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Genetic Variability and Evaluation of Cowpea [*Vigna Unguiculata* L.) Genotypes for Resistance to Cowpea Aphid Borne Mosaic Virus

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Abstract

Cowpea (Vigna unguiculata (L. Walp) is one of the most important leguminous crop to mankind because of its use as food, soil cover and Nitrogen fixation. Despite this, viral diseases have been reported to be a major biotic constrain against cowpea production and can lead to total crop failure (100% yield loss). Field studies were conducted using 44 cowpea varieties laid down in Randomized Completely Block Design (RCBD) with three replications. There was a significant difference P ≤ 0.05 for disease incidence among cowpea genotype in both locations and for both seasons except for incidence in Minjibir 2021. IT17-1157-3-2 recorded the least disease incidence (7.33), while IT18KD-391 recorded the highest disease incidence (32.08). In total, six genotypes showed resistant response, twenty showed tolerant and the remaining eighteen genotypes showed susceptible response. In terms of location, BUK 2022 recorded the highest disease incidence (34.30%) while Minjibir 2021 had the least incidence (1.33%). The results of genetic variability indicated that there was a considerable variability response to cowpea aphid borne mosaic virus (CABMV) which to a larger extent is influenced by the environment, as evidenced by the higher environmental variance (EV), environmental coefficient of variation (ECV), and lower heritability values.

Keywords: *Vigna unguiculata,* CABMV, incidence, Minjibir farm and BUK farm

INTRODUCTION

Cowpea (*Vigna unguiculata* (L. Walp) is the most economically important indigenous leguminous crop, which is believed to have Africa as its centre of domestication and origin. (Abebe & Alemayehu, 2022). It is a dicotyledonous, annual, herbaceous and leguminous plant from the order Fabales, Family Fabaceae and genus Vigna (Ogunsola, 2015). Global annual cowpea production was estimated to be 7.56 million tons out of which Africa produced 5.42 million tons and Nigeria, the largest producer of the crop produces over 3 million tons. (Isienyi, 2019).

Viruses are made of a nucleic acid (DNA or RNA) and protein coat (Hopfer *et al*., 2021). . They can only be seen using a transmission electron microscope (Hopfer *et al*., 2021). Since Tobacco mosaic virus (TMV) was first discovered over a century ago, more than 1000 plant viruses have

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been found (Gao *et al*., 2019). And more than 20 different Cowpea viruses have been recorded in different parts of the world and nine infect cowpea in Nigeria (Ogunsola *et al*., 2023). There is a lack of well-documented field research on the impact of viral infections on cowpea. Studies of this kind are challenging because surrounding treated plants' viruses commonly, if not always, contaminate virus-free control treatments (Chalam *et al.*, 2020).

Knowledge of the incidence of cowpea aphid borne mosaic virus (CABMV) disease is extremely important for rapid management interventions, the management of plant viral diseases based on direct methods have not been well documented yet. As such viral diseases are best controlled by indirect strategies such as: insect-viral-vector control, removing diseased plants, utilizing virus-free planting materials or planting resistant/tolerant varieties. (Jeong *et al*., 2014). The use of virus resistant cultivars is the cheapest and most effective method to controlling virus disease. (Haq & Ijaz, 2020). Despite several resistant cowpea lines to several cowpea viruses have been identified and documented at IITA gene bank, viruses are still detected and recorded in cultivated farms in Nigeria. Hence, there is need for production of more resistant lines. (Boukar *et al*., 2019). Also resistivity of a variety to a given pathogen is not a constant trait because new pathogens virulent to the given resistant genes multiply from time to time making a resistant variety to be susceptible over time, as such there is need to develop a new variety with a better resistivity to the available (Nelson *et al*., 2018). Given that resistance in plants is mostly regulated by quantitative genes, polygenic variants result, and can be phenotypic, genotypic, or environmental. According to Nausherwan *et al.* (2008) and Ndukauba *et al.* (2015), the relative values of these three coefficients for a trait will reveal information about the degree of variability. Genetic variability in crop breeding is important for successful plant breeding. Determining variability of different genotypes will enable a breeder to know to what extent the environment affects the expression of trait (Ullah *et al*., 2012). In this regard, this research was conducted to assess the level of disease incidence of CABMV through the various types of symptoms associated with CABMV infection and to determine the extent of genetic variability for resistant and tolerant response to CABMV in the genotypes.

MATERIALS AND METHODS

Experimental Sites

The experiments was conducted in Minjibir (lat. 12.08^0 N long. 80.32^0 E, 500 m above sea level) and BUK (lat.11.98^0 N long. 8.42^0 E, 475m above the sea levels) farms and the laboratory of the International Institute of Tropical Agriculture (IITA) Ibadan (latitude 70.31^0 N and longitude 30.45^0 E and 210 m above sea level). The soil of both experimental site was sandy loam.

Experimental Design and Source of Plant Materials

The experimental design for both two seasons and locations involves BUK2021, Minjibir2021, BUK2022 and Minjibir2022 as treatments laid down in a Randomized Completely Block Design (RCBD) with 44 entries and 3 replications. Each experimental site was demarcated into three blocks. Each block was further divided into plots with each experimental plot consisting of four (4) ridges, each 4 m long by 4m wide. A total of 44 cowpea varieties from IITA comprising of 43 improved varieties and one local variety (Danila) were used. Field experiments were conducted during two planting seasons for three months (August – October) of 2021 and (August – October) of 2022. At maturity, data were collected for incidence of cowpea aphid borne mosaic virus (CABMV) disease.

CABMV Disease Incidence

Disease incidence was calculated using the formula given below:

$$\text{Disease incidence (\%)} = \frac{\text{No. of plants infected}}{\text{Total no. of plants in the plot}} \times 100$$

This was used in grouping the Cowpea varietal response into Immune, Resistance, Tolerance, Susceptible and Highly susceptible (Muhammed *et. al*., 2012)

1 = no visible disease symptoms/symptomless, (Immune)
2 = mild symptoms, i.e 1-10% of plants showing symptoms (Resistant)
3 = pronounced foliar symptoms, i.e 11-20% of plants showing symptoms (Tolerant)
4 = severe symptoms, i.e 21-50% of plants showing symptoms (Susceptible)
5 = very severe foliar symptoms, i.e >50% of plants showing symptoms (Highly Susceptible)

Viral indexing

Leaf samples were randomly collected from 40 viral symptomatic plants and were indexed for three most common viruses in Northern guinea savannah as reported by Odedara and Kumar (2016) using antigen-coated plate enzyme-linked immunosorbent assay (ACP ELISA) as detailed in IITA Laboratory manual of 2010. Rabbit polyclonal antibodies against three cowpea viruses used include: Common bean mosaic virus (CBMV), Cowpea aphid borne mosaic virus (CABMV) and Cowpea severe mosaic virus (CSMV).

Viral Detection Using Direct Antigen-Coated Plate ELISA

Polyclonal antibodies were used to assay all the bulked and individual leaf samples by direct antigen coating-enzyme-linked immunosorbent assay (DAC-ELISA) as described by Hobbs *et al*. (1987).

Data Analysis

All the data collected were subjected to Two-way analysis of variance (ANOVA) using Genstat statistical package 17th edition. Treatment means, were significant, were separated using the Fischer protected range test at 5% level of probability. Means were also used to calculate genetic parameters to show genetic variability and Heritability among genotypes adopted from Chikezie *et. al.* (2016) as shown below:

Genotypic variance (σ^2_g) = $\frac{(MSg - MSe)}{r}$

Environmental variance ($\sigma^2 e$) = MSe

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2 e$

Genotypic Coefficient of variation (GCV) = $\frac{(\sqrt{\sigma 2 g})}{\bar{X}} x\ 100\%$

Environmental Coefficient of variation (ECV) = $\frac{(\sqrt{\sigma 2 e})}{\bar{X}} x\ 100\%$

Phenotypic Coefficient of variation (PCV) = $\frac{(\sqrt{\sigma 2 p})}{X} x\ 100\%$

Broad sense heritability (H^2_{Bs}) = $\frac{\sigma 2 g}{\sigma 2 p} x\ 100\%$

Genetic advance (GA) = $K(Sp)\ h^2_{bs}$

Genetic advance as % of mean (GAM) = $\frac{\text{GAM}}{\bar{X}} x\ 100\%$

Where MSg, MSe, and r are the mean squares of genotypes, mean squares of error, and number of blocks, respectively. X is the grand mean for measured trait, K is a constant (2.06) at 5% selection pressure, Sp is the phenotypic standard deviation $\sqrt{(\sigma 2p)}$ and H^2_{Bs} is the heritability ratio.

Note:
GMI (Grand Mean Incidence) was also obtained from the software, which represents the unabbreviated average mean incidence of each variety replicated thrice for both location and planting season.
The phenotypic variation for trait for each season and location was separated into genetic and non-genetic factors and estimated according to Ene *et al*. (2016)

RESULTS AND DISCUSSIONS

Mean Percentage Disease Incidence of CABMV among Genotypes

A combined analysis of variance results for the mean percentage disease incidence of CABMV among the genotypes was presented in Table 1. The result showed a significant differences ($p \leq 0.050$) among all the genotypes except for incidence in Minjibir 2021. Cowpea genotype IT17K-1157-3-2, recorded on average, the least attack (7.33%) by the virus and this could be associated with its superior inherent resistance to the disease attack over the other genotypes. Variety IT89KD-391 recorded the highest attack (32.08%) on an average probably because of its high susceptibility to the disease pathogens. For cowpea local cultivar Danila, susceptibility was also observed virtually across both locations and planting seasons this might be due to its spreading (since large succulent canopies i.e large leaf areas) typical of local cultivars are likely to be pre-disposed to viral attack as leaves are the major sites of infection and late maturing nature (which probably predisposes the crop to the disease pathogens over a period of time). All these imply that the occurrence of viral disease is significantly influenced by the type of plant and that variations in the susceptibilities and resistance among genotypes could be due to differences in their genetic makeup (Guerret *et al.,* 2016). Some of the other improved varieties have shown similar resistivity features in some work. Muhammed *et al*. (2012) for example, reported similar superiority of IT90K-277-2 over other improved varieties. However, few of the improved genotypes exhibited comparable disease incidence because their genetic compositions are alike while most of the improved varieties showed an overlapping result for incidence and this could be attributed to the effect of environment or planting season on incidence of CABMV disease. IT17K-1671-2-2 recorded a high viral incidence (68.33%) in BUK 2022 but recorded no viral incidence (0%) for Minjibir 2021. Similar trend was also observed in other genotypes like MAGIC245, IT17K-1251-1-2, IT17K-1707-2-2, IT17K-922-2-1 and IT98K-205-8. Mohammed and Miko (2007) claimed that the occurrence of agricultural diseases is significantly influenced by the variability of environmental elements including temperature, humidity, and rainfall. This hypothesis seems to be supported by this current investigation; the different impacts in the two sites and seasons indicated that the infections may have been significantly impacted by variations in the weather in both. Anyamba *et al*. (2014) confirmed this as well. The grand mean (GMI) of the combined analysis of variance table presented in table 1 showed six (6) genotypes with resistant response to the virus, Twenty (20) genotypes showed tolerant response and the remaining eighteen (18) genotypes showed susceptibility response.

Table 1: Mean Percentage Incidence of CABMV Disease among the Genotypes

SN	Genotypes	IB2021	IM2021	IB2022	IM2022	GMI	Status
1.	Danila	40.00^{gh}	3.33^{a}	23.33^{abcdefg}	22.67^{abcdefgh}	21.67^{bcdefghijklmn}	S
2.	IT15k-2411-1	23.33^{abcdefgh}	0.00^{a}	35.33^{abcdefghi}	14.67^{abcde}	19.50^{bcdefghijklm}	T
3.	IT16K-1965-2	36.00^{fgh}	4.33^{a}	46.00^{cdefghij}	16.00^{abcdef}	26.00^{ghijklmn}	S
4.	IT16K-2050-3	27.00^{abcdefgh}	0.00^{a}	9.00^{a}	18.33^{abcdefg}	14.00^{abcdef}	T
5.	IT16K-2091-7	24.67^{abcdefgh}	0.00^{a}	51.67^{defghij}	13.00^{abcde}	20.00^{bcdefghijklm}	T
6.	IT16K-2100-7	23.67^{abcdefgh}	0.00^{a}	40.33^{abcdefghij}	23.67^{bcdefgh}	21.92^{cdefghijklmn}	S
7.	IT16K-2351-10	27.33^{abcdefgh}	0.00^{a}	27.33^{abcdefgh}	17.33^{abcdefg}	18.00^{abcdefghijkl}	T
8.	IT16K-2556-1	32.67^{cdefgh}	3.33^{a}	38.00^{abcdefghij}	7.67^{abc}	20.75^{bcdefghijklmn}	S
9.	IT16K-2602-1	25.33^{abcdefgh}	1.66^{a}	25.33^{abcdefg}	12.00^{abcd}	17.00^{abcdefghij}	T
10.	IT16K-2675-3	33.33^{defgh}	3.33^{a}	30.00^{abcdefgh}	16.67^{abcdefg}	20.83^{bcdefghijklmn}	S
11.	IT17K-1107-3-1	17.33^{abcdef}	9.33^{a}	19.33^{abcde}	22.33^{abcdefgh}	17.33^{abcdefghijk}	T
12.	IT17K-1149-3-2	24.33^{abcdefgh}	6.33^{a}	16.33^{abc}	12.67^{abcd}	12.50^{abcd}	T
13.	IT17K-1157-3-2	11.67^{abc}	0.00^{a}	18.33^{abcde}	0.00^{a}	7.33^{a}	R
14.	IT17K-1165-5-4	31.33^{cdefgh}	0.00^{a}	61.33^{hij}	19.67^{abcdefg}	28.08^{ijklmn}	S
15.	IT17K-1181-1-2	25.00^{abcdefgh}	0.00^{a}	38.33^{abcdefghij}	11.67^{abcd}	19.17^{bcdefghijklm}	T
16.	IT17K-1190-1-5	24.67^{abcdefgh}	0.00^{a}	10.00^{ab}	9.67^{abcd}	10.25^{abc}	R
17.	IT17K-1251-1-2	26.00^{abcdefgh}	0.00^{a}	52.67^{efghij}	36.00^{efgh}	28.42^{jklmn}	S
18.	IT17K-1257-1-2	30.67^{bcdefgh}	0.00^{a}	17.33^{abcd}	30.67^{cdefgh}	19.42^{bcdefghijklm}	T
19.	IT17K-1267-2-1	26.33^{abcdefgh}	0.00^{a}	19.67^{abcde}	16.33^{abcdef}	15.33^{abcdefgh}	T
20.	IT17K-1279-3-2	25.33^{abcdefgh}	0.00^{a}	62.00^{hij}	22.00^{abcdefgh}	27.67^{ijklmn}	S
21.	IT17K-1310-1-2	17.00^{abcdef}	0.00^{a}	49.00^{cdefghij}	22.00^{abcdefgh}	22.33^{defghijklmn}	S
22.	IT17K-1367-2-4	14.67^{abcde}	0.00^{a}	21.33^{abcdef}	31.33^{defgh}	16.83^{abcdefghij}	T
23.	IT17K-1557-3-1	18.67^{abcdef}	3.33^{a}	32.00^{abcdefgh}	16.67^{abcdefg}	16.67^{abcdefghi}	T
24.	IT17K-1575-2-1	10.00^{ab}	0.00^{a}	23.33^{abcdefg}	10.00^{abcd}	10.83^{abcd}	R
25.	IT17K-1589-5-1	36.67^{fgh}	5.33^{a}	55.00^{fghij}	16.67^{abcdefg}	30.17^{mn}	S
26.	IT17K-1671-2-2	22.00^{abcdefgh}	0.00^{a}	69.00^{ij}	10.33^{abcd}	25.08^{fghijklmn}	S
27.	IT17K-1707-2-2	41.67^{h}	0.00^{a}	10.33^{ab}	23.33^{bcdefgh}	18.83^{abcdefghijklm}	T
28.	IT17K-1884-4	26.33^{abcdefgh}	4.66^{a}	43.00^{abcdefghij}	39.67^{gh}	28.83^{klmn}	S
29.	IT17K-2685-1	24.00^{abcdefgh}	0.00^{a}	26.00^{abcdefg}	43.67^{h}	24.33^{efghijklmn}	S
30.	IT17K-3113-2	31.00^{bcdefgh}	0.00^{a}	26.33^{abcdefg}	15.67^{abcdef}	16.67^{abcdefghi}	T
31.	IT17K-558-5-1	19.00^{abcdefg}	0.00^{a}	15.67^{abc}	5.67^{ab}	10.08^{ab}	R
32.	IT17K-817-7-1	7.00^{a}	3.66^{a}	42.00^{abcdefghij}	13.67^{abcde}	16.58^{abcdefghi}	T
33.	IT17K-922-2-1	19.00^{abcdefg}	0.00^{a}	69.00^{ij}	19.00^{abcdefg}	26.75^{hijklmn}	S
34.	IT17K-937-4-1	23.67^{abcdefgh}	0.00^{a}	17.00^{abcd}	13.67^{abcde}	13.33^{abcde}	T
35.	IT18K-586	8.67^{a}	0.00^{a}	42.33^{abcdefghij}	0.00^{a}	12.75^{abcde}	T
36.	IT18K-708-3	17.33^{abcdef}	0.00^{a}	22.33^{abcdefg}	14.00^{abcde}	13.42^{abcdef}	T

37.	IT18K-786-1	27.67^{abcdefgh}	0.00^{a}	71.00^{j}	17.67^{abcdefg}	29.08^{lmn}	S
38.	IT89KD-288	9.00 ^{a}	0.00^{a}	17.67^{abcd}	17.33^{abcdefg}	10.75^{abcd}	R
39.	IT89KD374	28.00^{abcdefgh}	0.00^{a}	44.67^{bcdefghij}	14.67^{abcde}	21.58^{bcdefghijklmn}	S
40.	IT89KD-391	35.00^{efgh}	0.00^{a}	55.00^{fghij}	38.33^{fgh}	32.08^{n}	S
41.	IT90K-277-2	31.00^{bcdefgh}	4.00^{a}	14.33^{abc}	11.00^{abcd}	15.17^{abcdefgh}	T
42.	IT98K-205-8	8.67^{a}	0.00^{a}	57.00^{ghij}	0.00^{a}	22.33^{defghijklmn}	S
43.	MAGIC245	13.00^{abcd}	3.66^{a}	21.67^{abcdef}	0.00^{a}	10.08^{ab}	R
44.	Striga_MABC-9	17.67^{abcdef}	5.66^{a}	22.67^{abcdefg}	14.33^{abcde}	14.42^{abcdefg}	T
	Grand Mean	23.70	1.33	34.30	17.10	19.19	
	LSD	21.12	6.10	34.97	23.25	11.68	
	SE (±)	10.63	3.07	17.60	11.70	5.94	

Means with different superscript along the columns are significant at P-value ≤0.05. IB2021 = % Incidence for BUK in 2021 planting season, IM2021 = % Incidence for Minjibir in 2021 planting season, IB2022 = % Incidence for BUK in 2022 planting season, IM2022 = % Incidence for Minjibir in 2022 planting season, GMI = Grand Mean % Incidence for BUK and Minjibir in 2021 and 2022 planting season, LSD = Least Significant Difference, SE= Standard Error and ST = status (R= resistant, T= tolerant, S= susceptible)

Mean Percentage Disease Incidence of CABMV between Locations and Seasons

The Incidence of CABMV for both seasons and locations is presented in Figure 1. BUK in 2022 planting season recorded the highest (34.30) disease incidence followed by BUK for 2021 planting season with (23.70) and Minjibir for 2022 planting season (17.10) respectively, while Minjibir for 2021 planting season had the least with (1.33) of disease incidence. The incidence for BUK was found to be higher for both 2021 and 2022 seasons (23.70, 34.30) respectively while Minjibir recorded (1.33, 17.10) respectively. The incidence for 2022 was found to be higher for BUK and Minjibir (34.30, 17.10) respectively than (23.70, 1.33) for 2021 respectively.

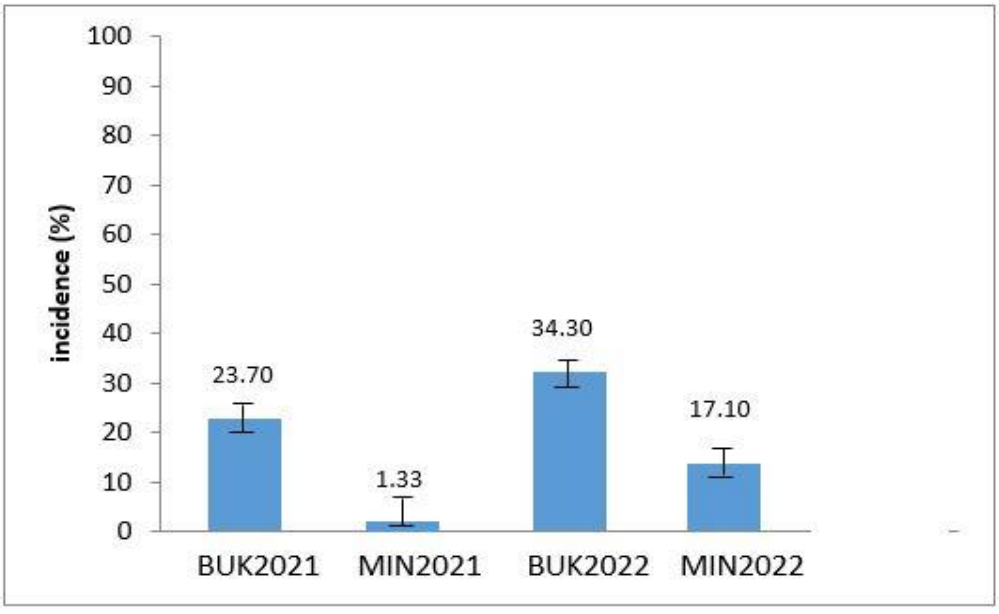
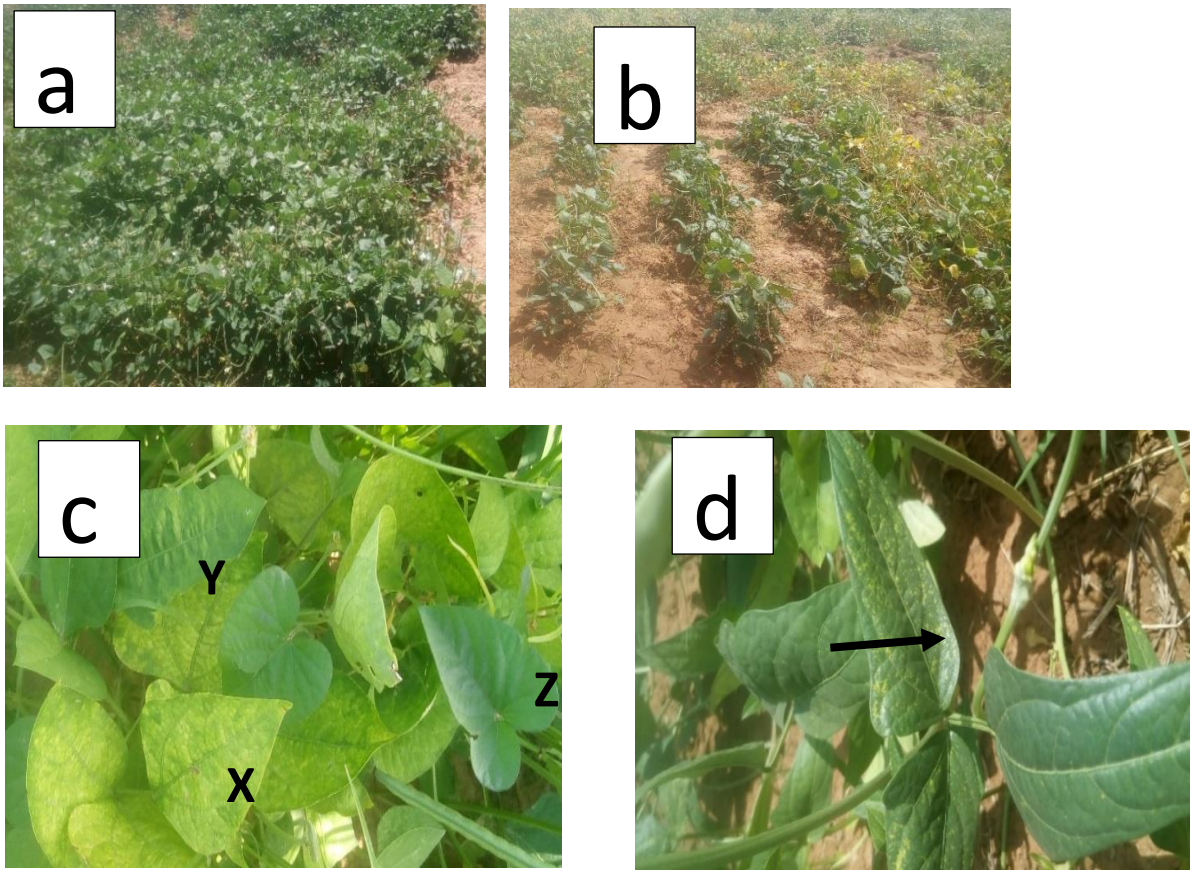


Figure 1: Mean Percentage Incidence of CABMV among the Locations and seasons

Symptoms Diversity of CABMV

There are numerous viruses causing mosaic diseases and mottle symptoms in cowpea. They are very difficult to differentiate based on field symptoms as several viruses can occur at the same time. The most prevalent viruses in the tropical regions are: Bean common mosaic virus-blackeye mosaic (BCMV-BlCM), Cowpea aphid-borne mosaic virus (CABMV) and Cowpea severe mosaic virus (CPSMV), with CABMV being the most prevalent in most of the growing regions in Nigeria. (Soyinka *et. al.,* 1997) and (Karim, 2016). Symptoms of CABMV produced vary according to the Cowpea cultivar and the possible interaction if any with other viruses (Karim, 2016). Symptoms diversity of CABMV is presented in Plate 1. Some of the observed symptoms in the field include: chlorosis and mosaic patterns as shown in leaf blade X, mottling in leaf blade Y. diffuse chlorotic spot patches as in Plate 1(b) and necrotic lesion as in Plate 1(d) while leaf blade Z shows no visible symptoms. This is consistent with the results of Bhat (2020) and Devi *et al.* (2024). However, symptoms may not always be visible (Ismail *et al.*, 2022).



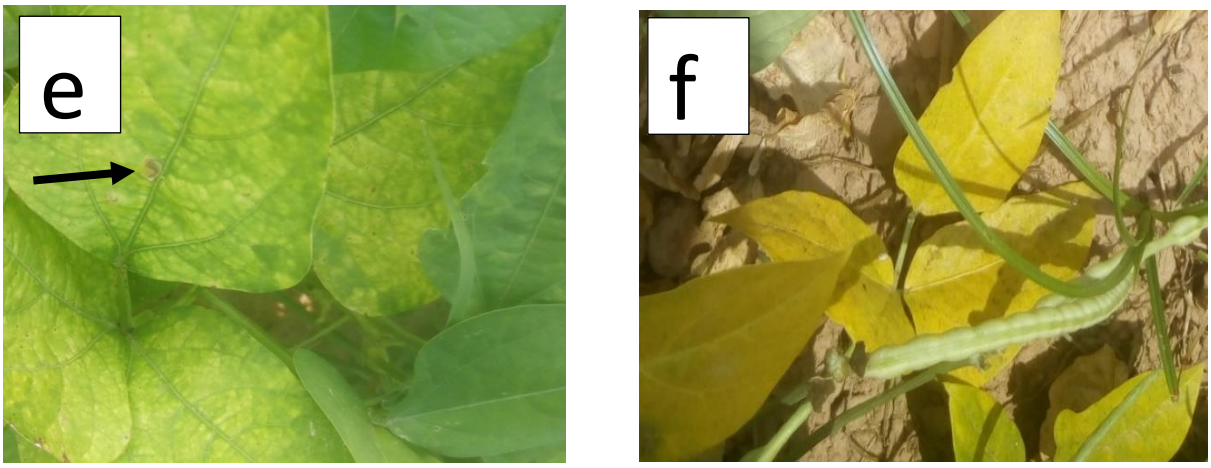


Plate 1: different symptoms diversity of forms of CABMV on cowpea (a) healthy plot showing no symptoms of CABMV (b) CABMV infected plots showing symptoms (c) CABMV infected leaves showing symptoms with chlorosis and mosaic patterns in leaf blade X, Mottling in leaf blade Y, while leaf blade Z shows no visible symptoms**.** Mosaic patterns with diffuse chlorotic spot patches as in (d) and necrotic lesion as in (e) while (f) is a Virus-like symptoms; Severe chlorosis which may be due to environmental stress such as nutritional imbalance

Viral Detection and Identification

In all, 40 symptomatic cowpea samples were collected and further confirmatory testing for single detection of virus in individual leaf samples collected showed 38 out of 40 (95.%) cowpea leaf samples collected to be infected either singly or with mixed virus infection (Table 2). CABMV was detected in 85% (34 out of 40) of the total samples, followed by BCMV-BlCM which had 42.5% (17 out of 40) and CPSMV had the least 32.5% (13 out of 40) as the percentage infection. This agrees with the work of Odedera and Kumar (2016) who reported that SBMV had the highest virus incidence in all the cowpea growing regions in Nigeria in 1991, while CABMV had it in 1992 and 1993 (Shoyinka *et al.* 1997), and BCMV had the highest disease incidence in 20016 (Odedera & Kumar, 2016). However in the present study, CABMV had the highest disease incidence. Probably this was due to the availability of insect vectors responsible for the transmission of the virus.

Table 2: Viral identification from leaf samples

S/N	VIRUS	No. of + in single	% + in single	Total No. of + in mixed	Total % + in mixed
1	CABMV	16	40	34	85
2	CPSMV	1	2.5	13	32.5
3	BCMV-BlCM	4	10	17	42.5
4	CABMV + CPSMV	5	12.5	-	-
5	CABMV + BCMV-BlCM	6	15	-	-
6	CPSMV + BCMV-BlCM	0	0	-	-
7	CABMV + CPSMV + BCMV-BlCM	7	17.5	-	-
8	No Virus Detected	2	5	-	-

Genetic Parameters for Incidence of CABMV

Genetic variability and the heritability of desired traits are major factors in the success of most crop improvement programmes. (Inuwa *et. al.,* 2012). Results of the study showed that there were considerable variations among the lines. The Genotypic variance (GV) was lower than the phenotypic variance (PV) for all and this is because the PV is the product of the interaction of the GV and EV (Chaudhari *et al*., 2017). Environmental variance (EV) values were higher

than GV values for all indicating that the incidence, to a large extent is influenced by the environmental component of the variation. This was also affirmed by Chaudhari *et al*. (2017), Kumar *et al*.(2019) and Khan *et al*. (2021). According to Chaudhari *et al*. (2017), PCV and GCV values below 10% were classified as low, 10% and 20% as moderate, and those beyond 20% as high. According to these parameters, the study's findings showed that both GCV and PCV were moderate to high. High PCV suggests that there may be more room for selection for a trait under consideration, depending on the degree of variability there is (Khan *et al*., 2021). The PCV and GCV values in the current study were high and the difference between them was quite large, also indicating a greater environmental influence on the trait's expression. Yusuf *et al.* (2017) and Bhargavi *et al.* (2016) also documented in the literature on the broader discrepancies between PCV and GCV. The ratio of genotypic variance to total phenotypic variance is used to estimate heritability. Heritability estimates show how much genetic control there is over a trait's expression and how much less environmental effect there is on the variance that is observed (Ene *et al*., 2016). Khan *et al*. (2021) reported heritability values of 0 - 30% as low, 30% - 60% as intermediate, and ≥60% as high. In the present study, Low to intermediate values of heritability were observed also indicating the influence of environment in the expression of these traits. However, broad sense heritability is also subjected to some experimental error. Hence, genetic advance along with heritability gives more reliable information for consideration of a character under selection (Ullah *et al*. 2012). The low heritability reported is as a result of the adverse effects of the environment than of genotype. High genetic advance indicates the presence of additive gene effect and similar observations were also recorded by Jaiswal *et al.* (2017). A comparative association of heritability alongside genetic advance as a percentage of the means shows the mode of gene action in the expression of a character, which aids in determining a suitable breeding technique. Even though the results of the study show more influence of the environment in the expression of this trait the values of genetic advance show that substantial residual genetic variability is still available to ensure good progress from further selection for the desired characters, which in turn will lead to increase in CABMV resistance.

Table 3: Genetic Parameters for Incidence of CABMV Disease

Traits	$\bar{X}$	Ms	σ^2e	σ^2p	σ^2g	PCV	GCV	ECV	H^2_B (%)	GA	GAM (%)
IB2021	23.70	225.30	169.40	188.03	18.63	57.86	18.21	54.91	9.91	279.92	1181.11
IM2021	1.33	15.98	14.14	14.76	0.61	288.80	58.88	282.73	4.16	32.89	2473.24
IB2022	34.30	945.60	464.50	624.87	160.37	72.88	36.92	62.83	25.66	1321.56	3852.95
IM2022	17.10	302.60	205.30	237.73	32.43	90.17	33.30	83.79	13.64	433.32	2534.06
GMI	19.19	330.8	211.6	251.33	39.73	82.61	32.85	75.80	15.81	516.29	2690.43

IB2021 = % Incidence for BUK in 2021 planting season, IM2021 = % Incidence for Minjibir in 2021 planting season, . IB2022 = % Incidence for BUK in 2022 planting season, IM2022 = % Incidence for Minjibir in 2022 planting season. σ^2p = phenotypic variance, σ^2g = genotypic variance, σ^2e = environmental variance, PCV = phenotypic coefficient of variance, GCV =genotypic coefficient of variance, ECV=environmental coefficient of variance, H^2_{bs}= heritability in broad sense, GA= genetic advance, GAM= genetic advance as percentage of mean

CONCLUSION

Results of this study have shown that the incidence of CABMV was significantly different among the 44 cowpea genotypes, the locations and planting seasons except for Minjibir 2021. Cowpea genotypes IT17K-1157-3-2, IT17K-1190-1-5, IT17K-1575-2-1, IT17K-558-5-1, IT89KD-288 and MAGIC245 are the promising resistant genotypes and can be used for CABMV screening. The study also showed various types of symptoms associated with CABMV infection among the cowpea genotypes. The results of genetic variability studies has indicated substantial variability among the studied genotypes. The larger environmental variance (EV), Environmental coefficient of variation (ECV) and the lower Heritability values obtained in the genetic variability results is an indication of the influence of the environment to a larger extent in the incidence of CABMV.

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