

**PHENOTYPIC SCREENING OF COWPEA (*VIGNA UNGUICULATA* (L.)  
WALP) GENOTYPES FOR RESISTANCE TO COWPEA VIRAL  
DISEASES**

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## ABSTRACT

Viruses are a major constraint to cowpea production in sub-Saharan Africa. Host plant resistance is the most effective and reliable method of managing viral diseases. In order to identify the source of resistance or tolerance, 38 cowpea genotypes were screened for virus infection under field conditions during the 2016 wet and dry seasons. The experiment was laid out in a randomized complete block design with four replications in both seasons. Disease severity was assessed fortnightly based on disease symptom using 1-5 visual scale (1=symptomless, and 5= very severe symptom). The cowpea genotypes exhibited varying reactions to viral infections with mean disease incidence ranging from 17.7% in the fourth week to 29.2% in the eighth week for the wet season and from 34.4% to 53.1% for the fourth and eighth week, respectively in the dry season. Symptoms observed were leaf mosaic (86.7%), leaf mottling (86.7%), chlorotic spots (34.2%), vein clearing (28.9%), leaf curl (26.3%), necrotic lesions (15.8%) and stunting (10.5%). Symptom severity in the rainy season ranged from symptomless (severity score of 1) in IT10K-819-4 and IT07K-297-13 to moderate symptom (severity score of 2.9) in Apagbaala. However, in the dry season, the symptom severity score ranged from 1.11 (mild symptom) in Marfo Tuya to a score of 2.4 (moderate symptom) in IT07K-298-9, thus demonstrating a significant genotype x season interaction effect. Incidence and severity were significantly higher in the dry season than in the rainy season. There was a strong positive correlation between the disease incidence and disease severity as well as AUDPC and no correlation between the cowpea incidence and the seed yield and plant height in the wet season. There was a negative correlation between the incidence and plant height in the dry season. Six genotypes (IT07-210-1-1, IT07K-297-13, IT08K-193-14, IT09-456, IT10K-817-3 and IT10K-819-4) exhibited mild symptoms and gave high yields in both seasons, thus demonstrating a stable G x E interaction effect. These disease resistant genotypes could be evaluated further before release to farmers.

**Key words:** Area Under Disease Progress Curve, Host resistance, *Vigna unguiculata*, Viral diseases



## INTRODUCTION

Cowpea, [*Vigna unguiculata* (L) Walp], is a dominant staple crop in some Sahelian countries. It is mainly grown to produce dry grains, but about 25 % is consumed on-farm or marketed as green pods [1]. Cowpea is a crop of major importance to the nutrition of both poor rural and resource poor urban households [2] who rely mostly on starchy foods such as millet, sorghum, maize and cassava as food. The grains, fresh peas and hay serve as a valuable source of proteins for human and animal nutrition [1]. Cowpea possesses several advantages for farmers in Ghana over other grain legumes and vegetables including high yields on poor, sandy soils, high rates of symbiotic nitrogen fixation and lower fertilizer requirements. It is also more tolerant to drought and high temperatures than other grain legumes [3]. These good attributes of cowpea make it an excellent food security crop in Ghana, especially in the northern regions and the coastal savannah where conditions of drought resulting in water deficiency and stress commonly affect crop production.

In spite of the significant contribution of cowpea to the nutrition and food security in Ghana, yields and the production of the crop in the country are very low and continue to decline over the years. Available data [4] indicate an average yield of cowpea of 1.3 mt ha<sup>-1</sup> which is lower than the achievable yield of 2.6 mt ha<sup>-1</sup>. The wide yield gap has been attributed to several abiotic and biotic constraints of which pests and diseases are major ones. Viral diseases are considered to be a major contributing factor to low productivity of cowpea in the tropical and sub-tropical countries [5] including Ghana [6]. About 140 cowpea viruses have been reported worldwide [7], of which only nine had been reported to occur in Africa [8]. Cowpea viruses reported so far in Ghana include southern bean mosaic virus (SBMV), cowpea aphid-borne mosaic virus (CABMV) [9], blackeye cowpea mosaic virus (BICMV), bean common mosaic virus (BICM) [6] and cowpea mild mottle virus (CPMMV) [10].

Symptoms of viral diseases in cowpea include mottling of the leaves, yellow mosaic patterns on the leaves, vein clearing, chlorotic and necrotic spots and stunting [11]. Losses due to viral infections are estimated to be between 10% and 100% [12]. A complete loss of irrigated cowpeas in northern Nigeria had been attributed to virus infection [13].

Effective management of these viral diseases is important in order to improve yields of cowpea. Conventional methods used by farmers to control viruses including broad-spectrum insecticides for the control of vectors that transmit the viruses are inadequate and not cost-effective to the peasant farmers. The use of host plant resistance is, therefore, considered to be the most economical and environmentally friendly approach in the management of viral diseases [14]. Identifying sources of resistance is an important objective of cowpea breeding programmes [15]. This study was conducted to assess the reaction of 38 cowpea genotypes to virus infection under field conditions both in the wet and dry seasons in order to identify sources of resistance.



## METHODOLOGY

### Study area

The study was conducted at the Teaching and Research farm of the School of Agriculture, College of Agriculture and Natural Sciences (CANS) of the University of Cape Coast, Ghana from June to August 2015 (major wet season) and from October 2015 to January 2016 (dry season). This site (5°10'N, 1.2°50'W) falls within the coastal savannah agro-ecological zone of the country with Acrisol soil type [16] and is a highly endemic site for viral diseases of cowpea. The area has a bi-modal rainy season from May to June and August to October, with an annual rainfall ranging between 50 mm and 1000 mm and temperatures ranging between 23.2 °C and 33.2 °C with an annual mean of 27.6 °C [17].

### Plant material

A total of 38 cowpea genotypes comprising thirty-three (33) elite lines from International Institute of Tropical Agriculture (IITA), Nigeria and five (5) local varieties were used for the study (Table 1).

### Experimental design and field layout

The experimental outlay was a randomized complete block design (RCBD) with three replicates consisting of two blocks each with nineteen (19) plots of 3m x 2m. Each subplot consisted of four rows of cowpea plants. Three seeds were sown per hill at an inter-row spacing of 50 cm and intra-row spacing of 30 cm apart. The plots were separated by 1 m alley and replicates were separated by 1.5 m alleys. Total field size was 75 m x 18 m (0.135 Ha). The experiment was repeated in the dry season.

### Cultural practices

Thinning out was conducted two weeks after sowing, leaving two plants per hill. Weeding was undertaken at four weeks intervals using a hoe and plants were watered using sprinkler when necessary. Insecticide PAWA 2.5 EC (Lambda-cyhalothrin 25 g L<sup>-1</sup>) was applied at seedling and flower initiation stages based on the manufacturer's recommended rate of 35 mL per 15 L water using a knapsack sprayer.

### Data collection

Data were collected on dry seed yield (kg ha<sup>-1</sup>), viral disease incidence and severity. Data were collected on ten plants in the middle row per plot and the means were taken. Disease assessment was conducted fortnightly starting four weeks after sowing (WAS) till senescence.

Disease incidence was based on disease symptoms described by Gumedzoe *et al.* [18]. Percentage disease incidence (DI) was then determined using the formula:

$$DI(\%) = \frac{\text{Number of plants infected in the inner rows}}{\text{Total number of plants in the two inner rows}} \times 100$$

The severity of viral diseases was assessed based on the intensity of disease symptoms using a modified 1-5 visual scale by Gumedzoe *et al.* [18]. Scores were described as 1



(unaffected shoots, no symptoms.), 2 (mild chlorosis, mild distortions at base of leaves, while the remaining parts of the leaves and leaflets appear green and healthy), 3 (pronounced mosaic pattern on most leaves, narrowing and distortion of the lower one-third of the leaflets), 4 (severe mosaic distortion of two thirds of most leaves and general reduction of leaf size and stunting of shoots) and 5 (very severe mosaic symptoms on all leaves, distortion, twisting, misshapen and severe leaf reductions of most leaves accompanied by severe stunting of plants).

Data on mean severity scores were used to calculate Area Under Disease Progress Curve (AUDPC) for each of the cowpea lines using the formula by Campbell and Madden [19]:

$$AUPDC = \sum_{i=1}^{n-1} ((y_i + y_{i+1}) / 2) (t_{i+1} - t_i)$$

Where “t” is the time of each reading (days after planting), “y” is the percent of affected foliage at each reading and “n” is the number of readings.

Plants with a mean AUDPC of less than 5 were classified as resistant (R), those with a AUDPC of 5-10 were classified as moderately resistant (MR), and those with a score > 10 were classified as susceptible (S).

### Data analyses

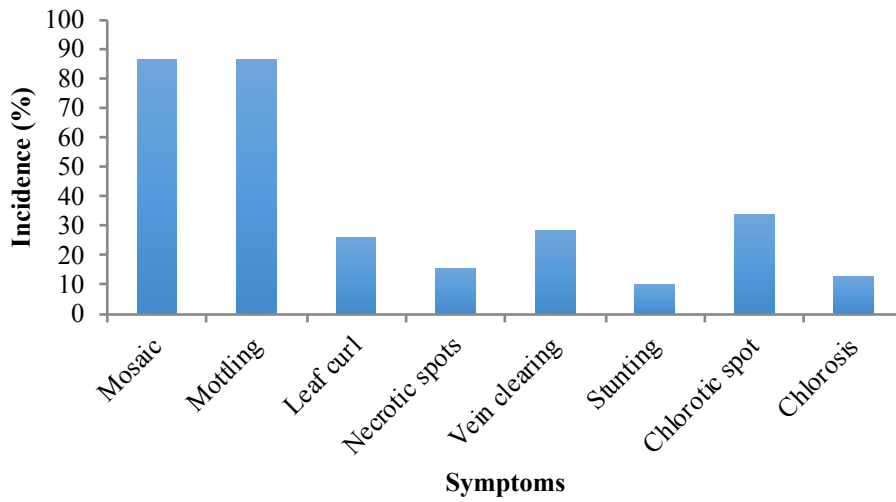
Data on disease incidence were arcsine-transformed to homogenize variances and reduce error before subjecting them to analysis of variance (ANOVA). The other quantitative data (AUDPC, final severity, plant height and seed yield) were subjected to ANOVA and the means separated by least significant difference (LSD) method at 5% level of probability. Pearson's correlation coefficients among the parameters (plant height, disease incidence, severity and AUPDC) were calculated. All statistical analyses were performed using GenStat Release 10.3 (VSN International).

## RESULTS AND DISCUSSION

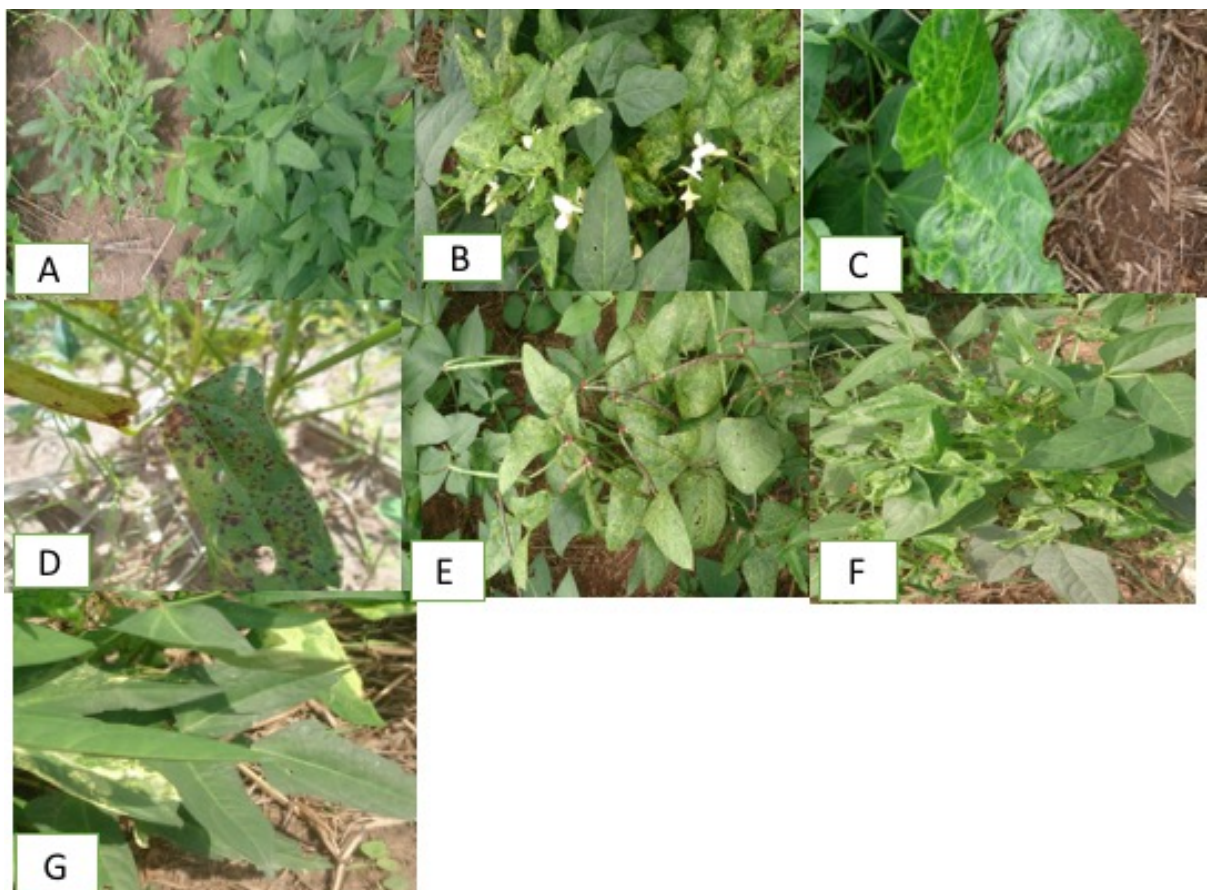
### Symptoms observed

The cowpea plants manifested varying symptoms of virus diseases during the study (Figs. 1 and 2). Leaf mosaic and mottling (86.7%) were the most common symptoms observed followed by chlorotic spots (34.2%), vein clearing (28.9%), leaf curl (26.3%), necrotic lesions (15.8%) whereas stunting was the least (10.5%). Similar symptoms were reported elsewhere on legumes affected by viral diseases [11, 20]. The symptoms observed in the present study are consistent with those associated with viral infection of cowpea in Ghana caused by BICMV, CABMV, CMEV and CYMV [6, 21]. The variations in symptoms observed on the field may be due to factors such as the type of viral strains, cowpea cultivar, the time of infection of the virus pathogen, mixed infections and/or the presence of unidentified viruses [22]. Variations in the cowpea viral disease symptoms development may also be as a result of factors such as changes in plant nutrients, physiological age of the plants and some environmental factors [23, 24].





**Figure 1: Incidence (%) of characteristic virus symptoms observed**



**Figure 2: Viral disease symptoms observed on the open field: A= stunted growth compared to a healthy plant of the same genotype, B= yellow mosaic leaves, C= vein clearing and mottling of the leaves, D= necrotic lesions, E= chlorotic spots, F= leaf curl, and G= leaf chlorosis**

Mean incidence (%) of viral diseases on 38 cowpea genotypes are shown in Table 2. Generally, for all the 38 cowpea genotypes, the mean incidence of viral diseases increased from 4 to 8 WAS, with overall mean incidences increasing from 17.7% to 29.2% in the wet season and from 34.4% to 53.1% in the dry season. The ANOVA showed no significant difference in mean incidence of viral disease during the wet season among the cowpea genotypes at 4 WAS ( $F_{41,84}=1.17$ ;  $P=0.274$ ), but differed significantly amongst them at 6 WAS ( $F_{41,84}=2.61$ ;  $P<0.001$ ) and 8 WAS ( $F_{41,84}=2.71$ ;  $P<0.001$ ). At the final observation (8 WAS), genotype IT10K-837-1 had the highest mean incidence (62.7%) in the wet season whereas genotype IT10K-819-4 showed no disease symptom (0%) (Table 2). On the contrary, in the dry season, ANOVA did not show significant difference in mean incidence of viral disease among the cowpea genotypes at 4 WAS ( $F_{41,84}=0.96$ ;  $P=0.547$ ), 6 WAS ( $F_{41,84}=1.36$ ;  $P=0.118$ ) and 8 WAS ( $F_{41,84}=1.45$ ;  $P=0.077$ ). At 8 WAS, genotype IT10K-827-11 had the highest mean disease incidence (90%) whilst Marfo Tuya had the lowest mean incidence of 11.8% (Table 2).

Differences in disease incidence observed among the cowpea genotypes in the wet season, suggests significant host-virus interaction effects. This variation in the host-virus interaction effects could be due to the differences in the genetic makeup of the different cowpea genotypes and viral species as reported in tomato-tomato yellow leaf curl virus pathosystem [25, 26]. It has been reported [27] that viral disease progression in a plant occurs only when new leaves develop, since symptoms cannot be expressed in already expanded leaves. This might have accounted for the increase in disease incidence among the cowpea genotypes from 4 WAS to 8 WAS in both seasons. It was also observed in this study that the level of disease incidence in some cowpea genotypes decreased between 4 WAS and 8 WAS. For instance, the level of disease incidence recorded for genotype IT07K-243-1-2 decreased from 36.1% to 19.9% between 4 WAS and 8 WAS (Table 2). This could be due to the fact that shortly after anthesis, some plants tend to become more resistant to viral infection and the number of healthy plants available for new infections also decreases as the season progresses [28].

### **Severity of viral disease, area under disease progress curve (AUDPC) and seed yield**

The cowpea genotypes showed significantly varying levels of disease severity ( $F_{37,74}=4.0$ ;  $P<0.001$ ) at the final observation (8 WAS) during the wet season (Table 3). Genotype Apagbaala had the highest symptom severity score of 2.9, whereas genotypes IT10K-819-4, and IT07K-297-13 did not show any symptom. On the contrary, in the dry season, there was no significant difference in the levels of viral symptom severity scores recorded for the cowpea genotypes ( $F_{37,74}=1.0$ ;  $P=0.45$ ). Genotype IT07K-298-9 had the highest mean symptom severity score of 2.4, whereas genotypes Marfo Tuya had the lowest disease severity score of 1.1, at 8 WAS (Table 3).

The AUDPC recorded for the 38 cowpea genotypes in the wet season varied significantly among them ( $F_{37,74}=4.0$ ,  $P<0.001$ ). The highest AUDPC of 9.1 was recorded for genotype Apagbaala, whereas genotype IT10K-819-4 had the lowest (4.1). There was, however, no significant difference ( $F_{37,74}=P>0.05$ ) among the cowpea genotypes during the dry season. The mean AUDPC values, however, ranged from 3.88 to 11.55 for genotypes IT10K-843 and GH3684, respectively (Table 3).



The variation in disease reactions for plants grown under the same environmental conditions may be due to inherent factors which control the ability of the plants to withstand viral infection, viral strain and the time of infection as postulated by Jones *et al.* [22]. Studies conducted by Schuerger and Hammer [29] also revealed that the genetic background or environmental factors might influence the apparent relative effectiveness of the resistant genes of the plant, resulting in a lot of genotypes becoming susceptible to a virus attack.

A 2-way ANOVA revealed a highly significant difference in disease incidence ( $F_{1,168}=76.14$ ,  $P<0.001$ ) between the wet and dry seasons. The dry season had the highest final mean incidence of 53.1% and the wet season had 30.9% (Table 2). The overall mean final disease severity score recorded in the dry season (1.71) was also significantly higher ( $F_{1,168}=10.66$ ,  $P=0.001$ ) than that of the wet season (1.47). Also, the ANOVA revealed significant difference ( $F_{1,168}=40.12$ ;  $P<0.001$ ) in AUDPC values between the wet (5.71) and dry (5.32) seasons (Table 3).

The higher disease incidence, severity and AUDPC recorded in the dry season compared to the wet season could be due to the higher temperatures (25-34°C) and low relative humidity experienced during the dry season compared to the wet season that might have influenced rapid disease development [30] and suppressed the plasticity and recovery rate of the cowpea genotypes [31]. Higher temperatures experienced in the dry season might have also favoured rapid development of aphid vectors, and hence increased the chances of transmitting viral diseases in the cowpea genotypes. A close relationship between aphids and viral incidences has been reported elsewhere [32]. Significant differences in the disease severity and incidence observed in two different growing seasons have also been attributed to varying weather conditions within seasons [33, 34]. Large populations of the virus vectors are usually found on the weeds, particularly during the minor growing season [35], which might have also accounted for the greater incidence and severity recorded during the dry season compared to the wet season.

### Genotype by season interaction

Genotype by season (G x S) interaction effect on disease severity ( $F_{41, 168}=1.24$ ,  $P = 0.177$ ) and AUDPC ( $F_{41, 168}=1.33$ ,  $P=0.110$ ) were not significant (Table 4). Mean severity scores ranged between 1.0 and 2.9 in the wet season and from 1.1 to 2.7 in the dry season. This finding indicates that all the cowpea genotypes were either resistant or moderately resistant in both wet and dry seasons. This could be due to the interplay between the viral pathogen, host (the cowpea genotypes) and environment, as have been earlier postulated by Engering *et al.* [36]. Thus, the cowpea genotypes exhibited a stable genotype x season interaction effect.

### Plant growth and seed yield

Shoot growth was more sensitive to increasing soil moisture stress [37] and this might have accounted for the difference in growth among the cowpea genotypes in the wet and dry seasons. Genotype SARC-1-57-1 had mean plant height of 41 cm in the wet season but had mean plant height of 17.7 cm in the dry season. Average plant height recorded in the wet season was much higher (26.27 cm) than that of the dry season (17.2 cm). The difference in the mean growth rate in the wet and dry seasons may be due to the





favourable environmental conditions of moisture during this period as well as the inherent differences among the cowpea genotypes. The low moisture and high temperatures recorded in the dry season might have affected the growth of the cowpea genotypes hence the lower mean plant height recorded for the dry season.

The yield was also not recorded during the dry season due to unfavourable environmental factors, which caused inflorescence to drop and also the continuous feeding on the fresh pods by birds due to lack of food during this period. The incidence of viral disease was also high which affected growth as well as pod formation. A preliminary experiment conducted during the dry season of 2002 by Taiwo and Akinjogunla [38] resulted in complete loss in pod and seed yield, which was attributed to the hot and low soil moisture level associated with the dry season, which is known to influence virus multiplication in cowpea. Hughes and Shoyinka [39] also indicated that yield loss in sub-Saharan Africa could be attributed to virus mixtures and cultivar-environment interactions. This finding, thus, shows a genotype-virus-environment interaction effect; hence, genotypes that showed stable viral disease reaction over the two seasons, as well as high yield could be selected for further evaluation.

### Correlation Analysis

Table 5 shows the correlation coefficients among the parameters studied. Incidence of viral disease in the wet season was significantly and positively correlated with disease severity ( $r=0.7721$ ;  $P < 0.05$ ) and AUDPC ( $r=0.8801$ ;  $P < 0.05$ ), but negatively correlated with plant height ( $r=-0.1320$ ;  $P > 0.05$ ) and seed yield ( $r=-0.1296$ ;  $P > 0.05$ ).

Genotypes IT10K-819-4 and Marfo Tuya had the lowest disease incidence in the wet and dry seasons, respectively. This did not, however, translate into the highest yield compared to GH3684 that recorded the highest yield of 8,010 kg ha<sup>-1</sup> with incidence and severity of 57.3% (2.0) and AUDPC of 6.2. This was further affirmed by the non-significant correlation between disease incidence and seed yield ( $r=-0.1296$ ;  $P > 0.05$ ) (Table 5). This may be due to the fact that genotype GH3684 may be more tolerant to the cowpea disease and adaptable than genotypes IT10K-819-4 and Marfo Tuya, which yielded dry cowpea seeds of 5,627 kg ha<sup>-1</sup> and 4,747 kg ha<sup>-1</sup>, respectively; this yield was more than the achievable yield of cowpea (2,600 kg ha<sup>-1</sup>) in Ghana [4]. The higher plant growth and spread of the cowpea plants observed on the field during the wet season, which translated into high yield in spite of incidence of viral disease could be attributed to favourable microclimate that favoured plant growth but affected the dynamics of virus vectors that transmit viruses to the cowpea plants [33, 34]. This also shows that cowpea plants are more tolerant to viral infection under favourable environmental conditions, which translates into yield and low incidence of the viral diseases.

### CONCLUSION

The cowpea genotypes evaluated were between resistant to moderately resistant to viral diseases and displayed varying symptoms including mosaic, mottling, necrosis, and deformation and stunting. Disease incidence and severity were significantly higher in the dry season than in the wet season. The cowpea genotypes also showed significant genotype-season interaction effects. Six genotypes (IT07-210-1-1, IT07K-297-13,



IT08K-193-14, IT09-456, IT10K-817-3 and IT10K-819-4) out of the 38 cowpea genotypes exhibited stable resistance both in the wet and dry seasons and also produced very high yields compared to the achievable yield of 2,600 kg ha<sup>-1</sup>. These high yielding resistant genotypes could be evaluated further multilocally for release to farmers in the coastal agro-ecological zones of Ghana. For maximum yield to be obtained, farmers in the coastal agro-ecological zone must grow cowpea when the major rains have peaked and about to subside and when there is effective management of birds and other insect pests.

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**Table 1: Thirty-eight cowpea genotypes assessed in an open field during the wet and dry seasons**

Cowpea genotype	Characteristic	Seed coat colour	Source
Apagbaala	Early maturing	White	SARI <sup>1</sup>
IT07K-243-1-2	Early maturing	Rough Brown	IITA <sup>2</sup>
IT07K-298-9	Early maturing	White	IITA
IT07K-299-6	Early maturing	White	IITA
IT08K-125-107	Early maturing	White	IITA
IT10K-836-2	Early maturing	Brown	IITA
IT10K-837-1	Early maturing	White	IITA
IT10K-843	Early maturing	White	IITA
IT10K-866-1	Early maturing	White	IITA
IT10K-973-1	Early maturing	White	IITA
IT10K832-3	Early maturing	Speckled White	IITA
IT11K-61-82	Early maturing	White	IITA
IT07-210-1-1	Medium maturing	White	IITA
IT07K-291-92	Medium maturing	White	IITA
IT07K-303-1	Medium maturing	White	IITA
IT08-125-100	Medium maturing	White	IITA
IT08-150-12	Medium maturing	White	IITA
IT08K-126-19	Medium maturing	White	IITA
IT08K-180-11	Medium maturing	White	IITA
IT09K-231-1	Medium maturing	Brown	IITA
IT10K-815-5	Medium maturing	Red	IITA
IT10K-817-7	Medium maturing	Red	IITA
IT10K-827-11	Medium maturing	White	IITA
MarfoTuya	Medium maturing	White	SARI
IT04K-321-2	Dual Purpose	White	IITA
IT07K-297-13	Dual Purpose	White	IITA
IT07K-298-15	Dual Purpose	White	IITA
IT08K-193-14	Dual Purpose	White	IITA
IT08K-193-15	Dual Purpose	White	IITA
IT09K-321-1	Dual Purpose	Brown	IITA
IT09K-456	Dual Purpose	Cream	IITA
IT10K-817-1	Dual Purpose	Red	IITA
IT10K-817-3	Dual Purpose	Red	IITA
IT10K-819-4	Dual Purpose	Red	IITA
IT10K-834-3	Dual Purpose	Mottled Red	IITA
Padi Tuya	Dual Purpose <sup>4</sup>	White	SARI
GH 3684	Striga-resistant	Red	UCC/PGRRI <sup>3</sup>
SARC-1-57-1	Aphid-resistant	White	SARI

1. SARI- Savanna Agriculture Research Institute, Bawku, Ghana

2. IITA- International Institute of Tropical Agriculture, Nigeria

3. UCC- University of Cape Coast and PGRRI- Plant Genetic Resource Research Institute, Bunso, Ghana

4. Dual Purpose- grown for the seeds and the leaves

**Table 2: Mean incidence of viral disease among 38 cowpea genotypes during the wet and dry seasons**

Cowpea Genotypes	Disease incidence					
	Wet season			Dry season		
	4WAS	6WAS	8WAS	4WAS	6WAS	8WAS
Apagbaala	26.1	57.8 <sup>ab</sup>	52.8 <sup>ab</sup>	23.1	60.0	51.5
GH3684	0	39.1 <sup>bcdefg</sup>	45.0 <sup>abcde</sup>	11.8	41.8	56.8
IT04K-321-2	17.7	8.9 <sup>hi</sup>	8.9 <sup>fgh</sup>	26.8	56.8	60.0
IT07-210-1-1	8.9	8.9 <sup>hi</sup>	8.9 <sup>fgh</sup>	31.1	53.0	45.0
IT07K-243-1-2	36.1	21.9 <sup>efghi</sup>	19.9 <sup>defgh</sup>	41.7	38.0	30.0
IT07K-291-92	13.1	25.4 <sup>cdefghi</sup>	21.1 <sup>cedfgh</sup>	26.8	63.7	60.0
IT07K-297-13	17.7	0.0 <sup>i</sup>	6.1 <sup>gh</sup>	<b>16.1</b>	26.3	41.8
IT07K-298-15	19.2	27.8 <sup>cdefghi</sup>	32.2 <sup>bcdefg</sup>	45.5	51.5	63.3
IT07K-298-9	54.1	48.9 <sup>abcde</sup>	51.1 <sup>ab</sup>	43.8	58.5	73.9
IT07K-299-6	23.1	30.3 <sup>bcdefgh</sup>	37.2 <sup>abcdef</sup>	<b>51.6</b>	58.9	78.3
IT07K-303-1	17.2	26.2 <sup>cdefghi</sup>	36.9 <sup>abcdef</sup>	48.3	63.7	55.7
IT08-125-100	6.1	47.3 <sup>abcdef</sup>	46.9 <sup>abcd</sup>	49.8	60.0	63.3
IT08K-125-107	6.1	52.1 <sup>abcd</sup>	54.1 <sup>ab</sup>	<b>55.2</b>	48.3	58.5
IT08-150-12	6.1	36.8 <sup>cdefgh</sup>	45.0 <sup>abcde</sup>	41.7	60.0	41.3
IT08K-126-19	17.2	28.1 <sup>bcdefghi</sup>	28.1 <sup>bcdefgh</sup>	41.3	55.7	62.2
IT08K-180-11	12.3	26.1 <sup>cdefghi</sup>	21.1 <sup>cedfgh</sup>	<b>16.1</b>	45.0	60.0
IT08K-193-14	18.4	17.7 <sup>fghi</sup>	17.2 <sup>efgh</sup>	26.3	45.0	48.3
IT08K-193-15	21.1	8.9 <sup>hi</sup>	8.9 <sup>fgh</sup>	30	48.7	60.0
IT09-456	13.1	17.2 <sup>ghi</sup>	8.9 <sup>gh</sup>	37	38.0	37.0
IT09K-231-1	15	37.2 <sup>bcdefgh</sup>	30.3 <sup>bcdefg</sup>	33.3	45.5	62.2
IT09K-321-1	8.9	13.1 <sup>ghi</sup>	18.9 <sup>defgh</sup>	33.3	41.8	51.5
IT10K-815-5	15	11.1 <sup>ghi</sup>	11.1 <sup>fgh</sup>	33.3	70.2	63.3
IT10K-817-1	8.9	0.0 <sup>i</sup>	8.9 <sup>fgh</sup>	45	51.5	58.5
IT10K-817-3	17.2	17.2 <sup>ghi</sup>	19.9 <sup>defgh</sup>	34.8	52.0	45.5



IT10K-817-7	12.3	8.9 <sup>hi</sup>	6.1 <sup>gh</sup>	36.5	53.5	63.3
IT10K-819-4	13.1	0.0 <sup>i</sup>	0.0 <sup>h</sup>	26.8	46.1	49.8
IT10K-827-11	6.1	13.1 <sup>ghi</sup>	19.2 <sup>defgh</sup>	45	48.3	90.0
IT10K-832-3	33	36.1 <sup>bcdefgh</sup>	36.8 <sup>abcdef</sup>	<b>11.7</b>	30.0	43.9
IT10K-834-3	11.1	0.0 <sup>i</sup>	33.0 <sup>bcdefg</sup>	26.8	54.7	70.2
IT10K-836-2	26.1	8.9 <sup>gi</sup>	19.2 <sup>d<sup>efgh</sup></sup>	48.6	82.0	63.3
IT10K-837-1	19.2	71.1 <sup>a</sup>	62.7 <sup>a</sup>	<b>54.4</b>	26.8	30.0
IT10K-843	6.1	49.6 <sup>abcde</sup>	53.9 <sup>abdefgh</sup>	41.7	38.0	38.0
IT10K-866-1	45	53.9 <sup>abc</sup>	30.3 <sup>bcdefg</sup>	30	45.0	38.0
IT10K-973-1	41.1	19.9 <sup>efghi</sup>	47.7 <sup>abcd</sup>	31.5	38.5	52.0
IT11K-61-82	27.3	27.3 <sup>cdefghi</sup>	18.9 <sup>defgh</sup>	38.1	48.7	48.3
MarfoTuya	0	27.3 <sup>cdefghi</sup>	53.9 <sup>ab</sup>	15	15.0	11.8
PadiTuya	15	23.9 <sup>defghi</sup>	36.1 <sup>abcdef</sup>	26.8	33.2	33.7
SARC-1-57-1	17.7	30.8 <sup>bcdefgh</sup>	50.8 <sup>abc</sup>	48.7	67.0	52.0
Grand mean	17.7	25.7	29.2	34.4	49.5	53.1
P-value	0.27	<. 001	<. 001	0.547	0.118	0.077
D.f.	41	41	41	41	41	41
l.s.d.	32.18	31.11	30.70	36.74	31.95	32.85

Each value is the mean of 3 replicates. In each column, means followed by the same letter are not significantly different ( $P < 0.05$ ) according to l.s.d. test at 5% level of probability

**Table 3: Mean viral disease severity scores, Area Under Disease Progress Curve (AUDPC), and mean seed yield for 38 cowpea genotypes screened during wet and dry seasons**

Genotypes	Wet season					Dry season				
	Plant height/cm	Final severity	AUDPC	Seed yield (kg ha <sup>-1</sup> )	Disease reaction	Plant height (cm)	Final severity	AUDPC	Seed yield (kg ha <sup>-1</sup> )	Disease reaction
Apagbaala	14.1 <sup>d</sup>	2.9 <sup>a</sup>	9.1 <sup>a</sup>	1543 <sup>ab</sup>	MR	15.6 <sup>b</sup>	1.7	5.0	N/A	R
GH3684	32.1 <sup>bc</sup>	1.6 <sup>cd</sup>	6.2 <sup>bcdefghi</sup>	8010 <sup>a</sup>	MR	20.8 <sup>a</sup>	1.9	6.6	N/A	MR
IT04K-321-2	27.6 <sup>c</sup>	1.1 <sup>cd</sup>	4.3 <sup>kl</sup>	3370 <sup>ab</sup>	R	17.1 <sup>b</sup>	1.9	5.3	N/A	MR
IT07-210-1-1*	22.9 <sup>cd</sup>	1.1 <sup>cd</sup>	4.6 <sup>hijkl</sup>	4063 <sup>ab</sup>	R	18.9 <sup>a</sup>	1.5	4.9	N/A	R
IT07K-243-1-2	27.3 <sup>c</sup>	1.5 <sup>cd</sup>	5.8 <sup>defghijkl</sup>	1733 <sup>ab</sup>	MR	20.4 <sup>a</sup>	1.4	4.5	N/A	R
IT07K-291-92	26.9 <sup>c</sup>	1.1 <sup>cd</sup>	4.9 <sup>ghijkl</sup>	1350 <sup>ab</sup>	R	18.9 <sup>a</sup>	2.2	5.7	N/A	MR
IT07K-297-13*	22.3 <sup>cd</sup>	1.0 <sup>d</sup>	4.4 <sup>jkl</sup>	4033 <sup>ab</sup>	R	16.9 <sup>b</sup>	1.4	4.0	N/A	R
IT07K-298-15	21.5 <sup>cd</sup>	1.4 <sup>cd</sup>	5.4 <sup>efghijkl</sup>	4707 <sup>ab</sup>	MR	15.8 <sup>b</sup>	1.8	5.1	N/A	MR
IT07K-298-9	21.3 <sup>cd</sup>	1.7 <sup>cd</sup>	7.1 <sup>bcde</sup>	2100 <sup>ab</sup>	MR	14.0 <sup>b</sup>	2.4	6.8	N/A	MR
IT07K-299-6	16.3 <sup>d</sup>	1.4 <sup>cd</sup>	5.5 <sup>efghijkl</sup>	2077 <sup>ab</sup>	MR	15.6 <sup>b</sup>	2.4	6.1	N/A	MR
IT07K-303-1	21.0 <sup>cd</sup>	1.4 <sup>cd</sup>	5.8 <sup>efghijkl</sup>	1873 <sup>ab</sup>	MR	16.5 <sup>b</sup>	2.1	6.1	N/A	MR
IT08-125-100	14.7 <sup>d</sup>	2.0 <sup>bc</sup>	7.7 <sup>abc</sup>	2513 <sup>ab</sup>	MR	18.5 <sup>a</sup>	2.1	5.7	N/A	MR
IT08-150-12	27.2 <sup>c</sup>	2.1 <sup>bc</sup>	6.8 <sup>bcdef</sup>	6223 <sup>ab</sup>	MR	21.1 <sup>a</sup>	1.6	5.3	N/A	MR
IT08K-125-107	22.2 <sup>cd</sup>	1.8 <sup>c</sup>	6.8 <sup>bcdef</sup>	4010 <sup>ab</sup>	MR	21.5 <sup>a</sup>	1.6	4.6	N/A	R
IT08K-126-19	23.0 <sup>cd</sup>	1.7 <sup>cd</sup>	6.4 <sup>bcdefgh</sup>	3463 <sup>ab</sup>	MR	18.9 <sup>a</sup>	2.0	5.3	N/A	MR
IT08K-180-11	23.9 <sup>cd</sup>	1.2 <sup>cd</sup>	5.2 <sup>fghijkl</sup>	2767 <sup>ab</sup>	MR	14.4 <sup>b</sup>	2.1	5.3	N/A	MR
IT08K-193-14*	24.3 <sup>cd</sup>	1.1 <sup>cd</sup>	4.6 <sup>ijkl</sup>	6867 <sup>ab</sup>	R	15.8 <sup>b</sup>	1.7	4.6	N/A	R
IT08K-193-15	27.0 <sup>c</sup>	1.1 <sup>cd</sup>	4.4 <sup>jkl</sup>	5717 <sup>ab</sup>	R	13.3 <sup>b</sup>	2.1	5.2	N/A	MR
IT09-456*	23.9 <sup>cd</sup>	1.1 <sup>cd</sup>	4.5 <sup>jkl</sup>	6770 <sup>ab</sup>	R	16.4 <sup>b</sup>	1.5	4.4	N/A	R
IT09K-231-1	24.4 <sup>cd</sup>	1.4 <sup>cd</sup>	5.5 <sup>efghijkl</sup>	3600 <sup>ab</sup>	MR	22.0 <sup>a</sup>	2.2	5.6	N/A	MR
IT09K-321-1*	23.2 <sup>cd</sup>	1.3 <sup>cd</sup>	4.8 <sup>ghijkl</sup>	5697 <sup>ab</sup>	R	17.4 <sup>a</sup>	1.7	4.9	N/A	R
IT10K-815-5	26.4 <sup>c</sup>	1.1 <sup>cd</sup>	4.7 <sup>ghijkl</sup>	4400 <sup>ab</sup>	R	17.6 <sup>a</sup>	2.1	5.6	N/A	MR



IT10K-817-1	22.2 <sup>cd</sup>	1.1 <sup>cd</sup>	4.2 <sup>l</sup>	5073 <sup>ab</sup>	R	18.1 <sup>a</sup>	1.9	5.3	N/A	MR
IT10K-817-3*	16.3 <sup>d</sup>	1.2 <sup>cd</sup>	4.8 <sup>ghijkl</sup>	5713 <sup>ab</sup>	R	12.5 <sup>b</sup>	1.7	5.0	N/A	R
IT10K-817-7	28.7 <sup>bc</sup>	1.1 <sup>cd</sup>	4.4 <sup>ijkl</sup>	2153 <sup>ab</sup>	R	14.8 <sup>b</sup>	1.9	5.5	N/A	MR
IT10K-819-4*	31.8 <sup>bc</sup>	1.0 <sup>d</sup>	4.1 <sup>l</sup>	5627 <sup>ab</sup>	R	18.2 <sup>a</sup>	1.7	4.8	N/A	R
IT10K-827-11	30.0 <sup>bc</sup>	1.1 <sup>cd</sup>	4.7 <sup>hijkl</sup>	2290 <sup>ab</sup>	R	17.5 <sup>a</sup>	2.7	6.0	N/A	MR
IT10K-832-3	26.4 <sup>c</sup>	1.4 <sup>cd</sup>	6.1 <sup>bcdefghij</sup>	3277 <sup>ab</sup>	MR	14.9 <sup>b</sup>	1.9	5.2	N/A	MR
IT10K-834-3	22.8 <sup>cd</sup>	1.2 <sup>cd</sup>	5.2 <sup>fghijkl</sup>	7040 <sup>ab</sup>	MR	15.5 <sup>b</sup>	2.4	6.4	N/A	MR
IT10K-836-2	26.1 <sup>c</sup>	2.8 <sup>b</sup>	4.5 <sup>ijkl</sup>	3257 <sup>ab</sup>	R	15.8 <sup>b</sup>	2.2	5.6	N/A	MR
IT10K-837-1	28.5 <sup>bc</sup>	2.2 <sup>bc</sup>	9.0 <sup>a</sup>	3483 <sup>ab</sup>	MR	21.8 <sup>b</sup>	1.4	4.6	N/A	R
IT10K-843	26.2 <sup>c</sup>	1.5 <sup>cd</sup>	7.6 <sup>abcd</sup>	3150 <sup>ab</sup>	MR	16.1 <sup>b</sup>	1.4	3.9	N/A	R
IT10K-866-1	26.7 <sup>c</sup>	1.6 <sup>cd</sup>	6.4 <sup>bcdefg</sup>	1313 <sup>b</sup>	MR	14.7 <sup>b</sup>	1.5	4.8	N/A	R
IT10K-973-1	23.2 <sup>cd</sup>	1.3 <sup>cd</sup>	5.1 <sup>fghijkl</sup>	3057 <sup>ab</sup>	MR	16.2 <sup>b</sup>	1.9	5.1	N/A	MR
IT11K-61-82	30.8 <sup>bc</sup>	1.1 <sup>cd</sup>	4.5 <sup>ijkl</sup>	3207 <sup>ab</sup>	R	15.0 <sup>b</sup>	1.9	5.3	N/A	MR
Marfo tuya	31.5 <sup>bc</sup>	2.2 <sup>bc</sup>	7.8 <sup>ab</sup>	4747 <sup>ab</sup>	MR	22.7 <sup>a</sup>	1.1	3.9	N/A	R
Padituya	31.7 <sup>bc</sup>	1.6 <sup>cd</sup>	6.0 <sup>cdefghijk</sup>	5027 <sup>ab</sup>	MR	15.4 <sup>b</sup>	1.5	4.2	N/A	R
SARC-1-57-1	41.0 <sup>a</sup>	1.6 <sup>cd</sup>	6.3 <sup>bcdefgh</sup>	5593 <sup>ab</sup>	MR	17.7 <sup>a</sup>	1.8	5.2	N/A	MR
Grand mean	26.27	1.47	5.71	4022		17.20	1.71	5.32		
P-value	<0.001	<0.001	<0.001	<0.001		<0.001	0.92	0.52		
l.s.d.	9.219	0.624	1.78	3362		5.751	0.79	3.32		

Each value is the mean of 3 replicates. In each column, means followed by the same letter are not significantly different ( $P < 0.05$ ) according to Least Significant Difference (LSD) test at  $P < 0.05$ . MR-moderate resistance, R-resistance. N/A-Yield was not assessed for the dry season due to lost of flowers and pods to birds

\* Genotypes showing resistance in both the wet and dry seasons



**Table 4: Mean sum of squares for viral disease incidence, final severity and AUPDC of viral diseases among the 38 genotypes of cowpea grown in wet and dry seasons**

Source	Df	Mean square		
		Disease incidence	Virus severity	AUPDC
Genotype (G)	41	633.50 <sup>ns</sup>	1.71 <sup>ns</sup>	3.00 <sup>ns</sup>
Season (S)	1	30835.70 <sup>***</sup>	16.16 <sup>**</sup>	96.62 <sup>***</sup>
G x S	41	863.20 <sup>***</sup>	1.87 <sup>ns</sup>	3.19 <sup>ns</sup>
Residue	168	405.00 <sup>ns</sup>	1.52 <sup>ns</sup>	2.41 <sup>ns</sup>

\*\* Significant at P<0.01;\*\*\* significant at P<0.001;ns, not significant (P>0.05), Df, degree of freedom

**Table 5: Association between the disease severity, incidence, AUPDC, plant height and seed yield among the cowpea genotypes in the wet and dry seasons**

1	AUPDC	Incidence	Severity	Plant height	Seed yield
AUPDC					
Incidence	0.8801 <sup>**</sup>				
Severity	0.8924 <sup>**</sup>	0.7721 <sup>**</sup>			
Plant height	-0.2163	-0.1320	0.0580		
Seed yield	-0.2397	-0.1296	-0.0368	0.5340 <sup>**</sup>	
2	AUPDC	Incidence	Plant height	Severity	
AUPDC					
Incidence	0.4722 <sup>**</sup>				
Plant_height	0.0654	-0.2749			
Severity	0.5178 <sup>**</sup>	0.9243 <sup>**</sup>	-0.2975		

\*\* Correlation is significant at 1% level of significance. 1=Wet season trial and 2=dry season trial





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