extract on the upper surface of the leaves that was dusted with carborundum powder (600- mesh). The leaves of inoculated plant were rinsed with sterile distilled water. Symptomatic cowpea leaves were collected from the infected plants at 3 weeks after inoculation (WAI) and used for inoculation during the main experiment. The leaves were preserved at room temperature (27^{o}C) in airtight via bottle on silica gels covered with a thin layer of non-absorbent cotton wool.

Sowing and Inoculation

Cowpea seeds were sown in plastic pots (30 cm diameter and 30 cm deep) at the rate of five seeds per pot and the seedlings were thinned to three plants per pot after emergence. Seedlings were inoculated with CMV extract at 10 days after sowing. Virus inoculum was extracted and inoculation performed as described above.

Data Collection and Statistical Analysis

Data were collected on CMV disease incidence, disease severity. Disease severity was based on a visual scale (1 – 5) of Abdulrahman *et al*. (2017). On the scale, 1 = no symptoms, 2 = slight mosaic; 3 = moderate mosaic, 4 = severe mosaic, leaf distortion and stunting, 5 = severe mosaic, stunting and plant death. Number of leaves per plant, leaf diameter, pod length and seed weight were also recorded. All data were subjected to analysis of variance (ANOVA) using the general linear model (PROC GLM) procedure of SAS (2008). Treatment means were separated using Duncan Multiple Range Test (DMRT) at $p \leq 0.05$. Cluster analysis was carried out on all the growth and yield data to determine the relationship among the selected genotypes.

RESULTS

Incidence and Severity of CMV infection

Disease symptoms were first sighted at 10 days after inoculation (DAI). All inoculated plants in trial 1 and 2 showed typical foliar symptoms of CMV infection at different level. The symptoms were mild leaf chlorosis and mosaic on the secondary leaves of the infected plants. At 1 WAI, the disease incidence varied significantly ($p<0.05$) between 0 and 88.9 % in trial 1. The highest disease incidence of 88.9 % was found in cowpea genotype 12K-809 followed by 12K -261 with 77.8

% incidence. Similarly, Ife Brown, TVU 408 and IT12K-13 exhibited 66.6 % level of infection, whereas 08K-193-15 and 09K-480 exhibited no disease incidence (Table 1). At 2 WAI in trial 1, disease incidence was significantly (p<0.05) highest (100 %) in Ife Brown, TVU 408, 07K-230-2-5, 07K-291-69, 12K-261, 12K-515, 12K-809, IT08K-125-100, IT08K-187-5, IT10K-292-10, IT10K-822-7, IT10K-830-9, IT10K-837-1 and IT12K-13. This was followed by cowpea genotypes 08K-125-107 which had 88.9 % disease incidence. In 11D-15-40, 10K-819-4 and 10K-836-3, disease incidence of 77.8 % was found whereas 09K-480 and IT10K-828-3 had the lowest disease incidence of 55.6 % and genotype 08K-193 -15 had no symptom (Table 1).

In trial 2, disease incidence differed significantly (p<0.05) amongst the twenty-three genotypes investigated at 1 WAI. The highest was observed in IT12K- 13 with 77.8 % followed by genotypes 10K-819-4 and IT10K-125-100 with 33.3 % disease incidence. Next were 09K-480 and IT08K-187-5 with 22.2 % disease incidence. Ife Brown, TVU 408,11D-15-40,07K-291-69, 08K-125-107, 10K-836-3, and 12K- 809 exhibited 11.1 % disease incidence while 04K-267-8, 07K-230-2-5, 08K-193-15, 12K-261, 12K-515, IT10K292-10, IT10K-822-7, IT10K-828-3, IT10K-830-9 and IT10K-837-1 had no symptom (Table 1). At 2 WAI in trial 2, the differences observed in disease incidence differed significantly (p<0.05). Cowpea genotypes 11D-15-40, 12K 515, IT08K-125-100, IT0 K-187-5 and IT10K-822-7 exhibited significantly (p<0.05) highest disease incidence of 100 %. Ife Brown, TVU 408, 07K-230-2-5 and IT12K-13 were next with 88.9 %, this was followed by genotypes 07K-291-69, 08K-125-24 and 10K- 836-3 with 77.8 % whereas disease incidence of 66.7 % was found in genotypes 04K-267-8, 10K-819-4, 12K-261, IT10K-292-10 and IT10K-837-1. The lowest disease incidence (22.2 %) was found in 09K-480 (Table 1).

At 3 WAI in trial 1, there were plants with severity score of 3.0 and this was peculiar to 04K-267-8 and IT10K-822-7. Genotypes 10K-836-3 and IT10K-837-1 exhibited 2.7 disease severity score whereas Ife Brown, TVU 408, 07K-230-2-5, 07K-291-69, 08K-125-107, 09K-480, 10K-819-4, 12K-809, IT10K-828-3 and IT10K-830-9 had a severity score of 2.3 (Table 1). At 5 WAI in trial 1, cowpea genotypes 09K-480, 10K-819-4 and 10K- 836-3 exhibited significantly (p<0.05) highest severity score of 4.0, 11D-15-40, 04K267-8, IT10K-822-7 and IT10K-837-1 elicited disease severity score 3.7, whereas the lowest severity score of 1.0 was observed in 08K-193-15 (Table 1). At 3 WAI in trial 2, the differences observed in disease severity differed significantly (p<0.05). The highest severity of 2.3 was observed in 07K-230-2-5. Ife Brown, TVU 408, 04K- 267-8, 07K-291-69, 08K-125-24, 08K-125-107, 08K-193-15, 09K-480, 10K-819-4, 10K-836-3, 12K-261, 12K 515, 12K-809, IT08K-125-100, IT08K-187-5, IT10K-292-10, IT10K-822-7, IT10K-837-1 and IT12K-13 exhibited a severity score of 2. The cowpea genotypes 11D-15-40 and IT10K-828-3 had 1.7 while cowpea genotype IT10K-830-9 had the lowest severity score of 1.3 (Table 1). At 5 WAI in trial 2, the genotypes IT10K-292-10 and IT10K-822-7 exhibited significantly (p<0.05) highest disease severity score of 3.3. Conversely, the cowpea genotypes 04K-267-8,07K-291-69, 08K-125-107,10K-819-4, 12K-515, IT08K-125-100, IT08K-187-5 and IT12K-13 had a severity score of 3 while Ife brown, 11D-15-40, 12K-261 and 12K-809 exhibited the lowest severity score of 2.3.

Effect of CMV on Plants' Growth and Yield Attributes

At 3 WAI in trial 1, number of leaves varied significantly between 10 and 18 leaves per plant. More number of leaves per plant (18 leaves) was found in genotypes 12K-261 and IT10K-292-10. Genotype 08K-125-24 had 16 leaves, 08K-193-15 and IT10K-828-3 produced 15 leaves each and Ife Brown, 07K-291-69, 08K-125-107, 10K-836-3, 12K-809, IT1-0K-837-1 had 14 leaves each which were similar statistically whereas the lowest of 10 leaves was found in IT10K-822-7 (Table 2). At 5 WAI in trial 1, more number of leaves (28 leaves) was observed per plant in 04K-267-8 followed by the cowpea genotype 09K-480 with 23 leaves per plant. Genotypes 08K-125-24 and 08K-125-107 had 21 leaves each. Ife Brown, 12K-261 and 12K-809 produced 19 leaves each while others gave numbers of leaves between 14 and 17 leaves per plant which were statistically similar (p>0.05) (Table 2). At 3 WAI in trial 2, Ife Brown, 07K-230-2-5, 08K-125-107 and 08K-125-107 produced significantly (p<0.05) more number of leaves per plant (17 leaves), 07K-291-69 and 08K-125-24 gave 16 leaves each per plant while the remaining genotypes produced number of leaves which did not differ from one another (Table 2). At 5 WAI in trial 2, significantly (p<0.05) more number of leaves per plant of 26 was observed in the genotypes 04K-267-8 and 04K-267-8 whereas genotypes IT08K-187-5, IT10K-822-7, IT10K-830-9 and IT12K-13 elicited the least of 14 leaves

each. The remaining genotypes had number of leaves which did not differ statistically.

Effect of *Cucumber mosaic virus* Disease on Leaf Diameter

As in other growth parameters, the leaf diameter differed significantly (p<0.05) among the genotypes. At 3 WAI in trial 1, leaf diameter varied between 2.9 cm (10K-836-3) and 4.8 cm (IT10K-292-10). The genotype IT10K-292-10 had 4.8 cm followed by IT10K-187-5 which had 4.5 cm leaf diameter. The genotypes. 10K-836-3 (2.9 cm) and 12K-515 (3.0 cm) were similar whereas the remaining genotypes did not differ in leaf diameter (Table 3). At 5 WAI in trial 1, the genotype with the widest leaf diameter was TVU 408 (6.1 cm), next to it was genotype IT10K-292-10 (5.8 cm) whereas the lowest in leaf diameter of 3.5 cm was found in 12K-515 (Table 3). At 3 WAI in trial 2, leaf diameter ranged between 3.3 and 6.4 cm. Ife Brown (5.8 cm) ran second after genotype TVU 408 which had a significantly (p<0.05) widest leaf diameter of 6.4 cm. This was followed by 11D-15-40 with 5.4 cm and the least in leaf diameter of 3.3 cm was observed in cowpea genotype 10K-836-3 (Table 3). Also, at 5 WAI in trial 2, the genotype TVU 408 exhibited significantly (p<0.05) widest leaf diameter of 7.4 cm. Next to this was genotype 11D-15-40 with 6.4 cm whereas genotypes IT10K-292-10 and 08K-193-15 had the lowest leaf diameter of 4.6 cm each (Table 3).

Effect of *Cucumber mosaic virus* Disease on Pod Length and Seed Weight Per Plant

In trial 1, genotype 10K-819-4 significantly (p<0.05) produced the longest pod length of 16.1 cm. The genotypes IT08K-187-5 and IT10K-822-7 gave 15.1 and 14.7 cm respectively which were similar whereas the shortest in pod length of 7.5 cm was found in genotypes TVU 408 (Table 5). Also, in trial 2, result on pod length did not differ from that recorded in trial 1 above (Table 4). In trial 1, the cowpea genotypes generally exhibited no significant (p>0.05) differences in seed weight. However, 07K-291-69 (1.1), 08K-125-107 (1.2), 08K-193-15 (1.1), 10K-836-3 (1.1), 12K-809 (1.2), IT08K-187-5 (1.1), IT10K-292-10 (1.2) and IT10K-828-3 (1.2) performed better than the rest genotypes. In trial 2, the differences observed among the genotypes were not significant (p>0.05) However, Ife brown (1.6 g) had the heaviest seed weight followed by 08K-125-107 and 10K-836-3 (1.5 g). The genotypes 08K-125-24, 08K-193-15, 12K-261, IT10K-830-9 and IT10K-837-1 had uniform seed weight (Table 4

Table 1: Incidence and Severity of *Cucumber mosaic virus* disease on the cowpea genotypes evaluated

	Disease incidence (%)				Disease severity			
	Trial 1		Trial 2		Trial 1		Trial 2	
Genotype	1 WAI	2 WAI	1 WAI	2 WAI	3 WAI	5 WAI	3 WAI	5 WAI
Ife Brown	66.7^{ab}	100.0^{a}	11.1^{b}	88.9^{a}	2.3^{ab}	3.0^{a}	2.0^{ab}	2.3^{a}
TVU 408	66.7^{ab}	100.0^{a}	11.1^{b}	88.9^{a}	2.3^{ab}	3.0^{a}	2.0^{ab}	2.7^{a}
11D-15-40	33.3^{ab}	77.8^{a}	11.1^{b}	100.0^{a}	2.0^{ab}	3.7^{a}	1.7^{ab}	2.3^{a}
04K-267-8	11.1^{ab}	66.7^{a}	0.0^{b}	66.7^{a}	3.0^{a}	3.7^{a}	2.0^{ab}	3.0^{a}
07K-230-2-5	22.2^{ab}	100.0^{a}	0.0^{b}	88.9^{a}	2.3^{ab}	3.3^{a}	2.3^{a}	2.7^{a}
07K-291-69	22.2^{ab}	100.0^{a}	11.1^{b}	77.8^{a}	2.3^{ab}	2.3^{a}	2.0^{ab}	3.0^{a}
08K-125-24	44.4^{ab}	66.7^{a}	11.1^{b}	77.8^{a}	2.0^{ab}	2.3^{a}	2.0^{ab}	2.7^{a}
08K-125-107	22.2^{ab}	88.9^{a}	11.1^{b}	55.6^{a}	2.3^{ab}	3.0^{a}	2.0^{ab}	3.0^{a}
08K-193-15	0.0^{b}	0.0^{b}	0.0^{b}	44.4^{a}	1.0^{b}	1.0^{b}	2.0^{ab}	2.7^{a}
09K-480	0.0^{b}	55.6^{a}	22.2^{b}	22.2^{b}	2.3^{ab}	4.0^{a}	2.0^{ab}	2.7^{a}
10K-819-4	22.2^{ab}	77.8^{a}	33.3^{b}	66.7^{a}	2.3^{ab}	4.0^{a}	2.0^{ab}	3.0^{a}
10K-836-3	44.4^{ab}	77.8^{a}	11.1^{b}	77.8^{a}	2.7^{ab}	4.0^{a}	2.0^{ab}	3.0^{a}
12K-261	77.8^{ab}	100.0^{a}	0.0^{b}	66.7^{a}	2.0^{ab}	2.7^{a}	2.0^{ab}	2.3^{a}
12K-515	55.6^{ab}	100.0^{a}	0.0^{b}	100.0^{a}	2.0^{ab}	3.0^{a}	2.0^{ab}	.3.0^{a}
12K-809	88.9^{a}	100.0^{a}	11.1^{b}	55.6^{a}	2.3^{ab}	3.0^{a}	2.0^{ab}	2.3^{a}
IT08K-125-100	11.1^{ab}	100.0^{a}	33.33^{b}	100.0^{a}	2.0^{ab}	2.7^{a}	2.0^{ab}	3.0^{a}
IT08K-187-5	22.2^{ab}	100.0^{a}	22.2^{b}	100.0^{a}	2.0^{ab}	2.7^{a}	2.0^{ab}	3.0^{a}
IT10K-292-10	11.1^{ab}	100.0^{a}	0.0^{b}	66.7^{a}	2.0^{ab}	2.7^{a}	2.0^{ab}	3.3^{a}
IT10K-822-7	33.3^{ab}	100.0^{a}	0.0^{b}	100.0^{a}	3.0^{a}	3.7^{a}	2.0^{ab}	3.3^{a}
sIT10K-828-3	22.2^{ab}	55.6^{a}	0.0^{b}	66.6^{a}	2.3^{ab}	3.3^{a}	1.7^{ab}	2.7^{a}
IT10K-830-9	22.2^{ab}	100.0^{a}	0.0^{b}	55.6^{a}	2.3^{ab}	3.3^{a}	1.3^{b}	2.7^{a}
IT10K-837-1	33.3^{ab}	100.0^{a}	0.0^{b}	66.7^{a}	2.7^{ab}	3.7^{a}	2.0^{ab}	2.7^{a}
IT12K-13	66,7^{ab}	100.0^{a}	77.8^{a}	88.9^{a}	2.0^{ab}	3.0^{a}	2.0^{ab}	3.0^{a}
± SEM	15.5	10.6	9.6	19.7	0.3	0.3	0.1	0.3

Means followed by different letter (s) in the same column are significantly different at 5 % probability level of significance using Duncan Multiple Range Test (DMRT)

Table 2: Effect of *Cucumber mosaic virus* disease on number of leaves per plant

	Trial 1		Trial 2	
Genotype	3 WAI	5WAI	3 WAI	5 WAI
Ife Brown	14^{a-f}	19^{b-e}	17.0^{ab}	20.0^{ab}
TVU 408	11^{ef}	16^{b-e}	15.0^{a-d}	19.0^{ab}
11D-15-40	11^{def}	10^{e}	14.0^{a-d}	17.0^{b}
04K-267-8	17^{abc}	28^{a}	19.0^{a}	26.0^{a}
07K-230-2-5	13^{c-f}	17^{b-e}	17.0^{ab}	20.0^{ab}
07K-291-69	14^{a-f}	20^{bcd}	16.0^{abc}	19.0^{ab}
08K-125-24	16^{a-d}	21^{bc}	16.0^{abc}	18.0^{b}
08K-125-107	14^{a-f}	21^{bc}	17.0^{abc}	19.0^{ab}
08K-193-15	15^{a-f}	17^{b-e}	15.0^{a-d}	17.0^{b}
09K-480	13^{b-f}	23^{b}	13.0^{bcd}	20.0^{ab}
10K-819-4	12^{c-f}	16^{b-e}	13.0^{bcd}	15.0^{b}
10K-836-3	14^{a-f}	20^{bcd}	16.0^{abc}	19.0^{ab}
12K-261	18^{a}	19^{b-e}	16.0^{abc}	20.0^{ab}
12K-515	13^{c-f}	15^{b-e}	15.0^{a-d}	16.0^{b}
12K-809	14^{a-f}	19^{b-e}	14.0^{a-d}	19.0^{ab}
IT08K-125-100	13^{c-f}	14^{b-e}	14.0^{a-d}	17.0^{b}
IT08K-187-5	13^{c-f}	17^{b-e}	11.0^{d}	14.0^{b}
IT10K-292-10	18^{a}	15^{b-e}	14.0^{bcd}	19.0^{ab}
IT10K-822-7	10^{f}	10de	12.0^{cd}	14.0^{b}
IT10K-828-3	15^{a-f}	16^{b-e}	14.0^{a-d}	18.0^{b}
IT10K-830-9	13^{c-f}	15^{b-e}	13.0^{bcd}	14.0^{b}
IT10K-837-1	14^{a-f}	17^{b-e}	12.0^{bcd}	16.0^{b}
IT12K-13	12^{c-f}	13^{cde}	12.0^{bcd}	14.0^{b}
± SEM	1.0	1.9	1.0	1.6

Means followed by different letter (s) in the same column are significantly different at 5% probability level of significance using Duncan Multiple Range Test (DMRT).

Table 3: Effect of *Cucumber mosaic virus* disease on leaf diameter

	Leaf Diameter (cm)			
	Trial 1		Trial 2	
Genotype	3WAI	5WAI	3WAI	5 WAI
Ife Brown	4.1^{abc}	.5^{abc}	5.8^{ab}	6.9^{ab}
TVU 408	3.9^{abc}	6.1^{a}	6.4^{a}	7.4^{a}
11D-15-40	3.8^{abc}	4.1^{cde}	5.4^{abc}	6.4^{ab}
04K-267-8	3.4^{abc}	4.3^{cde}	4.4^{bcd}	5.5^{b-e}
07K-230-2-5	3.3^{bc}	5.0^{a-e}	3.8^{cd}	4.8^{cde}
07K-291-69	4.2^{abc}	4.9^{a-e}	4.2^{cd}	4.7^{cde}
08K-125-24	4.1^{abc}	5.2^{a-d}	4.4^{bcd}	5.2^{cde}
08K-125-107	3.7^{abc}	4.4^{b-e}	4.2^{cd}	5.0^{cde}
08K-193-15	3.6^{abc}	4.1^{cde}	4.1^{cd}	4.6^{cde}
09K-480	3.1^{bc}	4.2^{cde}	3.5^{d}	4.7^{cde}
10K-819-4	3.7^{abc}	4.7^{a-e}	4.6^{bcd}	4.6^{cde}
10K-836-3	2.9^{c}	4.2^{cde}	3.3^{d}	4.2^{de}
12K-261	4.0^{abc}	5.4^{a-d}	4.2^{cd}	6.0^{bcd}
12K-515	3.0^{c}	3.5^{e}	3.5^{d}	3.9^{e}
12K-809	3.4^{abc}	5.1^{a-d}	3.4^{d}	4.8^{cde}
IT08K-125-100	4.0^{abc}	4.9^{a-e}	4.2^{cd}	5.0^{cde}
IT08K-187-5	4.5^{ab}	5.3^{a-d}	4.0^{cd}	5.5^{b-e}
IT10K-292-10	4.8^{a}	5.8^{ab}	4.0^{cd}	4.6^{cde}
IT10K-822-7	3.8^{abc}	4.5^{b-e}	3.6^{d}	5.3^{de}
IT10K-828-3	3.4^{abc}	3.9^{de}	3.8^{cd}	4.9^{cde}
IT10K-830-9	3.6^{abc}	4.0^{cde}	3.5^{d}	4.3^{de}
IT10K-837-1	3.9^{abc}	4.1^{cde}	3.6^{d}	4.5^{de}
IT12K-13	4.2^{abc}	5.1^{a-d}	4.6^{bcd}	5.2^{cde}
± SEM	0.3	0.3	0.3	0.4

Means followed by different letter (s) in the same column are significantly different at 5% probability level of significance using Duncan Multiple Range Test (DMRT).

Table 4: Effect of *Cucumber mosaic virus* disease on pod length and seed weight

Genotype	Pod Length (cm)		Seed Weight (g)	
	Trial 1	Trial 2	Trial 1	Trial 2
Ife Brown	10.4[ab]	13.0[a]	1.0[a]	1.6[a]
TVU 408	7.5[b]	11.4[a]	1.0[a]	1.0[a]
11D-15-40	13.4[ab]	14.0[a]	1.0[a]	1.0[a]
04K-267-8	11.8[ab]	8.7[a]	1.0[a]	1.0[a]
07K-230-2-5	12.7[ab]	11.6[a]	1.0[a]	1.0[a]
07K-291-69	13.1[ab]	12.3[a]	1.1[a]	1.1[a]
08K-125-24	13.0[ab]	13.4[a]	1.0[a]	1.2[a]
08K-125-107	12.5[ab]	14.5[a]	1.2[a]	1.5[a]
08K-193-15	11.8[ab]	12.8[a]	1.1[a]	1.2[a]
09K-480	8.4[ab]	12.2[a]	1.0[a]	1.0[a]
10K-819-4	16.1[a]	13.7[a]	1.0[a]	1.0[a]
10K-836-3	12.8[ab]	14.4[a]	1.1[a]	1.5[a]
12K-261	12.4[ab]	12.4[a]	1.0[a]	1.2[a]
12K-515	13.3[ab]	12.4[a]	1.0[a]	1.0[a]
12K-809	12.4[ab]	12.4[a]	1.2[a]	1.0[a]
IT08K-125-100	12.2[ab]	14.2[a]	1.0[a]	1.3[a]
IT08K-187-5	15.1[ab]	14.0[a]	1.1[a]	1.0[a]
IT10K-292-10	13.0[ab]	13.0[a]	1.2[a]	1.1[a]
IT10K-822-7	14.7[ab]	12.9[a]	1.0[a]	1.0[a]
IT10K-828-3	11.8[ab]	14.1[a]	1.2[a]	1.4[a]
IT10K-830-9	7.7[b]	12.2[a]	1.0[a]	1.2[a]
IT10K-837-1	10.8[ab]	10.1[a]	1.0[a]	1.2[a]
IT12K-13	12.3[ab]	13.8[a]	1.0[a]	1.1[a]
± SEM	1.5	1.5	0.2	0.2

Means followed by different letter (s) in the same column are significantly different at 5% probability level of significance using Duncan Multiple Range Test (DMRT).

Relationships among the Cowpea Genotypes based on Cluster Analysis

In trial 1, the first cluster (cluster 1) consisted of ten genotypes which were Ife Brown, 10K-836-3, IT10K-830-9, IT12K-13, 12K-261, 12K-515, TVU 408, IT10K-837-1, 11D-15-40 and IT10K-822-7. Two sub-groups emerged within the first cluster. Cowpea genotypes Ife Brown, 10K-836-3, IT10K-830-9, IT12K-13, 12K-261 and 12K-515 formed a sub-group. Ife Brown and 10K-836-3 were more closely related while IT10K-830-9 and IT12K-13 formed the second pair of closely related genotypes. Similarly, 12K-261 and 12K-515 formed the third pair of closely related genotypes and this third pair was related to pair 1 and 2 in the sub group 1.TVU 408, IT10K-837-1, 11D-15-40 and IT10K-822-7 formed the sub group 2. TVU 408 and IT10K-837-1 were closely related while 11D-15-40 and IT10K-822-7 formed a pair of closely related genotypes. Cluster 2 consisted of twelve genotypes (07K-230-2-5, 09K-480, 07K-291-69, 08K-125-24, 08K-193-15, 10K-819-4, 08K-125-107, 12K-809, IT08K-125-100, IT08K-187-5, IT10K-828-3 and IT10K-292-10) genotypes. This cluster consisted of two sub groups. 07K-230-2-5 and 09K-480 genotypes formed closely related association and in relationship with sub group 2. Similarly, 07K-291-69, 08K-125-24, 08K-193-15, 10K-819-4, 08K-125-107, 12K-809, IT08K-125-100, IT08K-187-5, IT10K828-3 and IT10K-292-10 formed sub group 2. This sub group consisted of four pairs of closely related genotypes and two outliers. 07K-291-69 and 08K-125-24 formed a pair of closely related genotypes. 08K-193-15 and 10K-819-4 formed the second pair while 08K-125-107 and 12K-809 formed the third pair. IT08K-125-100 formed the outlier. The fourth pair of closely related genotype was formed by IT08K-187-5 and IT10K-828-3 while the second outlier was formed by IT10K-292-10 and it had relationship with the fourth pair of closely related genotypes in sub group 2 of cluster 2. Conversely, 04K-267-8 was distinct to be the only member of cluster 3.

In trial 2, five genotypes (Ife Brown, 07K-230-2-5, IT10K-828-3, 11D-15-40 and 04K-267-8) out of the twenty-three aggregated to form cluster 1. The genotypes 07K-230-2-5 and IT10K-828-3 were closely related while Ife Brown, 11D-15-40 and 04K-267-8 formed the outliers. Cluster 2 consisted of sixteen genotypes which were 07K-291-69, 08K-125-24, 08K-125-107, IT08K-125-100, 09K-480, 08K193-15, 10K-836-3, 10K-819-4, IT08K-187-5, 12K-261, 12K-515, 12K-809, IT10K-292-10, IT10K-822-7, IT10K-837-1, IT10K-830-9 and IT12K-13. Four sub groups were observed in cluster 2. 07K-291-69, 08K-125-24, 08K-125-107, IT08K-125-100 and 09K-480 formed the first sub group where 08K-125-24 and IT08K-125-107 were closely related. 07K-291-69, IT08K-125-100 and 09K-480 formed the outliers for the closely related genotypes in this cluster. The second sub group was formed by 08K-193-15, 10K-836-3, and 10K-819-4 and IT08K-187-5 Cowpea genotypes. 08K-193-15 and 10K-836-3 were the only closely related genotypes in this sub group. The sub group 3 was formed by 12K-261, 12K-515, 12K-809 and IT10K-292-10 genotypes. 12K-515 and 12K-809 were the only closely related genotypes while 12K-261 and IT10K-292-10 formed the outliers. The sub group 4 was formed by four (IT10K-822-7, IT10K-837-1, IT10K-830-9 and IT12K-13) genotypes which were in relationship with sub group 3. This sub group consisted of two pairs (IT10K-822-7 and IT10K-837-1 that formed pair 1, IT10K-836-3 and IT12K-13 that formed pair 2) of closely related genotypes. Similarly, TVU 408 was distinct to be the only member of cluster 3 as 04K-267-8 in cluster 3 of trial 1.

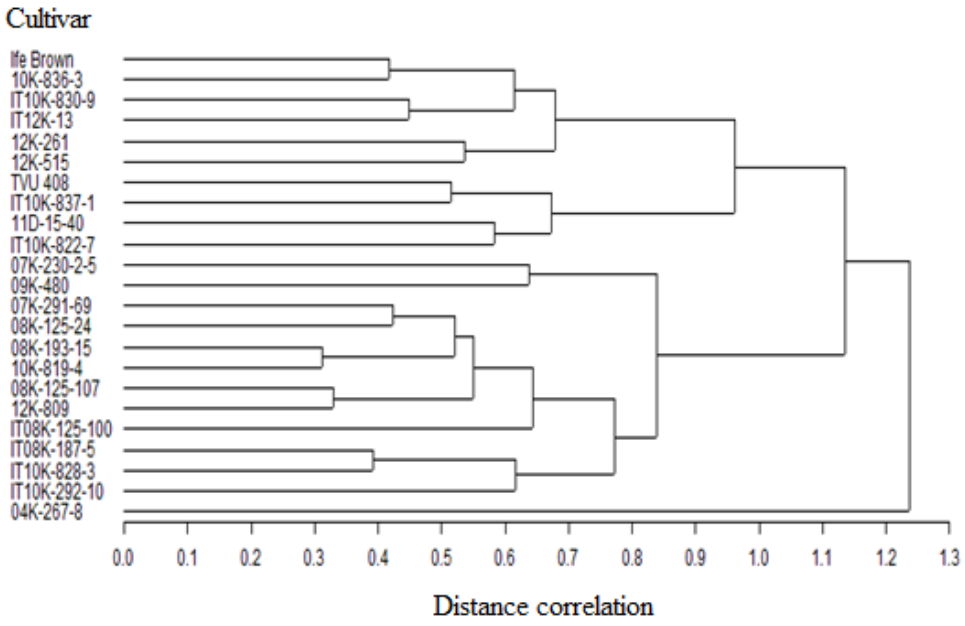

Fig.1: Dendogram of growth and yield attributes from cowpea genotypes infected with *Cucumber mosaic virus*, using Unweighted Pair Group Method with Arithmetic (UPGMA) mean in trial 1

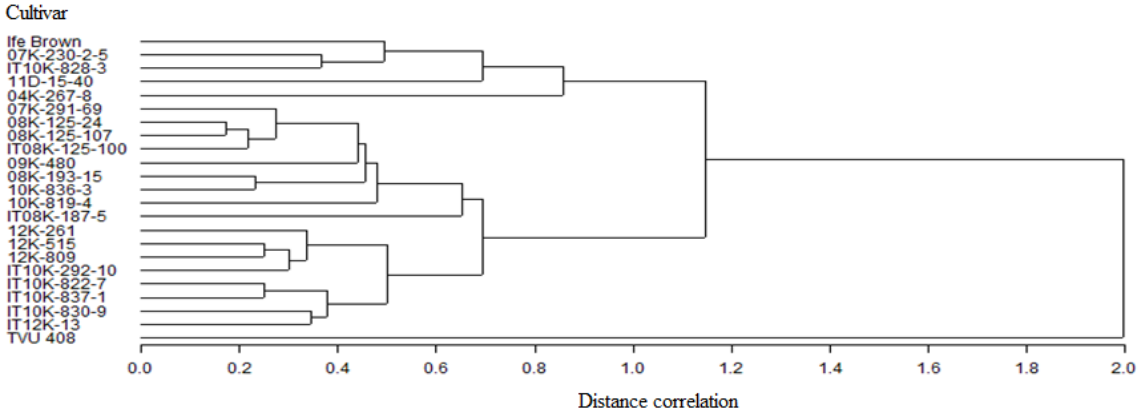

Fig. 2: Dendogram of growth and yield attributes from cowpea genotypes infected with *Cucumber mosaic virus*, using Unweighted Pair Group Method with Arithmetic (UPGMA) mean in trial 2

DISCUSSION

Cucumber mosaic virus disease causes significant yield losses in cowpea and several crops of economic importance. The symptoms observed on the infected plants were in agreement with those reported by Aliyu *et al*. (2012). The mosaic symptoms observed on the infected plants reveals that none of the twenty-three cowpea genotypes was completely resistant to the virus. This is in consonance with the findings of Arogundade *et al*. (2010). Disease severity was varied among the cowpea cultivars owing to the differences in their genetic background. Similarly, the higher number of leaves in some of the cowpea genotypes investigated was in tandem with the findings of Pazarlar *et al*. (2013). The variability in reductions of the growth and yield parameters was an indication of the differences in genotypes' genetic architecture. This corroborates the findings of Paga'n *et al*. (2008), who recorded substantial negative consequences in the CMV infected *Arabidopsis thaliana*. Seed weight is an important character in cowpea breeding and selection normally favours varieties with appreciable yield. None of the cowpea cultivars exhibited consistent performance for the morphological and yield attributes probably due to different gene actions required for each plant trait. Studies showed that quantitative traits are controlled by two or more genes which may operate synergistically or antagonistically (Malmberg *et al*., 2005). The deleterious effect of CMV disease could impact negatively on cowpea productivity and food security**.** In spite of this, 08K-125-107 was detected as the most promising genotype for seed production. Conversely, cowpea genotype 04K-267-8 could be regarded as the best genotype for hay and fodder production.

CONCLUSION AND RECOMMENDATIONS

This study has established the virulence and pathogenicity of CMV on the evaluated cowpea genotypes. Moreover, the results obtained revealed that the best cowpea genotypes for seed (08K-125-107) production and fodder (04K-267-8) were the most tolerant to CMV infection. Cultivation of these varieties was recommended in areas that are prone to CMV disease in order to reduce malnutrition and food insecurity. More so, based on the inconsistencies of the evaluated genotypes to growth and yield parameters, it was recommended that a further research on this work be carried out.

REFERENCES

Abdulrahman, A., Salaudeen, M. T. and Gana, A. S. (2017): Tolerance levels of cowpea (*Vigna unguiculata* L. Walp) cultivars to cucumber mosaic disease in Minna, Northern Nigeria. Edited by Nasir, A., Dauda, S. M., Onimanyi, A., Abdulkareem, A. S., Isah, A. G., Muriana, D. A., Alenoghena, C., Bello-Salau, H., Ohiza, H., Olatomiwa, L., Masin, M., Umar, M., Abubakar, M., Talha, F., Aminulai, H. O. and Yusuf, A. Proceedings of the 2nd International Engineering Conference. Held at the Federal University of Technology, Minna, Niger State, 17th – 19th October, 2017. p 87 – 92.

Adeboye, M. K. A., Bala, A., Osunde, A. O., Uzoma, A. O., Odofin, A. J. and Lawal, B. A. (2011). Assessment of soil quality using soil organic carbon and total nitrogen and microbial properties in tropical agroecosystem. Agric. Sci., 2, 34-40.

Aliyu, T. H., Balogun, O. S. and Kumar, L. (2012). Survey of the symptoms and viruses associated with cowpea (*Vigna unguiculata* (L).) in the Agroecological zones of Kwara State, Nigeria. Ethiopian J. Environ. Studies Manage., 5, 613-619.

Arogundade, O., Balogun, O. S., Shokalu, O. and Aliyu, T. H. (2010). Influence of *Cowpea mottle virus* and *Cucumber mosaic virus* on the growth and yield of six lines of soybean (*Glycine max* L. Merrril). J. Agric. Sci**.**, 2, 72-78.

Asiwe, R, Miko, S. and Mohammed, I. B. (2009). Performance of improved cowpea genotypes in the Sudan Savannah: I. Growth and dry matter production. Biol. Environ. Sci. J. Tropics, 4, 12-18.

Crescenzy, M. J. (2003). Rearrangements in the 5' non-translated region and phytogenetic analysis of cucumber mosaic virus RNA_3 indicate radial evolution of three subgroups. J. Virol.,73, 6752 – 6758.

Food and Agriculture Organization (FAO, 2016). Cowpea FAO, Rome, available at http://fao.org

Kumar, L. (2009). Methods for the diagnosis of Plants Virus diseases. Laboratory Manual, Ibadan IITA, 94p.

Malmberg, R. L., Held, S., Waits, A. and Mauricio, R (2005). Epistasis for fitness-related quantitative traits in Arabidopsis thaliana grown in the field and in the greenhouse. Genetics, 171, 2015-2027.

Nault B. A., Shah D. A. and Taylor A. G. (2006). *Viruses and aphids everywhere in New York snap bean fields in 2005*, 74-76. In: proceedings of the 2006 Empire State Fruit and vegetable EXPO. February 13-16, 2006. Cornell Cooperation Extension, Syracuse, NY. Nigeria IITA pp 143-146

Paga'n, I, Alonso – Blanco, C, and Garcia'a – Arenal, F. (2008). Host responses in life – history traits and tolerance to virus infection in Arabidopsis thaliana. PLoS Pathog. 4:e1000124.

Pazarlar, S., Gümüş, M. and Öztekin, G. B. (2013+. The effects of tobacco mosaic virus infection on growth and physiological parameters in some pepper varieties (*Capsicum annuum* L.). Not Bot Horti Agrobo,. 41, 427–433.

SAS (Statistical Analysis System) (2008). Statistical Analysis System SAS/STAT User's guide, ver. 9.2. SAS, Institute Inc., Cary NC.