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EVALUATION OF SELECTED COWPEA (*Vigna unguiculata* L. Walp) GENOTYPES FOR RESISTANCE TO COWPEA APHID- BORNE MOSAIC VIRUS DISEASE

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Abstract

Cowpea (*Vigna unguiculata*), is one of the most important and versatile nutritive grain legume crops native to Africa. However, disease induced by *Cowpea aphid-borne mosaic virus* (CABMV; Potyvirus) causes significant yield losses. Adoption of cultivars with inherent genetic resistance is the most effective and sustainable management option to limit the effect of pathogen.Twenty-four cowpea genotypes were evaluated under screenhouse conditions for resistance to CABMV disease. The experiment was laid out in completely randomised design with three replications. Seedlings were mechanically inoculated with virus extract at 10 days after sowing. Observations were made on percentage disease incidence, symptom severity, days to flowering, number of pods per plant, pod length per plant and number of seeds per pod. The data were subjected to analysis of variance and Duncan Multiple Range Test was used for means separation. All the cowpea genotypes infected with CABMV showed mosaic, vein yellowing and leaf deformation symptoms. Disease incidence varied from 11.1 to100 % at 3 weeks after inoculation (WAI). The cowpea genotypes: 11D-24-25 (symptom score = 1.3), 99K-573-2-1 (symptom score = 2) and IT12K-425 (symptom score = 2) exhibited the mildest disease severity. The cowpea genotype IT12K-425 combined low symptom expression with the highest seed production (9 seeds per pod). However, the genotype IT12K-488 also combined high number of pods (3 pods per plant) and seed (10 seeds per pod) production attributes. Therefore, IT12K-425 and IT12K-488 which were the most promising under CABMV infection are recommended for further evaluations and possible candidate for release for commercial production.

Keywords: Disease incidence, Severity, Genetic resistance, CABMV, Food security

Introduction

Cowpea (*Vignaunguiculata* L. Walp) is one of the most important and versatile nutritive grain legumes native to Africa (Francisco *et al.*, 2014). It is amajor source of dietary protein for hundreds of millions of people in Africa and Asia. Cowpea is also a valuable component of livestock feeds. The crop is widely cultivated in mixtures or rotation with cereals with the purpose of fixing atmospheric nitrogen into the soil (Batiano, 2011). In 2016, the world cowpea output stood at approximately sevenmillion tonnes, harvested from about 12.3 million hectares (FAO, 2016). Cowpea production of about 6.7 million tonnes was obtained in Africa from 12 million hectares of land. Nigeria with approximately three million tonnes from 3.6 million hectares was the highest cowpeaproducer in Africa.Apart from Nigeria, a lot of cowpea is grown in Nigér, Burkina Faso, Cameroon,United Republic of Tanzania, Sudan, Kenya and Mali (FAO, 2016).

Although cowpea is cultivated on a wide expanse of land in Nigeria, its productivity is threatened by an arrayof insect pests and diseases. The yield limiting diseases are usually induced by bacteria, fungi, nematodes, parasitic flowering plants and viruses. Studies have revealed the occurrences of*Cowpeaaphid-borne mosaic virus* (CABMV) as an economically important virus of cowpea in Nigeria (Alegbejo, 2015).*Cowpea aphid-borne mosaic virus*is a filamentous and positive sense RNA virus. Its particles are about 750 $\pm$ 15 nm in size and infected cells have cylindrical inclusions. The virus is widely distributed in the world and causes >70 % yield losses either alone or in combination with other viruses (Taiwo, 2001; Ayeleke *et al*., 2018). Susceptible cowpea plants exhibit symptoms such as dark-green veinal necrosis, vein-yellowing, diffused chlorotic spots/patches or intense chlorosis, blistering, stunting and severe mosaic symptoms (Aliyu *et al*., 2012).Generally, severity of CABMV infection depends on the genetic background of the host cultivar and virulence of the virus strain. The virus can be transmitted by sap inoculation, seeds of infected plants and aphid vectors (Alegbejo, 2015).The prominent aphids transmitting CABMV are*Aphids craccivora*, *A. gossypii*, *Acyrthosiphum* sp., *Macrosiphum* sp., *Myzus persicae*, *Rhopalosiphum maids* and *Cerataphis* sp in a non-

persistent manner. Seed yield can be reduced or completely lost in highly susceptible cultivars resulting in huge financial losses.

Cultural practices such close spacing, early planting and intercropping cowpea plants with tall cereals such as maize or sorghum have been recommended to restrict the movement of aphid vectors (IITA, 2013). However, adoption of resistant cultivars is the most promising and sustainable option. In Nigeria, different cowpea genotypes are being evaluated with the ultimate goal of improving food and nutrition security.Therefore, this study was conducted to identify cowpea genotypes which combined CABMV disease resistance with desirable growth and seed production.

Materials and Methods

Description of the Study Site

The experiment was carried out under screenhouse conditions with temperature ranging between 36 and 40^{o} C and 55 % relative humidity at the Teaching and Research Farm, Federal University of Technology (FUT), Minna (9^{O} 51′ N, 6 ^{O} 44′ E and 212m above sea level), Niger State, Nigeria. Minna is located in the Southern Guinea Savanna agro-ecology with annual mean rainfall of 1200mm. The rainfall is normally distributed between April and early October with peak around September and the relative humidity varies between 40 and 80 %.

Treatments and Experimental Design

The trial comprised of 24 cowpea genotypes, which were obtained from the germplasm of the International Institute of Tropical Agriculture (IITA), Kano, Nigeria. The materials included Ife-Brown, TVU408, 06K-180-11, 07K-210-1-1, 09K-456, 10K-816-1, 10K-816-3, 12K-487, 12K—489, 12K-612, 98K-1092-1, 99K-573-2-1, 11D-24-25, 11D-24-29, 11D 24 40, IT11D-21-143, IT08K-150-11, IT09K-269-1, IT10K-817-1, IT10K-817-7, IT10K-821-6, IT12K-420, IT12K-425 and IT12K-488. They were arranged as completely randomised design with three replications.

Sowing and Inoculation

The seeds were sowed in pots (bottom diameter of 15 cm and 30 cm deep) at the rate offour seeds per pot. Water was sprinkled on the pots to field capacity immediately after sowing and seedlings were thinned to three plants per pot at one week after emergence (WAE).At 10 days after sowing, cowpea seedlings were inoculated with CABMV extract. Extract for inoculation was prepared by grinding CABMV-infected leaves, obtained from the stock in the Department of Crop Production, Federal University of Technology, Minna with inoculation buffer (0.1M sodium phosphate dibasic, 0.1M potassium phosphate monobasic, 0.1M ethylene diamine tetra acetic acid and 0.001M L-cysteine per litre of distilled water, adjusted to pH 7.2) using cold sterile mortal pestle. Grinding was done at the rate of 1gmL^{-1} of the buffer. Just before the inoculation the upper leaf surface was dusted with 600-mesh carborundum powder (Aliyu *et al*., 2011). This was to create openings on the leaf surface for the virus particles to penetrate. Cowpea seedlings were inoculated by dipping a piece of cheesecloth in virus extract and gently rubbed on the carborundum-dusted leaf surface. The infected plants were rinsed with distilled water so as to prevent leaf shading by the powder.

Data Collection and Analysis

Incidence of CABMV disease was recorded at 1 and 3weeks after inoculation (WAI).It was calculated as percentage of total plants exhibiting symptoms of CABMV infection. Disease severity was rated using a visual scoring scale. On the scale,1= no symptoms (apparently healthy plant), 2=mild mosaic (10-30 % infection), 3=moderate mosaic (31-50 % infection), 4=severe mosaic, chlorosis and stunting (51-70 % infection), 5=very severe mosaic, chlorosis, stunting and plant death (>70 % infection) (Ayeleke *et al*., 2016). The growth parameter(number of days to flowering) and yield components (number of pods per plant, pod length and seeds per pod) parameters were also recorded.Data were subjected to Analysis of variance (ANOVA) at $p<0.05$ using Statistical Analysis System (SAS, 2008).The differences in growth and yield of the cowpea genotypes were separated using Duncan Multiple Range Test (DMRT) at 5% probability level.

Results

Genotypic responses to CABMV infection

All the inoculated plants exhibited typical foliar symptoms of CABMV infection but at various levels. Symptoms were first observed at 10 days after inoculation (DAI). Mild leaf chlorisis was the major symptom observed at this stage of infection. Subsequent symptoms included mosaic and vein clearing symptoms on the inoculated and newly formed leaves. In trial 1, the differences in disease incidence among the genotypes were significant ($p<0.05$) at 1 and 3 WAI (Table1). At 1 WAI, disease

incidence of 11 % was observed in 06K-180-11, 10K-816-1, 10K-817-3 and IT12K-488. In 99K-573-2-1 and IT09-269-1,22.2 % infection was found. The highest disease incidence (33.3 %) was observed in Ife Brown, 12K-487, 98K-1092-1 and IT08K-150-11, whereas the plants of the remaining genotypes were apparently symptomless. At 3 WAI,the percentage of infections varied between 11.1(11D-24-29, 11D-24-40 and IT10K-817-1) and 100 (Ife Brown and 07K-210-1-1). High disease incidence was also observed in TVU408 (88.9%), 10K-816-1(88.9 %), 06K-180-11 (77.8 %), 09K-456 (77.8 %), 10K-817-3 (77.8 %),12K-632 (77.8 %)and 98K-1092-1 (77.8 %). This was followed by 11D-24-25, IT08K-150-11, IT09K269-1 and IT12K-488, which had 66.7 % disease incidence. However, 12K-489, 99K-573-2-1, IT11D-21-143, IT10K-817-7 and IT10K-821-6 exhibited 55.5 % level of infection. The cowpea genotype IT12K-420 had 22.2 %, whereas 12K-487 and IT12K-425 elicited 33.3 and 44.4 %disease incidence, respectively.

At 1 WAI in trial 2, the highest disease incidence was observed in IT12K-420 (33.3 %), followed by TVU 408 and IT10K-821-6 (22.2 %). The genotypes 07K-210-1-1, 12K-487, 12K-632, IT08K-150-11, IT09K-269-1, IT10K-817-1 and IT10K-817-7 showed 11.1 % level of infection. However, Ife Brown, 06K-180-11, 09K-456, 10K -816-1, 10K-817-3, 12K-489, 98K-1092-1, 99K-573-2-1, 11D-24-25, 11D-24-29, 11D-24-40, IT11D-21-143, IT12K-425 and IT12K-488 were apparently symptomless.At 3WAI, the differences in disease incidence among the infected plants were also significant (p<0.05).The percentage of infection ranged between 11.1 (09K-456) and 100 (10K-816-1, 10K-817-3, 12K-487, 11D-24-29, 11D-24-40, IT08K-150-11, IT09K-269-1, IT10K-821-6 and IT12K-488).High disease incidence was also observed in Ife Brown, TVU 408, 06K-180-11, 11D-24-25 and IT11D-21-143 with 88.9 % infection. Next were 07K-210-1-1, 98K-1092-1, IT10K-817-1 and IT10K-817-7 which exhibited 77.8 % disease incidence. Disease incidence of 55.6 and 44.4 % was found in 12K-488 and 12K-632, respectively. Conversely, an incidence of 33.3 % was found in 99K-573-2-1 and IT12K-420. Disease incidence of 22.2 % was observed in IT12K-425 (Table 1).

In trial 1, the differences in disease severity among the genotypes were significant (p<0.05) (Table1).The symptoms observed varied from mild to moderate level of infection. At 3WAI, the highest level of disease severity (score= 3.3) was observed in 06K-180-11. This was followed by Ife Brown, 12K-487 and IT09K-269-1 which elicited a disease severity score of 3. Next was a severity score of 2.7 observed in 12K-632, 11D-24-29, IT08-150-11, IT10K-821-6, IT12K-420 and IT12K-488. However, 07K-210-1-1, 10K-816-1, 10K-817-3, 98K-1092-1, 11D-24-40 and IT10K-817-7 had a severity score of 2.3 while the lowest disease severity of 2 was found in the remaining genotypes (TVU 408, 09K-456, 12K-489, 99K-573-2-1,11D-24-25, IT11D-21-143, IT10K-817-1 and IT12K-425).At 5WAI, significant (p<0.05) differences were also observed with Ife Brown, 12K-487 and IT10K-821-6 eliciting the highest disease severity (score=4). This was followed by a score of 3.7 observed in IT09K-269-1. The genotypes 07K-210-1-1, IT10K-817-3, 11D-24-29, 11D-24-40 and IT08K-150-11 had a severity score of 3.3. However, 06K-180-11, 09K-456,10K-816-1, 12K-489-632, 99K-573-2-1, 11D-24-25, IT11D-21-1430, IT10K-817-7 and IT12K-420 had a uniform disease severity (score= 3). The remaining genotypes exhibited disease severity ranging from 2 to 2.7 with the lowest observed in IT12K-425.

At 3WAI in trial 2, the differences in disease severity were significant (p<0.05) among the genotypes (Table 1). The highest level of disease severity (score = 3.7) was observed in 98K-1092-1.This was followed by IT09K-269-1 which showed a disease severity score of 3. On the other hand, IID-24-29, IID-24-40, IT10K-817-1, IT10K-821-6 and IT12K-488 showed a symptom score of 2.7.The genotypes 10K-817-3, IT10K-817-7 and IT12K-420 had a disease severity score of 2.3. Moreover, Ife Brown, TVU 408, 06K-180-11, 09K-456, 10K-816-1, 12K-487, 12K-489, 99K-573-2-1, IT11D-21-143 and IT12K-425 had a uniform disease severity score of 2. However, 07K-210-1-1 elicited a severity score of 1.7 while 12K-632, 11D-24-25, IT08K-150-11 exhibited the lowestdisease severity (score = 1.3).At 5 WAI, there were significant (p<0.05) disease severity differences among the genotypes (Table 1).The highest level of severity (score = 4.7) was observed in IT11D-21-143. This was also followed by 10K-817-3, IT09K-269-1 and IT10K-817-1 (score = 4.3). Next were Ife Brown, 12K-487, 11D-24-40 and IT10K-821-6 which had a disease severity score of 4.Disease severity score of 3.3 was found in 09K-456, 98K-1092-1, 11D-24-29 and IT10K-817-7. A moderate level of severity (score = 3) was observed in TVU 408, 06K-180-11, 07K-210-1-1, 10K-816-1, 12-489, IT08K-150-11, IT12K-420 and IT12K-488. On the other hand, low level of infection (score = 2) was found in 99K-573-2-1 and IT12K-425, whereas, the lowest was observed in 11D-24-25 (score = 1.3).

Table 1. Incidence and severity of *Cowpea aphid-borne mosaic virus* disease on cowpea genotypes at various weeks after inoculation (WAI)

	Disease incidence (%)				Disease severity			
	Trial 1		Trial 2		Trial 1		Trial 2	
Genotype	1 WAI	3 WAI	1 WAI	3 WAI	3 WAI	5WAI	3 WAI	5 WAI
Ife Brown	33.3 ^{a}	100^{a}	0.0^{b}	88.9^{ab}	3.0^{ab}	4.0^{abc}	2.0^{bcd}	4.0^{abc}
TVU408	0.0^{b}	88.9^{ab}	22.2^{ab}	88.9^{ab}	2.0^{b}	2.7^{def}	2.0^{bcd}	3.0^{cd}
06K-180-11	11.1^{b}	77.8^{abc}	0.0^{b}	88.9^{ab}	3.3^{a}	3.0^{c-f}	2.0^{bcd}	3.0^{cd}
07K-210-1-1	0.0^{b}	100^{a}	11.1^{ab}	77.8^{abc}	2.3^{ab}	3.3^{b-e}	1.7^{bcd}	3.0^{cd}
09K-456	0.0^{b}	77.8^{abc}	0.0^{b}	11.1^{e}	2.0^{b}	3.0^{c-f}	2.0^{bcd}	3.3^{bcd}
10K-816-1	11.1^{b}	88.9^{ab}	0.0^{b}	100.0^{a}	2.3^{ab}	3.0^{c-f}	2.0^{bcd}	3.0^{cd}
10K-817-3	11.1^{b}	77.8^{abc}	0.0^{b}	100.0^{a}	2.3^{ab}	3.3^{b-e}	2.3^{bcd}	4.3^{ab}
12K-487	33.3 ^{a}	33.3^{bcd}	11.1^{ab}	100.0^{a}	3.0^{ab}	4.0^{abc}	2.0^{bcd}	4.0^{abc}
12K-489	0.0^{b}	55.5^{a-d}	0.0^{b}	55.6^{bdc}	2.0^{b}	2.7^{def}	2.0^{bcd}	3.0^{cd}
12K-632	0.0^{b}	77.8^{abc}	11.1^{ab}	44.4^{cde}	2.7^{ab}	3.0^{c-f}	1.3^{d}	2.3^{d}
98K-1092-1	33.3 ^{a}	77.8^{abc}	0.0^{b}	77.8^{abc}	2.3^{ab}	2.3^{ef}	3.7^{a}	3.3^{bcd}
99K-573-2-1	22.2 ^{a}	55.5^{a-d}	0.0^{b}	33.3^{de}	2.0^{b}	3.0^{c-f}	2.0^{bcd}	2.0^{cd}
11D-24-25	0.0^{b}	66.7^{a-d}	0.0^{b}	88.9^{ab}	2.0^{b}	3.0^{c-f}	1.3^{d}	1.3^{c}
11D-24-29	0.0^{b}	11.1^{d}	0.0^{b}	100.0^{a}	2.7^{ab}	3.3^{b-e}	2.7^{abc}	3.3^{bcd}
11D-24-40	0.0^{b}	11.1^{d}	0.0^{b}	100.0^{a}	2.3^{ab}	3.3^{b-e}	2.7^{abc}	4.0^{abc}
IT11D-21-143	0.0^{b}	55.5^{a-d}	0.0^{b}	88.9^{ab}	2.0^{b}	3.0^{c-f}	2.0^{bcd}	4.7^{a}
IT08K-150-11	33.3 ^{a}	66.7^{a-d}	11.1^{ab}	100.0^{a}	2.7^{ab}	3.3^{b-e}	1.3^{d}	3.0^{cd}
IT09K-269-1	22.2 ^{a}	66.7^{a-d}	11.1^{ab}	100.0^{a}	3.0^{ab}	3.7^{a-d}	3.0^{ab}	4.3^{ab}
IT10K-817-1	0.0^{b}	11.1^{d}	11.1^{ab}	77.8^{abc}	2.0^{b}	2.7^{def}	2.7^{abc}	4.3^{ab}
IT10K-817-7	0.0^{b}	55.5^{a-d}	11.1^{ab}	77.8^{abc}	2.3^{ab}	3.0^{c-f}	2.3^{bcd}	3.3^{bcd}
IT10K-821-6	0.0^{b}	55.5^{a-d}	22.2^{a}	100.0^{a}	2.7^{ab}	4.0^{abc}	2.7^{abc}	4.0^{abc}
IT12K-420	0.0^{b}	22.2^{cd}	33.3^{a}	33.3^{de}	2.7^{ab}	3.0^{c-f}	2.3^{bcd}	3.0^{cd}
IT12K-425	0.0^{b}	44.4^{a-d}	0.0^{b}	22.2^{de}	2.0^{b}	2.0^{f}	2.0^{bcd}	2.0^{cd}
IT12K-488	11.1^{b}	66.7^{a-d}	0.0^{b}	100.0^{a}	2.7^{ab}	2.7^{def}	2.7^{abc}	3.0^{cd}
±SEM	6.4	18.8	6.5	77.3	0.3	0.3	0.3	0.3

Means with dissimilar letter (s) within the same column differ significantly (p<0.05) according to Duncan Multiple Range Test (DMRT)

Effect of *Cowpea aphid-borne mosaic virus* Disease on Number of Days to Flowering

In trail 1, the number of days to flowering differed significantly (p<0.05) among the cowpea genotypes infected with CABMV (Table 2). Time of flowering varied from 39 days (IT08K-150-11, IT09K-269-1, IT19K-817-7, IT12K-425, IT12K-488)to 63 days(10K-816-1). The genotypes 10K-817-3, 12K-489, 12K-632 and 11D-24-25 depicted a uniform number of days to flowering (53 days).In trial 2, number of days to flowering differed significantly (p<0.05) between 36 days (IT08K-150-11) and 69 days (10K-816-1). The early maturing genotypes were Ife Brown, TVU 408, 06K-180-11, 07K-210-1-1, 09K-456, 12K-487, 98K-1092-1, 99K-573-2-1, 11D-24-29, 11D-24-40, IT11D-21-143, IT08K-150-11, IT09K-269-1, IT10K-817-1, IT10K-817-7, IT10K-821-6, IT12K-420 IT12K-425 and IT12K-488. The medium maturing genotypes were 10K-817-3, 12K-489 and 12K-632 while 10K-816-1exhibited late maturity.

Effect of *Cowpea aphid-borne mosaic virus* Disease on Number of Pods per Plant

The effects of virus significantly (p<0.05) reduced pod production (Table 2).In trial 1, the infected plants produced a range of one to three pods per plant. The

plants of 06K-180-11, 98K-1092-1, IT08K-150-11, IT10K-817-1, IT10K-817-7, IT10K-821-6 and IT12K-488 had three pods per plant. Conversely, 09K-456,10K-816-1,10K-817-3, 12K-489, 99K-573-2-1,11D-24-25 and IT09K-269-1produced an average of one pod per plant, whereas the remaining genotypes produced an average of two pods per plant.In trial 2, the number of pods also varied significantly (p<0.05) between one and three pods per plant among the genotypes (Table 2). The infected plants of Ife Brown, 06K-180-11, 11D-24-29, IT12K-425 and IT12K-488 produced threepods per plant. On the other hand, 07K-210-1-1, 10K-816-1,12K-487, 12K-632, 98K-1092-1, 99K-573-2-1,11D-24-25, 11D-24-40, IT10K-817-1, IT10K-817-7, IT10K-821-6 and IT12K-420 produced two pods per plant. The remaining genotypes produced a mean of one pod per plant.

Effect of *Cowpea aphid-borne mosaic virus* Disease onPodLength

In trial 1, significant (p<0.05) differences in pod length were observed among the genotypes infected with CABMV (Table 2). Curled and shortened pods were common in susceptible plants. Pod length varied from 4.3 cm (10K-816-1) to 17.4 cm (12K-489). The differences in pod length among 06K-180-11 (14.3 cm), 07K-210-1-1 (15.2 cm), 09K-456 (14.8 cm),10K-817-3 (13.8 cm), 12K-632 (14.8 cm), 98K-1092-1 (13 cm), 99K-573-2-1 (14.5 cm), 11D-24-29(14.8 cm), 11D-24-40 (15.5 cm), IT11D-21-143 (11.3 cm), IT08K-150-11 (12.1 cm), IT09K-269-1 (14.6 cm), IT10K-817-7 (14.1 cm), IT10K-821-6 (12.8 cm), IT12K-420 (12.8 cm), IT12K-425 (15.7 cm) and IT12K-488 (11.8 cm) were not significant (p>0.05). Also, there was no significant difference between the pod length of 12K-487 (11.3 cm) and 11D-24-25 (8.4 cm). Additionally, non-significant differences in pod length were observed among Ife-Brown (10.2 cm), TVU 408 (10 cm) and IT10K-817-1 (9.3 cm).

In trial 2, significant (p<0.05) differences in pod length were found among the genotypes (Table 2). Pod length varied between 3.2 cm (IT08K-150-11) and 16.3 cm (98K-1092-1). The genotypes 06K-180-11 (14.8 cm), 07K-210-1-1 (15.8 cm), 12K-632 (15 cm), 11D-24-25 (15 cm), IT12K-420 (14.5 cm) and IT12K-488 (15.2 cm) exhibited statistically similar pod lengths. Moreover, there were no significant (p>0.05) differences in pod length among Ife-Brown (12.9 cm), TVU 408 (5.9 cm), 09K-456 (9.3 cm), 10K-816-1 (13.7 cm), 10K-817-3 (7.9 cm), 12K-487 (9.9 cm), 12K-489 (12.4 cm), 99K-573-2-1 (13.4 cm), 11D-24-29 (11.3 cm), 11D-24-40 (13.3 cm), IT09K-269-1 (10.3 cm), IT10K-817-1 (13.8cm), IT10K-817-7 (12.4 cm), IT10K-821-6 (12.3 cm) and IT12K-425 (8.7 cm). The pod length observed in IT08K-150-11 (3.2 cm) was not significantly (p>0.05) different from that of IT11D-21-143 (4.7 cm).

Effect of *Cowpea aphid-borne mosaic virus* Disease on Number of Seeds per Pod

The pathogen suppressed seed production significantly (p<0.05) (Table 2). In trial 1, the values ranged between three and 11 seeds per pod. The infected plants of 10K-816-1 (three seeds) had the lowest seeds per pod, whereas the highest was observed in IT10K-817-1 (11 seeds). This was followed by 99K-573-2-1(10 seeds), 11D-24-40 (10 seeds), 06K-180-11 (nine seeds), 10K-817-3 (9 seeds), 98K-1092-1 (nine seeds) and ITIID-21-143 (nine seeds). The number of seeds per pod in TVU 408 (seven seeds), 07K-210-1-1 (eight seeds), 12K-489 (7 seeds),IT08K-150-11 (sevenseeds), IT10K-817-7 (seven seeds), IT10K-821-6 (seven seeds), IT12K-420 (eight seeds) and IT12K-488 (eight seeds) were all statistically at par. Moreover, similar number of seeds per pod was found in the genotypes 12K-487 (six seeds), 12K-632 (six seeds) 11D-24-29 (six seeds), IT09K-269-1 (six seeds) and IT12K-425 (six seeds). The genotypes 11D-24-25 produced an average of four seeds per pod.

In trial 2, the number of seeds per pod ranged from two to 10. The lowest was observed in IT11D-21-143 and IT08K-150-11 while the highest was found in IT12K-488. This was followed by the genotypes Ife Brown (nine seeds), 06K-180-11 (nine seeds), 11D-24-40 (nine seeds), IT10K-817-1 (nine seeds), IT12K-420 (nine seeds) and IT12K-425 (nine seeds). Similarly, the number of seeds per pod in 07K-210-1-1 (eight seeds), 12K-632 (eight seeds), 98K-1092-1 (eight seeds), 99K-573-2-1 (six seeds), IT10K-817-7 (eight seeds) and IT10K-821-6 (eight seeds) was uniform. Moreover, the cowpea genotypes 12K-489 (six seeds), 11D-24-25 (six seeds),11D-24-29 (six seeds), 09K-456 (five seeds), 10K-816-1 (five seeds), 10K-817-3 (five seeds), 12K-487 (five seeds) and IT09K-269-1 (five seeds) had statistically similar number of seeds per pod

.Table 2. Growth and seed production of cowpea genotypes infected with *Cowpea aphid-borne mosaic virus* disease

	Days to flowering (no.)		Pods per plant (no.)		Pod length (cm)		Seeds per pod (no.)	
Genotype	Trial 1	Trial 2	Trial 1	Trial 2	Trial 1	Trial 2	Trial 1	Trial 2
Ife Brown	47^{d}	47^{e}	2^{b}	3^{a}	10.2^{abc}	12.9^{abc}	6^{b-e}	9^{ab}
TVU 408	48^{c}	48^{d}	2^{b}	1^{c}	10.0^{abc}	5.9^{abc}	7^{a-d}	4^{cd}
06K-180-11	47^{d}	48^{d}	3^{a}	3^{a}	14.3^{ab}	14.8^{ab}	9^{abc}	9^{ab}
07K-210-1-1	47^{d}	47^{e}	2^{b}	2^{b}	15.2^{ab}	15.8^{ab}	8^{a-d}	8^{abc}
09K-456	47^{d}	43^{h}	1^{c}	1^{c}	14.8^{ab}	9.3^{abc}	7^{a-d}	5^{a-d}
10K-816-1	63^{a}	69^{a}	1^{c}	2^{b}	4.3^{c}	13.7^{abc}	3^{e}	5^{a-d}
10K-817-3	53^{b}	54^{b}	1^{c}	1^{c}	13.8^{ab}	7.9^{abc}	9^{abc}	5^{a-d}
12K-487	45^{e}	47^{e}	2^{b}	2^{b}	11.3^{bc}	9.9^{abc}	6^{b-e}	5^{a-d}
12K-489	53^{b}	53^{c}	1^{c}	1^{c}	17.4^{a}	12.4^{abc}	7^{a-d}	6^{a-d}
12K-632	53^{b}	48^{d}	2^{b}	2^{b}	14.8^{ab}	15.0^{ab}	6^{b-e}	8^{abc}
98K-1092-1	48^{c}	47^{e}	3^{a}	2^{b}	13.0^{ab}	16.3^{a}	9^{abc}	8^{abc}
99K-573-2-1	48^{c}	46^{f}	1^{c}	2^{b}	14.5^{ab}	13.4^{abc}	10^{ab}	8^{abc}
11D-24-25	53^{b}	46^{f}	1^{c}	2^{b}	8.4^{bc}	15.0^{ab}	4de	6^{a-d}
11D-24-29	47^{d}	47^{e}	2^{b}	3^{a}	14.8^{ab}	11.3^{abc}	6^{b-e}	6^{a-d}
11D-24-40	47^{d}	47^{e}	2^{b}	2^{b}	15.5^{ab}	13.3^{abc}	10^{ab}	9^{ab}
IT11D-21-143	45^{e}	48^{d}	2^{b}	1^{c}	11.3^{ab}	4.7^{bc}	9^{abc}	2^{d}
IT08K-150-11	39^{g}	36^{j}	3^{a}	1^{c}	12.1^{ab}	3.2^{c}	7^{a-d}	2^{d}
IT09K-269-1	39^{g}	46^{f}	1^{c}	1^{c}	14.6^{ab}	10.3^{abc}	6^{b-e}	5^{a-d}
IT10K-817-1	48^{c}	46^{f}	3^{a}	2^{b}	9.3^{abc}	13.8^{abc}	11^{ab}	9^{ab}
IT10K-817-7	39^{g}	38^{i}	3^{a}	2^{b}	14.1^{ab}	12.4^{abc}	7^{a-d}	8^{abc}
IT10K-821-6	41^{f}	40^{h}	3^{a}	2^{b}	15.7^{ab}	12.3^{abc}	7^{a-d}	8^{abc}
IT12K-420	41^{f}	38^{i}	2^{b}	2^{b}	12.8^{ab}	14.5^{ab}	8^{a-d}	9^{ab}
IT12K-425	39^{g}	44^{g}	2^{b}	3^{a}	15.7^{ab}	8.7^{abc}	6^{b-e}	9^{ab}
IT12K-488	39^{g}	38^{i}	3^{a}	3^{a}	11.8^{ab}	15.2^{ab}	8^{a-d}	10^{a}
±SEM	0.3	0	0.4	0.4	1.6	2.1	1.3	1.5

Means with dissimilar letter (s) within the same column differ significantly (p<0.05) according to Duncan Multiple Range Test(DMRT)

Discussion

*Cowpea aphid-borne mosaic virus*has been identified as one of the major viruses threatening cowpea productivity globally. Adoption of cultivars with inherent genetic resistance is the most effective and sustainable management option to the pathogen. The observation that all the inoculated plants exhibited typical symptoms of CABMV disease implies that none of them was immune to the virus. This corroborates the findings of Ayeleke*et al.* (2016) in an experiment when some groundnut cultivars were inoculated with the virus.The cowpea genotypes 12K-632, 99K-573-2-1, 11D-24-25 and IT12K-425 which exhibited consistently lowest disease severity ratings could be described as the most tolerant. Although CABMV causes significant yield losses in legumes, identification of some tolerant cowpea cultivars has been reported (Lima*et al*., 2011). Cultivation of tolerant varieties has been recognized as an effective alternative measure against plant pathogenic viruses. Although infection occurs in such plants, there is no complete yield loss.

Cultivation of virus-tolerant variety is considered an ideal practice in the absence of immune cultivars because the former is capable of producing acceptable yield under disease pressure. According to Agnew *et al*. (2000), tolerance as one of the well-known mechanisms for compensating the stresses imposed by parasites is elicited by reducing the deleterious impacts of parasite infection which could be manifested as alteration of host life-history characteristics. Disease severity increased in some infected cowpea genotypes at 5WAI, confirming the fact that some viruses have the capacity to escape plant's defense barriers (Boualem *et al*., 2016). Some infected plants exhibited high symptom severity due to rapid and unrestricted movement of virus particles. This is consistent with the findings of Hong and Ju (2017) who reported that intercellular movement of virus particles is an avenue that favours systemic infection. Following infection, the virus replicates at infection foci and subsequently spreads to adjacent cells as virions or viral ribonucleoprotein (vRNP)complexes. In plant virus pathotype, plant use mechanisms such as antiviral RNA silencing but viruses fight back using silencing-repressors.

The data on the evaluated parameters for both trials indicated that the impact of CABMV disease was similar among the cowpea genotypes. The results of time of flowering revealed that all the evaluated genotypes are extra-early maturing. Adoption of extra-early maturing cowpea varieties is gaining popularity in the drought-prone regions of sub-Saharan Africa (IITA, 2010). In addition to their ability to escape drought, early maturing cultivars have the potential to escape insect infestations, provide the first food grain and marketable product and be grown in a diverse array of cropping systems (Singh *et al*., 2014). The differences in growth and yield of the cowpea genotypes could be attributed to their inherent genetic background and partly due to deleterious effect of CABMV infection. Similar observations were recorded when some cowpea genotypes were challenged with CABMV disease (Taiwo and Akinjogunla, 2011). Some genotypes that exhibited low level of disease severity produced relatively low number of pods and seeds per plant. This was probably due to antagonistic actions of the genesinvolved. Conversely, some genotypes combined low level of infection with high pod and seed production, indicating synergistic gene action.

Conclusion and Recommendation

This study revealed that CABMV disease incidence and severity were genotype dependent. Although the twentyfour cowpea genotypes evaluated were susceptible to CABMV, the cowpea genotype IT12K-425 combined low symptom expression with the highest seed production. However, the genotype IT12K-488 also exhibited combined high pod and seed production attributes.Therefore, IT12K-425 and IT12K-488 which were the most promising under CABMV infection are recommended to farmers in order to enhance food and nutrition security.

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