





Evaluation of Cowpea (*Vigna unguiculata*) Genotypes for Resistance to Web Blight Caused by *Rhizoctonia solani*

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Authors' contributions

This work was carried out in collaboration between all authors. Author FK designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors ENKS and AI managed the analyses of the study. Author ENKS managed the literature searches. All authors read and approved the final manuscript.

Article Information

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Original Research Article

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ABSTRACT

Aims: Soil borne fungi such as *Rhizoctonia solani* are among the pathogens that infect cowpea (*Vigna unguiculata*) causing web blight which results in yield loss of 30% worldwide. Disease infection is mostly controlled by the use of chemicals, which occasionally reaches the level of toxicity thereby polluting the environment as well as killing beneficial microorganisms in soil. The present study was conducted to evaluate seven cowpea genotypes for their resistance to *Rhizoctonia solani*.

Place and Duration: The study was carried out during the 2017 cropping season at the experimental fields of the University for Development Studies, Nyankpala, Northern Region of Ghana.

Methodology: The field was laid in a randomized complete block design (RCBD) with seven treatments and each treatment replicated three times. Data was collected on disease incidence, severity and grain yield.

Results: The results showed that IT99K-1122 had the least incidence and severity whereas Sanzi

recorded the highest disease incidence and severity. The results showed that IT99K-1122 was moderately resistant and also recorded the highest yield.

Conclusion: It was recommended that farmers cultivate IT99K-1122 as it was found to be the most suitable genotype offering resistance to *R. solani*. Thus, IT99K-1122 which was also moderately resistant was suggested to be used as a source of resistance to *R. solani* in future breeding works.

Keywords: Resistance; disease incidence; Rhizoctonia solani; susceptible; cowpea genotype.

1. INTRODUCTION

Cowpea (Vigna unguiculata (L.) Walp) is one of the most important legumes in the farming systems particularly in the Northern part of Ghana. It is mostly grown by smallholders in the hot, drought-prone savannas and very arid Sahelian agro-ecological zones where it is often intercropped with sorghum and pearl millet [1]. In comparison to cereals, cowpea is a cheap source of proteins and amino acids [2]. Depending on the variety or cultivar, the crop may exhibit different morphological features such as climbing, erectness, semi erect, prostate or creeping and usually indeterminate under favourable environmental conditions [3]. Due to its valuable and dependable nature, cowpea provides income to many small holder farmers and traders in sub-Saharan Africa [4]. All parts of the plant are used as food and provide nutrient such as proteins and vitamins [5]. Cowpea thrives very well in the tropics particularly Africa with Nigeria and Niger accounting for 66% of world production. Nigeria produced an average of 3.5 ton of cowpea followed by Niger with 1.6 ton between 2010 and 2014 [6]. Cowpea is adapted to different soil types; and has been observed to grow well in sandy soils where root growth is not restricted [7]. The crop requires well-drained soils with a pH of 5.6 - 6.0 but can still produce reasonable yield in waterlogged and heavy soils [8]. The optimum rainfall conditions for cowpea range from 400 to 700 mm per annum [8].

Yields are significantly low despite the numerous significance cowpeas existence in regions such as sub-Saharan Africa. In Ghana, pests and diseases, low soil fertility, as well as drought, are the major constraints of cowpea production [9]. Also, the production of cowpea without the control of insect pests as well as various bacterial and fungal diseases are high in Africa which result in the severe damage by pests and diseases hence the reduction in yields [3,10]. Soil and seed - borne fungi are among the pathogens that infect cowpea causing web blight,

stem rot, seedling decay and damping - off complex which result in low yield [10].

The most frequently used control measure against pests and diseases is by synthetic pesticides usage whose intensive and indiscriminate use in agriculture has caused many problems to the environment [11]. Such problems include water, soil, animals, food contamination; poisoning of farmers; elimination of non-target organisms, selection of pest and weed tolerance to certain pesticides [12]. Alternative control measures of plant diseases include cultural, biological, regulatory and the use of crops resistant to certain pests and diseases [13]. The use of resistant crop varieties is the most economical, easiest, and safest and one of the most effective means of managing plant diseases in crops [13,14]. It is therefore important to give appropriate research attention to finding cowpea varieties resistant to stem rot so as to minimise losses caused by the disease in a manner that will not pose threat to the environment, human and beneficial animals.

The present study was, therefore, set up to evaluate seven genotypes of cowpea for their resistance to web blight caused by wild relatives of *Rhizoctonia solani*.

2. MATERIALS AND METHODS

2.1 Study Area

The study was conducted at the "Farm for Future" of the University for Development Studies (UDS), Nyankpala campus in the Tolon District of Northern Region, Ghana. Nyankpala is within the Guinea-Savanna zone with annual rainfall of about 1200 mm. It lies between latitude 9°, 25 ° North and longitude 0°, 25° West on altitude 183 m above sea level. The distribution of temperature is fairly uniform with a maximum relative humidity of 76.8% and minimum of 46%. The area has a monomodal rainfall pattern which starts in May and ends in October. The cropping season, therefore, starts in mid-June to October with the rest of the year being dry and hazy [15]. The study was carried out between the months of August and November 2017.

2.2 Experimental Design and Treatments

The experiment was laid in randomized complete block design with seven treatments replicated three times.

2.3 Land Preparation and Layout

The total area used was 351 m^2 with $13 \text{ m} \times 27$ m dimensions. The plot size was $3 \text{ m} \times 3$ m made up of 5 rows x 15 stands giving the total number of stands on each plot to be 75 per replicate and in the three replicates giving a total of 1575 plants. The plots and replications were separated by a distance of 2 m between replications and 1m between plots. Weeding was done regularly until maturity.

Refilling was carried out 10 days after planting (DAP) as a result of poor germination of seeds. Plants were also thinned to two plants per stand 10 days after planting. At 30 DAP, Cypermethrin 10 EC in 200 ml/200 L of water insecticide was foliar - sprayed using a Knapsack sprayer and was applied thrice at weekly intervals on all replications. Data on yield components, pod number per plot were collected at harvest and grain yield per plot was obtained after threshing.

2.4 Data Collection

Data collection commenced three (3) weeks after seedling emergence. Five plants were randomly selected and tagged from each plot for data collection. The tagging was done by tying a coloured thread at the base of the selected plants for easy identification of the selected plants throughout the data collection period. The following data were taken on selected plants at three (3) weeks interval beginning from the 3rd week after seedling emergence.

2.4.1 Number of leaves

Leaf numbers were determined by counting the number of leaves on 5 tagged plants in the two middle rows and the mean recorded.

2.4.2 Plant height

Plant height was measured with a metre rule on 5 tagged plants of each plot. Height was measured from ground level to the topmost leaf

axil of the main stem and the mean height was expressed in centimetres.

2.4.3 Number of pods per plant

This was estimated by counting the number of pods from the 5 tagged plants harvested from the two middle rows and the mean recorded.

2.4.4 100 seed weight

A random 100 dried seed were taken from the harvested bulk and weighed to the nearest 0.1 g.

2.4.5 Seed yield

The pods from the harvested plants from the two middle rows were shelled and the weight of the seed recorded at 12% moisture content and later converted using the formula:

Seed yield (kg/ha) = Seed yield (kg) / Harvested area $(m^2) \times 10000 m^2$

Seed yield (t/ha) = Seed yield (kg/ha) × 1000

2.4.6 Disease assessment

The web blight disease severity was recorded using Web blight disease severity rating scale (1-9) [16] with modification. The detailed rating scale was as follows: 1 = No lesions on leaves; 3 = 1-25% area covered by lesions; 5 = 25.1-50%area covered by lesions; 7 = 50.1-75% area covered by lesions; 9 = 75.1-100% area covered by lesions.

Disease incidence (DI) percentage was calculated using the following formula:

$$DI = \frac{\text{Number of infected plants}}{\text{Total number of plants assessed}} \times 100$$

Disease severity (DS) percentage was determined using the following formula:

Disease severity (%) =
$$\frac{\text{Sum of disease rating}}{\text{Highest rating} \times \text{total number of plants rated}} \times 100$$

Using the severity values, the cowpea genotypes were grouped into five different classes based on a modified scale of [17] where lines with severity (%) of;

0 = immune, 1 - 15 = highly resistant, 16 - 30 = moderately resistant, 31 - 45 = moderately susceptible, > 45 = highly susceptible.

2.5 Statistical Analyses

GenStat (18th edition) statistical package was used to analyse all data taken by subjecting it to analysis of variance (ANOVA). Means were separated using the least significant difference (LSD) at 5%.

3. RESULTS

3.1 Incidence and Severity of Web Blight on Cowpea Genotypes

Table 1 shows that significant differences (P <0.05) existed in disease incidence among the cowpea genotypes. At 3 WAP, Sanzi recorded the highest disease incidence (35.1%) which was significantly different from the remaining six cowpea genotypes. Genotype IT99K-1122 recorded the least incidence (13.2%) which did not differ significantly from IT07K-299-6, Songotra and Zaayura. Padituya did not also differ significantly from Songotra and Zaayura. At 6 WAP, IT99K-1122 recorded the least incidence of 20% which was significantly different from Padituva, Songotra, Apagbaala, IT07K-299-6, Sanzi and Zaavura. Sanzi recorded the highest incidence of 57.9% which was also significantly different from the rest of the cowpea genotypes evaluated. At 9 WAP, Sanzi again recorded the highest incidence of 75.5% which differed significantly from the remaining cowpea genotypes. Genotype IT99K-1122 recorded the least incidence of 25.6% which was also significantly different from the rest of the cowpea genotypes. The control (Apagbaala) did not differ significantly from Padituva and Zaayura whiles Songotra did not differ statistically from genotype IT07K-299-6.

From Table 1, there was significant difference (P < 0.05) in disease severity in cowpea genotypes. At 3 WAP, Sanzi recorded the highest severity of 36.7% which was significantly different from the remaining treatments. Genotype IT99K-1122 recorded the least severity of 22.8% which also differed significantly from the remaining genotypes. Songotra did not differ significantly from IT07K-299-6 while Padituya did not differ significantly from the control (Apagbaala). At 6 WAP, IT99K-1122 recorded the least severity of 29.3% which was not significantly different from IT07K-299-6 and Zaayura. Sanzi recorded the highest severity of 55.6% which was significantly different from Padituya, Songotra, Apagbaala, IT07K-299-6, Sanzi and Zaayura. Padituya did not differ significantly from Songotra and Apagbaala (Control). At 9 WAP, Sanzi recorded

the highest severity of 76.5% which was significantly different from the rest of the treatments. Genotype IT99K-1122 recorded the least severity (30.8%) which did not differ significantly from IT07K-299-6, Padituya and Songotra. Padituya was not also significantly different from Apagbaala (Control) and Zaayura.

3.2 Yield Components, Yield and Disease Rating of Cowpea Genotypes

At 3 WAP, Padituya recorded the highest plant height of 12.2 cm which was not significantly different from Songotra and Zaayura (Table 2). Sanzi recorded the lowest plant height of 7.8 cm which was not significantly different from IT0K-299-6, Apagbaala (Control) and IT99K-1122. At 6 WAP. IT0K-299-6 recorded the highest plant height of 20.3 cm which was not significantly different from the remaining six treatments. Apagbaala (Control) recorded the least plant height of 14.8 cm. There was no significant difference among the cowpea genotypes. At 9 WAP, IT99K-1122 recorded the highest plant height of 29.7 cm which was significantly different from Zaayura, Padituya, Apagbaala (Control), IT07K-299-6, Sanzi and Songotra. Sanzi recorded the least plant height of 19.1 cm which was also significantly different from the rest of the genotypes. There was however no significant difference between Songotra and Apagbaala (Control) and also no significant difference existed between Padituya, IT07K-299-6 and Zaayura.

From Table 2, there was significant difference in the number of leaves among the cowpea genotypes. At 3WAP, Sanzi recorded the highest number of leaves which was significantly different from the rest of the treatments. Zaayura recorded the least number of leaves which was not significantly different from IT07K-299-6, Apagbaala (Control) and Padituya. At 6 WAP, IT99K-1122 recorded the highest number of leaves which was not significantly different from Sanzi. Padituya recorded the least number of leaves which was not significantly different from Apagbaala, Zaayura and IT07K-299-6. At 9 WAP, IT07K-299-6 recorded the least number of leaves which was not significantly different from Songotra, Zaayura and Padituya. IT99K-1122 recorded the highest number of leaves which was not significantly different from Sanzi.

From Table 2, also, the number of pods per plant, number of seeds per pod and total grain yield varied significantly. IT07K-299-6 recorded the highest number of pods per plant which was

not significantly different from Padituya, Zaayura and IT99K-1122. Sanzi, on the other hand, recorded the least number of pods per plant which was not significantly different from Songotra, Apagbaala (Control) and IT99K-1122.

Zaayura recorded the highest 100 seed weight which did not vary significantly from Padituya and IT99K-1122 (Table 2). Sanzi recorded the least 100 seed weight which was significantly different from Songotra, IT07K-299-6, Zaayura, Padituya, Apagbaala and IT99K-1122. Songotra was not significantly different from Apagbaala (Control) and IT07K-299-6.

In terms of grain yield, IT99K-1122 recorded the highest yield, which varied significantly from Zaayura, Padituya, Apagbaala (control) IT07K-299-6, Sanzi, and Songotra (Table 2). Sanzi recorded the least grain yield which was significantly different from Zaayura, Padituya, Apagbaala (control), IT07K-299-6, IT99K-1122 and Songotra. The yield Songotra was not significantly different from those of IT07K-299-6, Apagbaala (Control) and Zaayura.

The cowpea genotypes were separated into different host reaction groups based on the scale described by [17]. The field evaluation showed that Padituya, Songotra, and IT07K-299-6 were moderately susceptible; Apagbaala (Control), Sanzi and Zaayura were highly susceptible while IT99K-1122 was moderately resistant (Table 2).

4. DISCUSSION

Rhizoctonia solani produced reddish brown lesions on the leaves and also on the stem at soil level resulted in stem girdled which agrees with the report of [18] that seedling infected with *R. solani* had reddish brown lesions on leaves and cankers on the stem and roots. The results show that no cowpea genotype tested was immune to

the disease even though some genotypes showed different level of resistance to the disease. The study recorded significant differences in web blight incidence and severity among the cowpea genotypes evaluated and IT99K-1122 recorded the least web blight incidence and severity while Sanzi recorded the highest incidence and severity. It was observed during the study that cowpea genotypes that exhibited prostrate or indeterminate growth habit particularly Sanzi recorded the highest incidence and severity of web blight whereas cowpea genotypes that exhibited erect or determinate growth habit particularly genotype IT99K-1122 recorded the least incidence and severity. This could be due to the fact that the leaves and of cowpea genotypes branches with indeterminate or spreading growth habit were almost touching the ground and so were exposed to R. solani pathogens in the soil. Also, splashes of soil during rainfall could easily get into contact with the branches and leaves of the plants which could lead to increased population of the pathogen hence increased severity of web blight.

Incidence and severity of web blight could be associated to the fact that the cowpea genotypes were cultivated as a sole crop in the field which allowed for the quick increase in pathogen population which conformed to findings of [19] who also recorded high disease severity in cowpea caused by R. solani. Disease incidence and severity may also be attributed to the growth forms of the various cowpea genotypes. Also, higher incidences and severities recorded in the field could be attributed to the fact that the soil was not sterilised. The report of [20] showed that cowpea web blight and stem rot were caused by complex of soil fungi which included S. rolsii, R. solani and Pythium ultimum. Also [21] showed that cowpea stem rot caused by complex of soil borne fungi was more severe than those caused by a single fungus.

 Table 1. Incidence and severity of web blight on cowpea genotypes at three weeks interval

 after planting

Treatments	Dis	ease incidence	Disease severity (%)			
	3WAP	6WAP	9WAP	3WAP	6WAP	9WAP
Padituya	21.13cd	37.93c	46.0c	34.23c	39.60c	44.3bc
Songotra	18.10bc	26.63d	30.3d	29.67d	35.23cd	36.9b
IT99K-1122	13.23b	20.00b	25.6b	22.87b	29.33b	30.8b
IT07K-299-6	15.73b	24.90de	30.5d	28.40d	33.50bd	38.9bc
Sanzi	35.10a	57.90a	75.5a	36.77a	55.60a	76.5a
Zaayura	18.67bc	27.97d	51.9c	25.27e	29.57b	48.5c
Apagbaala (Control)	24.20d	37.07c	47.0c	34.37c	43.07ce	48.6c
LSD (0.05)	2.97	2.81	10.65	2.21	4.35	10.16
CV (%)	8.00	4.60	13.90	4.10	6.30	12.50

Figures with the same alphabets in a column are not significantly different ($P \ge 0.05$)

Treatments	Plant height			Number of flowers			Number	100	Grain	Host
	3WAP	6WAP	9WAP	3WAP	6WAP	9WAP	of pods/ plant	seed weight (g)	yield (t/ha)	reaction group
Padituya	12.23a	17.17a	27.07c	15.67c	49.7b	69.0b	9.67a	19.20a	0.907c	MS
Songotra	10.87a	16.70a	24.13d	17.33c	55.3ab	67.3b	7.67b	16.23c	0.803d	MS
IT99K-1122	9.60ac	19.33a	29.73a	17.67c	66.7a	93.3a	8.00ab	19.03a	1.023a	MR
IT07K-299-6	8.73ab	20.30a	26.57c	15.00c	49.7b	65.3b	10.33a	17.67ca	0.817d	MS
Sanzi	7.80b	15.93a	19.17b	20.33a	61.7a	88.0ac	4.67b	11.73b	0.627b	HS
Zaayura	10.23a	17.80a	28.17c	14.33b	54.0b	71.0b	8.67ab	21.37a	0.853cd	HS
Apagbaala (Control)	8.47ab	14.83a	23.23d	16.67c	52.3b	78.0c	6.00b	15.70c	0.737d	HS
LSD (0.05)	2.30	7.14	2.13	2.77	9.32	11.03	3.40	3.30	0.09	
CV (%)	13.30	23.00	4.70	9.30	9.40	8.20	4.30	10.70	6.40	

 Table 2. Yield components, yield and disease rating of cowpea genotypes at three weeks

 interval and at harvest

Figures with the same alphabets in a column are not significantly different at 5% level of significance ($P \ge 0.05$). Keys: MS = Moderately susceptible. MR = Moderately resistant. HS = Highly susceptible. HR=Highly resistant

From the study, genotype IT07K-299-6 recorded the highest number of pods per plant. However, its superior performance might be due to the good agronomic practices on the field. The study recorded significant difference in number of pods per plant. Sanzi recorded the least number of pods per plant and this could be attributed to the fact that Sanzi recorded the highest incidence and severity of web blight. IT99K-1122 recorded the highest grain yield and this could also be attributed to the fact that this cowpea line recorded the least severity and incidence of web blight. The results showed that the number of pods and grain yield significantly decreased with an increase in incidence and severity. This shows that cowpea web blight caused significant reduction in yield. This agrees with [22] who reported a negative and significant correlation between cowpea scab severity and grain yield in Samaru Zaria. Also, [23] recorded significant negative correlation between yield of maize and severity of root and basal stem rots caused by R. solani. The present study has shown that cowpea web blight is a serious limiting soil-borne pathogen to cowpea production in Northern region of Ghana and calls for provision of concomitant management strategies for it by relevant stakeholders in the region.

5. CONCLUSION

There were significant differences in disease severity and incidence among the cowpea genotypes evaluated. Sanzi recorded the highest disease incidence and severity from the third week to ninth week while IT99K-1122 recorded the least incidence and severity. However, the superior performance of genotype IT99K-1122 could be due to certain inherent abilities which could prevent damage from *R. solani* and also could withstand damage in case it occurred. The study revealed that among the seven cowpea genotypes used IT99K-1122 was the most resistant cowpea genotype, followed by IT07K-299-6, Songotra, Padituya, Zaayura, Apagbaala (Control) and Sanzi. Genotype IT99K-1122 could, therefore, form part of Integrated Disease Management (IDM) strategy for web blight of cowpea in areas where the disease is reported to cause yield loss.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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