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Research Article

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Response of cowpea germplasm to bacterial blight in Uganda

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ABSTRACT

Cowpea (*Vigna unguiculata* (L.) walp) is a legume crop mainly grown on small scale in low–input farming systems in Uganda. Cowpea bacterial blight (CoBB) disease caused by *Xanthomonas axonopodis* pv. *vignicola* (Burkh.) Dye is increasingly becoming a major hindrance to cowpea productivity. Sixty-four cowpea genotypes were evaluated for their response to bacterial blight disease (CoBB). Field experiments were carried out during the first and second rainy seasons using alpha lattice design with three replications. Data on disease incidence and severity, grain yield, days to 50% flowering, number of seeds per pod, pod length, number of peduncles per plant, and number of branches per plant were collected. Disease severity and incidence data was used to determine relative Area Under Disease Progress Curve (rAUDPC). Results showed significant differences ($P \leq 0.001$) among the genotypes for rAUDPC in each season. The rAUDPC across the seasons indicated that genotypes NE 32, WC 32A, WC 26 and NE 44 with rAUDPC values ranging from 0.22 to 0.26 were resistant to CoBB whereas genotypes NE 31 and NE 40 with rAUDPC values 0.44 and 0.46 respectively were susceptible. The rAUDPC did not show any significant correlation with days to 50% flowering, yield and its components. This study suggested that the genotypes NE 32, WC 32A, NE 44, and WC 26 be used as prospective parents in breeding initiatives to develop bacterial blight-resistant varieties due to their high yields and resistance to CoBB.

Keywords: Cowpea, Bacterial blight, disease response, Uganda

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INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) walp.), is one of the major food legumes cultivated for human consumption, particularly in East Africa (Orawu *et al.*, 2013). In Uganda, 90% of the cowpea is grown in the Northern and North Eastern regions (Tumwegamire *et al.*, 1998). Globally, cowpea cultivation is increasing from 2.41 million hectares to 10.68 million hectares over the last six decades (FAOSTAT, 2010). Approximately 30 countries cultivate cowpea globally (Singh, 2005) and it forms a primary source of income for small scale farmers in the Savannah region of Sub-Saharan Africa and to a greater extent in other developing countries. Increasing grain yield and quality are therefore the primary breeding objectives of nearly all cowpea breeding programs (Agbicodo, 2009).

The global population is continuously increasing and is expected to reach nine billion by 2050 (Bohra *et al.*, 2014) and such a huge population pressure will lead to severe food, natural resources and arable land shortages (FAO, 2009). Cowpea contains more than 25% protein in dry seeds as well as in young leaves (dry weight basis) and thus plays an important role in achieving food and nutritional security (Timko *et al.*, 2007). The high protein content of cowpea grain represents a major advantage for use in infant and children's food (Lambot, 2002). Legumes complement cereal-based carbohydrate rich diets of households as a key source of protein, vitamins and minerals. It is equally important as nutritious fodder for livestock (Singh *et al.*, 2003).

Cowpea is a particularly valuable component of low–input farming systems of resource-poor farmers because of its productivity, yield stability in the face of abiotic stress (drought, heat and low soil fertility) and the ability of the crop to enhance soil fertility for succeeding cereal or tuber crops grown in rotation (Sanginga *et al.*, 2003). Additionally, cowpea is an important warm season grain legume and forms excellent heavy vegetative growth which covers the ground so well that it checks soil erosion. As a leguminous crop, cowpea fixes about 70 - 240 kg per ha of nitrogen per year when cultivated commercially in most tropical and sub-tropical regions (Singh *et al.*, 2003).

Cowpea has greater tolerance to heat, drought and low soil fertility, and close evolutionary relatedness to other economically important grain legumes such as common bean

(*Phaseolus vulgaris* L.) and soybean (*Glycine max* (L.) Merr.), and renders it able to serve as a model species for crop adaptation to the stresses above (Hall, 2004). The importance and diverse role played by cowpea in the farming systems and in the diets of poor people makes it potentially ideal for achieving the goal of reducing poverty and hunger, improving human health and nutrition, and enhancing ecosystem resilience (World Bank, 2008).

Despite the numerous benefits of cowpea as food and a component of the farming system, the productivity of the crop, especially among smallholder farmers has remained very low, averaging 0.5 t/ha (FAO, 2012) compared to the potential yield of 3 t/ha reported for some varieties (McKnight Foundation Collaborative Crops Research, 2003; Miesho, 2019). The miserably low productivity of cowpea (approximately 0.47 t/ha) is largely attributable to a number of constraints including diseases such as bacterial blight caused by *Xanthomonas axonopodis* pv. *vignicola* (Burkh.) Dye. Cowpea bacterial blight (CoBB) is one of the major diseases of cowpea, with the capacity to cause up to 92% yield loss worldwide under severe infections (Agbicodo, 2009). This pathogen is widespread in many agro-ecological zones of tropical and sub-tropical countries (Ajeigbe *et al.*, 2008). The pathogen is the seed-borne and causes discoloration of seeds and cotyledons, seed mortality, stem cankers, bushy and stunted growth, leaf and pod blight (Okechukwu & Ekpo, 2004).

In the eastern part of Africa, information on bacterial blight is scanty and the disease is reported to be common in Uganda and Tanzania (Bua *et al.*, 1998). Additionally, there are limitations in the study of the disease due to the lack of access to cowpea varieties that are resistant to CoBB (IAASTD, 2009). Moreover, cowpea producers in Sub-Saharan Africa are mostly small scale, resource-poor farmers who cannot afford the management strategies that have been proposed such as regular spraying or timing of planting (Mbong *et al.*, 2010), and there is a lack of knowledge regarding the response of cowpea genotypes to CoBB.

In Uganda, the occurrence of CoBB was reported in the early 1990s (Edema *et al.*, 1997) and since then no major progress has been made in characterising the strains of the pathogen in Uganda and developing cowpea varieties that are resistant to the pathogen. Field observations have indicated that CoBB is increasingly becoming a major problem for farmers in cowpea growing areas in Uganda (NARO Report, 2014). The prevalence of the disease can ably be associated with changes in weather patterns, for instance, long rainfall durations. Such a condition has been noted to favour CoBB epidemics, resulting in significant yield losses in the semi-arid regions of Uganda, where the crop is commonly grown (Stern, 2007). Moreover, most of the recently released cowpea varieties (SECOW 1T, SECOW 2W, SECOW 3B, SECOW 4W and SECOW 5T) are susceptible to the pathogen (NARO Report, 2014). This is consequently leading to the decline in the production of cowpea in Uganda, a situation that is likely to worsen if CoBB is not managed (Orawu *et al.*, 2013). This study therefore aimed at determining the response of Ugandan cowpea germplasm to CoBB infection and associated yield in Uganda under natural field infestation. This knowledge will be critical to identify sources of host resistance for use in cowpea breeding programs in the region.

MATERIALS AND METHODS

Plant Materials Screened

A total of 64 cowpea genotypes comprising 5 improved varieties, 10 inbred lines and 49 land races obtained from the National Semi Arid Resources Research Institute (NaSARRI) Serere, Uganda were used in the study. The genotypes were categorized into three maturity groups; 26 early maturing, 24 medium maturing and 14 late maturing (Table S1).

Site Description

Two field experiments were conducted at Makerere University Agricultural Research Institute - Kabanyolo (MUARIK), located in the Central part of Uganda – Wakiso district, 17.3 km North of Kampala (0°28'N and 32°37'E; 1200 m above sea level). The first field experiment was conducted during the first rainy season (April to July 2020 (MUARIK 20A)) and the second during the second rainy season (September to December 2020 (MUARIK 20B)). All experiments were conducted in naturally infested fields. The average rainfall and relative humidity recorded during the first experimental period were 162.8 mm and 69 - 87%, respectively. In the second experimental period, average rainfall and relative humidity were 230.4 mm and 73 - 96%, respectively.

Experimental Design

Field trials at each site were laid out in an alpha lattice design of 8 blocks x 8 plots and replicated thrice with a spacing of 1 m between plots and 2 m between replicates. Each genotype was planted in a 4 row 3 m long plot, with 0.6 m inter row spacing and 0.3 m inter plant spacing. Using a calibrated planting rope and dibbling stick, small holes for planting were made, and 2 seeds were sowed and later thinned to 1 plant per hole 3 weeks after planting. Hand hoe weeding was done twice while insect pest management was done also twice using Roket 44 EC (Profenofos 40% + Cypermethrin 4%) one just before flowering and the second during pod setting. No fertilizer or fungicide was applied during the entire growing period.

Data Collection

The plants were rated for disease severity 6 weeks after planting and subsequently at 7 days intervals for 4 weeks (Jackai & Singh, 1988; Shi *et al.*, 2016). Disease severity was scored on 5 selected plants from two middle rows of each plot excluding plants at the beginning and end of rows. Disease severity was evaluated using a disease scale of 1 - 5 (Withanage, 2005), with modification to assess the percentage of leaf surfaces covered by the CoBB symptoms, where 1 = 0% or No symptoms (immune); 2 = 1 to 15% (resistant); 3 = 16 to 30% (moderately resistant), 4 = 31 - 45% (moderately susceptible) and 5 = 46% and above (susceptible). For all plots and assessment dates, the relative Area Under the Disease Progress Curve rAUDPC (Fry, 1978;

Lima-Primo *et al.*, 2019) was calculated using the following formula:

$$rAUDPC = \frac{\sum (T_{i+1} - T_i) * \left(\frac{D_{i+1} + D_i}{2} \right)}{T_{Total} * 100}$$

Where T_i = the ith day when an estimation of percent CoBB was made
D_i = the estimated percentage of area with CoBB at T_i
T_{Total} = the number of days at which the final assessment was recorded

Days to 50% flowering was recorded for all genotypes. At maturity, plants were harvested manually from each plot and data collected for traits such as grain yield, number of seeds per pod, pod length (cm), number of peduncles per plant and number of branches per plant.

Data Analyses

The data were subjected to Restricted Maximum Likelihood (ReML analysis) and generalized analysis of variance (ANOVA) in GENSTAT statistical program (18 edition). During the analysis, genotypes were considered as fixed factors while replication and blocks were random factors as shown in the linear model of Equation below. The predicted genotype mean performance under each trait found significant from the analysis was separated using Fisher's Protected Least Significant Difference (LSD) test at an alpha level of $P \leq 0.05$.

Linear Model: $Y_{ijkl} = \mu + S_i + B / R / S_{ijk} + G_l + G * S_{li} + e_{ijkl}$

Where Y_{ijkl} = observed value from each experimental unit,
μ = general mean, S_i = season effect,
$S_{i=}$ season effect,
G_l = genotype effect,
B/R_{jk} = block means effect nested in the replication,
$G*S_{li}$ = genotype by season interaction effect and
$e_{ijkl.}$ = the experimental error.

To calculate disease reaction scale value (DrSv) from rAUDPC values, we followed a method proposed by Yuen and Forbes (2009) with modification as described below;

$$DrSv = Sy \frac{Dx}{Dy}$$

Where Sy = the assigned disease reaction scale value,
Dy = observed disease reaction measure (rAUDPC) for the standard genotype (genotype with the highest rAUDPC),
DrSv = the calculated disease reaction scale value and
Dx = observed disease measurement for the genotype in question.

The rAUDPC values obtained for genotypes were sorted from the lowest to highest. Then, following a disease reaction scale of 1-5, the disease reaction scale values (DrSv) were calculated by dividing the assigned disease reaction value (*Sy* = 5) by the observed disease reaction measure (*Dy* = highest rAUDPC value) to get a constant. This was then multiplied by the disease reaction measure (*Dx*) of each genotype to get the DrSv of that genotype (Forbes *et al.*, 2014).

The following ranges were used to classify the resulting disease reaction scale values (DrSv) of the genotypes. That is 1 = immune (0%), 1.1-2.0 = resistant (1 to 15%), 2.1-3.0 = moderately resistant (16 to 30%), 3.1-4.0 = moderately susceptible (31 to 45%), and 4.1-5 = susceptible (46% and above).

Correlation analysis of the predicted means was performed in GENSTAT 18th edition between days to 50% flowering, rAUDPC, number of branches per plant, number of peduncles per plant, pod length (cm), number of seeds per pod and yield to determine if there was a significant relationship between the traits studied.

RESULTS

Variations in rAUDPC Among Seasons and Genotypes

The relative Area Under Disease Progress Curve (rAUDPC) was significantly different for seasons 1 and 2 ($P \leq 0.001$). The effects of genotype and genotype by season interactions were not significant ($P \leq 0.05$) for rAUDPC across seasons. However, analysis of variance for individual seasons revealed significant differences ($P \leq 0.001$) for rAUDPC among genotypes (Table 1).

During season 1 (MUARIK 20A), the mean rAUDPC showed that none of the genotypes was resistant (*DrSv = 1.1-2.0*), 54 genotypes were moderately resistant (*DrSv = 2.1-3.0*), 8 were moderately susceptible (*DrSv = 3.1-4.0*) and 2 genotypes were susceptible (*DrSv = 4.1-5.0*). The mean rAUDPC ranged from 0.20 (*DrSv*= 2.3) to 0.44 (*DrSv*= 5.0) with genotypes WC 32A, NE 44,WC 26, NE 37, ACC 12 x SECOW 3B, ACC 26 x ACC 2, SECOW 2W x SECOW IT and SECOW 2W x ACC 2 exhibiting the least mean rAUDPC of 0.20 (*Drive*= 2.3) and were therefore considered moderately resistant. Genotypes WC 36 and NE 21 had the greatest rAUDPC mean values of 0.44 (*DrSv*= 5.0) and 0.37 (*DrSv*= 4.2) respectively and were considered susceptible. The average rAUDPC at MUARIK 20A was 0.24 (*DrSv*= 2.7) which was much lower than that at MUARIIK 20B (0.43, *DrSv*= 3.2) Table 2.

During season 2 (MUARIK 20B), the mean values for rAUDPC showed that out of the 64 genotypes evaluated, only 3 were resistant, 18 moderately resistant, 41 moderately susceptible and only 2 were susceptible to CoBB. Genotypes NE 32, WC 32A and NE 44 had the least mean rAUDPC (0.23 (*DrSv*= 1.7), 0.25 (*DrSv*= 1.9) and 0.27 (*DrSv*= 2.0) respectively) and were therefore considered to be resistant to CoBB. Genotypes NE 40 and WC 31 had the greatest mean rAUDPC values of 0.67 (*DrSv*= 5.0) and 0.64 (*DrSv*= 4.8) respectively and were the most susceptible. The average mean rAUDPC for season 2 for the 64 genotypes evaluated was 0.43 (*DrSv*= 4.2) (Table 2).

Table 1: Mean squares for rAUDPC for seasons MAURIK 20A and MAURIK 20B

COMBINED SEASONS			SOV	DF	MUARIK 20A	MUARIK 20B
SOV	df	MS			MS	MS
Gen	63	0.003	Gen	63	0.005***	0.011***
Seas	1	1.130***	Rep	2	0.006*	0.001
Gen.Seas	63	0.003	Rep.Blk	21	0.002	0.004
Error	282	0.004	Error	87	0.002	0.005
CV (%)		18.1	CV (%)		17.7	16
Sed		0.037	Sed		0.069	0.25
Sem		0.026	Sem		0.025	0.04

*,** and ***=significance at Probability levels 0.05, 0.01, and 0.001 respectively, df=Degree of freedom, MS=Mean squares, Gen=Genotype effect, Seas=Season effect, Gen.Seas=Genotype by Season interaction effect, Rep.Blk=Blocks within replication effect, CV (%)= Percentage coefficient of variation, Sed=Standard Error Difference, Sem=Standard Error of the mean, rAUDPC=Relative Area Under Disease Progress and SOV=Source of variation.

Variations in Agronomic Traits Among Seasons and Genotypes

Across seasons analysis of variance revealed significant differences ($P \leq 0.001$) due to season effect for grain yield, days to 50% flowering, number of seeds per pod, peduncles per plant, and number of branches while pod length was non-significant ($P \leq 0.05$). There were non-significant ($P \leq 0.05$) differences among genotypes for all traits studied except pod length which was significant ($P \geq 0.05$). (Table 3).

During season 1, significant differences were observed between genotypes for 50% flowering ($P \leq 0.001$), pod length ($P \leq 0.001$) and the number of branches ($P \leq 0.01$). However, the number of seeds per pod, peduncles per plant, and grain yield were not significantly different among genotypes (Table 3). During season 2, genotypes were significantly different for grain yield, days to 50% flowering, pod length, peduncles per plant, and the number of branches ($P \leq 0.001$), but not the number of seeds per pod ($P \geq 0.05$).

There was a higher mean performance of genotypes for grain yield during season 1 (mean grain yield = 1.9 t/ha) than in season 2 (mean grain yield = 1.6 t/ha). During season 1 (MUARIK 20 A), 64.1% of the genotypes got high yields ranging from 1.9 to 2.8t/ha and the remaining 35.9% got below average yield (below 1.9 t/ha) while during season 2 (MUARIK 20 A), only 39.1% of the genotypes evaluated in this study got high yields ranging from 1.6 to 2.9 t/ha with the remaining genotypes (60.9%) getting below average grain yields (below 1.6 t/ha). Genotypes SECOW 5T (2.8 t/ha) and NE 5 (2.6 t/ha) were the best grain yielders while WC 29 was the worst performer for grain yield during season 1. Genotypes NE 40 (2.9 t/ha), SECOW 2W x SECOW 1T (2.9 t/ha) and WC 7 (2.8 t/ha) showed the greatest yield while ALEGI x SECOW 3B, SECOW 2W, NE 70, WC 29, WC 46, WC 64, WC 66 got the lowest grain yield (1.1 t/ha) during the second season (Table 4).

The days to 50% flowering of genotypes varied from 54 to 57 days with an average of 52 days and 48 to 68 days with an average of 58 days during seasons 1 and 2 respectively. Genotypes ACC 12 x SECOW 3B, SECOW 5T x SECOW 3B, and NE 70 took the longest time (57 days) and WC 65 took the shortest time (45 days) to 50% flowering during season 1 while SECOW 1T, WC 32A, and NE 70 took the longest (68 days) and NE 32 took the shortest time (48 days) to 50% flowering during season 2 (Table 4).

The mean performance of genotypes for the number of seeds per pod was higher during season 1 (ranging from 12 to 19 seeds with an average of 16 seeds) than in season 2 (ranging from 9 to 17 seeds with an average of 13 seeds), pod length was similar with an average of 15.8cm during the two seasons, number of peduncles per plant was greater during season 1(ranging from 16 to 44 peduncles with an average of 26 peduncles) than season 2 (ranging from 5 to 49 peduncles with an average of 20 peduncles) and the number of branches per plant was lower during season 1 (range of 3 to 7 branches with an average of 5 branches) than season 2 (range of 4 to 15 branches with an average of 7 branches) (Table 4).

Relationship Between Resistance (rAUDPC) and Agronomic Traits

The relative Area Under Disease Progress Curve (rAUDPC) did not show any significant correlation with days to 50% flowering (r =-0.11), number of branches per plant (r=0.11), number of peduncles per plant (r=-0.03), pod length (r=0.10), number of seeds per pod (r=0.60), and grain yield (r =0.10). A significant ($P \leq 0.05$) positive correlation (r = 0.26) between grain yield and the number of branches per plant was observed. In addition, there was a highly significant ($P \leq 0.001$) positive correlation (r = 0.6) between the number of seeds per pod and pod length (Table 5).

DISCUSSION

This study evaluated 64 cowpea genotypes in two seasons for their reaction to cowpea bacterial blight and agronomic traits (grain yield, days to 50% flowering, number of seeds per pod, pod length, peduncles per plant and number of branches per plant) at Makerere University Agricultural Research Institute - Kabanyolo (MUARIK) in central Uganda.

In the current study, differences among genotypes for rAUDPC and agronomic trait, were not significant across seasons. Whereas significant differences were observed among genotypes for the variables assessed in both seasons. There were variations in genotypes performance for rAUDPC, grain yield, days to 50% flowering, number of seeds per pod, pod length, peduncles per plant and number of branches grain indicating the presence of wide genetic variability among the genotypes. Genetic variation is a prerequisite for establishing any crop improvement programme (Nwosu *et al.*, 2013). The existence of differences among genotypes presents the opportunity for the selection of genotypes with better attributes for yield and CoBB resistance. We, therefore, envisage that breeding for varieties with resistance to bacterial blight disease and high yield using

Table 2: Mean performance for rAUDPC of genotypes at MUARIK 20B and MUARIK 20A

Season 1 (MUARIK 20A)				Season 2 (MUARIK 20B)			
Genotype	rAUDPC	DrSv	HoR	Genotype	rAUDPC	DrSv	HoR
NE 32	0.21	2.4	MR	NE 32	0.23	1.7	R
WC 32A	0.21	2.4	MR	WC 32A	0.25	1.9	R
NE 44	0.25	2.8	MR	NE 44	0.27	2.0	R
WC 26	0.21	2.4	MR	WC 26	0.29	2.2	MR
WC 18	0.24	2.7	MR	WC 18	0.37	2.8	MR
NE 6	0.21	2.4	MR	NE 6	0.38	2.8	MR
WC 44	0.24	2.7	MR	WC 44	0.38	2.8	MR
NE 36	0.26	3.0	MR	NE 36	0.39	2.9	MR
ACC 12 x SECOW 3B	0.20	2.3	MR	ACC 12 x SECOW 3B	0.40	3.0	MR
ALEGI x ACC 2	0.21	2.4	MR	ALEGI x ACC 2	0.40	3.0	MR
NE 23	0.21	2.4	MR	NE 23	0.40	3.0	MR
WC 48	0.21	2.4	MR	WC 48	0.40	3.0	MR
WC 35B	0.22	2.5	MR	WC 35B	0.40	3.0	MR
WC 62	0.23	2.6	MR	WC 62	0.40	3.0	MR
NE 50	0.24	2.7	MR	NE 50	0.40	3.0	MR
WC 35A	0.24	2.7	MR	WC 35A	0.40	3.0	MR
SECOW 2W	0.25	2.8	MR	SECOW 2W	0.40	3.0	MR
ACC 2 x ACC 12	0.26	3.0	MR	ACC 2 x ACC 12	0.40	3.0	MR
WC 52	0.26	3.0	MR	WC 52	0.40	3.0	MR
NE 41	0.28	3.2	MS	NE 41	0.40	3.0	MR
WC 36	0.44	5.0	S	WC 36	0.40	3.0	MR
ACC 26 x ACC 2	0.20	2.3	MR	ACC 26 x ACC 2	0.41	3.1	MS
SECOW 5T x SECOW 3B	0.21	2.4	MR	SECOW 5T x SECOW 3B	0.41	3.1	MS
NE 4	0.22	2.5	MR	NE 4	0.41	3.1	MS
SECOW 1T	0.23	2.6	MR	SECOW 1T	0.41	3.1	MS
SECOW 4W	0.24	2.7	MR	SECOW 4W	0.41	3.1	MS
NE 46	0.27	3.1	MS	NE 46	0.41	3.1	MS
SECOW 5T	0.29	3.3	MS	SECOW 5T	0.41	3.1	MS
NE 21	0.37	4.2	S	NE 21	0.41	3.1	MS
WC 68	0.23	2.6	MR	WC 68	0.42	3.1	MS
WC 8	0.24	2.7	MR	WC 8	0.42	3.1	MS
NE 49	0.25	2.8	MR	NE 49	0.42	3.1	MS
NE 55	0.26	3.0	MR	NE 55	0.42	3.1	MS
ALEGI x SECOW 3B	0.29	3.3	MS	ALEGI x SECOW 3B	0.42	3.1	MS
WC 29	0.30	3.4	MS	WC 29	0.42	3.1	MS
WC 66	0.20	2.3	MR	WC 66	0.43	3.2	MS
NE 30	0.22	2.5	MR	NE 30	0.43	3.2	MS
NE 5	0.22	2.5	MR	NE 5	0.43	3.2	MS
WC 46	0.23	2.6	MR	WC 46	0.43	3.2	MS
WC 48A	0.23	2.6	MR	WC 48A	0.43	3.2	MS
WC 67B	0.20	2.3	MR	WC 67B	0.44	3.3	MS
NE 53	0.21	2.4	MR	NE 53	0.44	3.3	MS
ALEGI	0.22	2.5	MR	ALEGI	0.44	3.3	MS
WC 21	0.22	2.5	MR	WC 21	0.44	3.3	MS
WC 42	0.31	3.5	MS	WC 42	0.44	3.3	MS
WC 41	0.20	2.3	MR	WC 41	0.45	3.4	MS
WC 32	0.21	2.4	MR	WC 32	0.45	3.4	MS
NE 18	0.22	2.5	MR	NE 18	0.45	3.4	MS
NE 70	0.21	2.4	MR	NE 70	0.46	3.4	MS
SECOW 1T x ACC 23	0.25	2.8	MR	SECOW 1T x ACC 23	0.46	3.4	MS
WC 33	0.22	2.5	MR	WC 33	0.47	3.5	MS
SECOW 2W x ACC 2	0.20	2.3	MR	SECOW 2W x ACC 2	0.48	3.6	MS
SECOW 2W x SECOW 1T	0.20	2.3	MR	SECOW 2W x SECOW1T	0.48	3.6	MS
WC 63	0.25	2.8	MR	WC 63	0.48	3.6	MS
WC 17	0.25	2.8	MR	WC 17	0.49	3.7	MS
NE 37	0.28	3.2	MS	NE 37	0.49	3.7	MS
WC 67	0.21	2.4	MR	WC 67	0.50	3.7	MS
WC 53	0.24	2.7	MR	WC 53	0.50	3.7	MS
WC 7	0.24	2.7	MR	WC 7	0.50	3.7	MS
WC 64	0.20	2.3	MR	WC 64	0.51	3.8	MS
SECOW 3B	0.22	2.5	MR	SECOW 3B	0.52	3.9	MS
ACC 26 x SECOW 1T	0.31	3.5	MS	ACC 26 x SECOW 1T	0.52	3.9	MS
NE 31	0.24	2.7	MR	WC 31	0.64	4.8	S
NE 40	0.26	3.0	MR	NE 40	0.67	5.0	S
MEAN	0.24			MEAN	0.43		
Max	0.44			Max	0.67		
Min	0.2			Min	0.23		
$LSD_{0.05}$	0.07			$LSD_{0.05}$	0.25		

DrSv=Susceptibility Scale Value, HoR=Host Response, MR=Moderately Resistant, MS=Moderately Susceptible, rAUDPC=Relative Area Under Disease Progress Curve, $Lsd_{0.05}$=Least significant difference at probability level of 0.05, N=total number of genotypes evaluated, Max=Maximum Value and Min=Minimum Value.

Table 3: Analysis of variance for grain yield, days to 50% flowering, number of seeds per pod, pod length, peduncles per plant and number of branches for cowpea genotypes screened for two seasons at MUARIK

Season	SOV	df	GY	DTF	No. SpP	PdL	Ped/Pt	No. Br
Across Seasons	Gen	63	2.39	15.9	2.2	3.75*	68.8	2.3
	Seas	1	25.70***	1241.7***	185.0***	0.01	906.8***	120.60***
	Gen.Seas	63	2.27	10.9**	1.9	2.98	70.6	2.4
	Error	282	1.81	6.9	5.2	2.52	78.1	2.2
	CV (%)		56.2	4.8	15.6	10.04	38.3	26.4
	Sed		0.78	1.5	1.3	0.92	5.1	0.86
	Sem		0.55	1.1	0.9	0.65	3.6	0.61
Season 1 (MUARIK 20A)	Gen	63	0.31	25.7***	5.1	11.83***	109.2	2.46**
	Rep	2	2.97***	3.7	18.5*	7.09	887.8***	23.08***
	Rep.Blk	21	0.38	5.8	7.9	4.04	127.6	1.09
	Error	87	0.3	6.3	4.9	2.4	108.1	1.43
	CV (%)		28.2	4.8	14	9.8	40.4	25.8
	Sed		0.9	4.1	3.6	2.54	17	1.94
	Sem		0.32	1.4	1.3	0.89	6	0.69
Season 2 (MUARIK 20B)	Gen	63	12.57***	57.7***	7.3	8.10***	302.5***	11.33***
	Rep	2	5.06	14.1	12.4	4.93	12.1	1.68
	Rep.Blk	21	3.35	4.6	3.4	2.23	45.4	1.62
	Error	87	3.39	7.5	5.4	2.61	44.4	3.04
	CV (%)		64.8	4.7	17.3	10.22	32.7	26.5
	Sed		3.01	4.4	3.8	2.64	10.9	2.83
	Sem		1.06	1.6	1.3	0.93	3.9	1.01

SOV=Source of variation, Seas=Season effect, Rep.Blk=Blocks within replication effect, Gen=Genotype effect, Gen.Seas=Genotype by Season interaction effect, CV (%)= Percentage coefficient of variation, Sed=Standard Error Difference, Sem=Standard Error of the mean, df=Degree of freedom, GY=Grain yield, DTF=Days to 50% flowering, , No.SpP=Number of Seeds per Pod, PdL=Pod Length, Ped/Pt=Peduncles per Plant, No.Br=Number of Branches and *, ** and ***=significance at Probability levels 0.05, 0.01, and 0.001 respectively.

Table 4: Mean grain yield, days to 50% flowering, number of seeds per pod, pod length, peduncles per plant and number of branches for genotypes evaluated at MAURIK

Genotypes	Season 1 (MUARIK 20A)						Season 2 (MUARIK 20B)					
	GY	DTF	No.SpP	PdL	Ped/Pt	No.Br	GY	DTF	No.SpP	PdL	Ped/Pt	No.Br
ACC 12 x SECOW 3B	2.5	57	13	12.5	23	5	2.0	66	10	13.5	6	6
ACC 2 x ACC 12	1.5	50	14	14.6	16	4	1.2	62	11	12.6	9	5
ACC 26 x ACC 2	1.7	55	16	20.2	21	3	1.2	59	13	19.3	12	6
ACC 26 x SECOW 1T	1.6	52	17	16.3	25	5	1.8	63	9	14.0	6	8
ALEGI	1.9	52	13	13.2	44	5	1.2	65	13	15.3	18	5
ALEGI x ACC 2	1.9	56	17	17.7	24	6	1.8	66	16	19.5	7	7
ALEGI x SECOW 3B	2.1	55	16	15.8	24	7	1.1	57	13	16.3	14	7
NE 18	2.0	52	15	14.2	24	4	1.5	58	14	15.0	18	7
NE 21	2.4	53	15	15.3	23	6	1.4	57	13	15.3	23	9
NE 23	1.9	49	15	13.7	24	4	2.3	57	16	16.8	49	7
NE 30	1.4	55	16	18.6	28	5	1.4	53	14	15.8	20	11
NE 31	1.5	49	15	15.3	18	4	1.4	56	14	15.3	21	4
NE 32	2.0	51	16	15.8	33	4	1.7	48	14	15.3	23	5
NE 36	1.8	53	16	15.4	39	6	1.7	58	14	14.4	11	4
NE 37	2.2	50	16	16.5	19	3	1.5	54	14	18.2	21	6
NE 4	1.8	51	16	14.7	29	5	1.6	58	9	14.0	36	6
NE 40	2.0	51	17	17.9	21	6	2.9	55	14	13.8	20	8
NE 41	1.3	55	16	14.3	20	6	1.8	56	15	17.2	12	5
NE 44	2.3	53	16	17.7	21	4	1.7	62	11	16.1	18	5
NE 46	2.4	47	14	14.4	27	5	2.1	56	14	16.9	12	8
NE 49	1.8	47	16	13.4	20	5	1.2	62	14	17.0	11	5
NE 5	2.6	52	16	13.6	32	4	1.2	58	11	13.6	17	7
NE 50	2.1	51	16	14.6	19	5	1.5	61	11	14.6	20	5
NE 53	1.7	50	17	17.2	17	4	1.5	55	15	16.2	26	6
NE 55	1.8	46	15	14.0	28	4	1.3	57	15	15.1	19	7
NE 6	1.8	51	15	12.7	33	5	1.4	55	13	17.2	19	6

(Contd...)

Table 4: *(Continued)*

Genotypes	Season 1 (MUARIK 20A)						Season 2 (MUARIK 20B)					
	GY	DTF	No.SpP	PdL	Ped/Pt	No.Br	GY	DTF	No.SpP	PdL	Ped/Pt	No.Br
NE 70	1.9	57	15	16.9	26	3	1.1	68	12	14.3	9.0	5
SECOW 1T	2.0	55	15	15.6	20	5	1.8	68	13	15.3	31	7
SECOW 1T x ACC 23	1.3	53	19	19.1	23	5	1.7	58	14	18.5	10	6
SECOW 2W	2.2	53	15	13.2	29	5	1.1	57	14	15.6	5	6
SECOW 2W x ACC 2	2.1	56	17	21.1	26	4	1.9	66	13	14.8	26	7
SECOW 2W x SECOW 1T	1.9	55	15	14.8	26	3	2.9	53	11	16.3	6	11
SECOW 3B	1.9	55	15	15.3	21	5	1.4	58	14	16.7	15	6
SECOW 4W	2.3	51	17	15.6	22	3	1.8	55	14	16.9	39	5
SECOW 5T	2.8	53	16	16.9	23	6	1.3	55	15	18.1	17	5
SECOW 5T x SECOW 3B	2.2	57	15	14.5	18	4	1.2	56	13	15.6	16	9
WC 17	1.8	50	16	15.9	20	4	1.3	54	13	15.9	27	5
WC 18	2.0	53	18	17.6	26	6	1.9	60	14	15.2	22	5
WC 21	2.0	53	17	14.9	21	4	1.3	54	14	16.2	14	8
WC 26	2.1	53	16	17.5	20	4	1.9	55	12	15.0	16	6
WC 29	1.0	54	15	15.5	26	5	1.1	59	13	16.4	18	4
WC 32	1.7	53	16	14.8	27	3	1.2	58	13	15.8	18	8
WC 32A	1.7	52	15	15.4	29	6	1.3	68	14	12.9	17	6
WC 33	1.9	53	16	19.5	36	6	1.7	55	12	11.1	27	4
WC 35A	2.1	50	17	19.1	19	5	1.2	61	11	16.6	22	6
WC 35B	2.0	53	17	18.4	35	6	1.4	55	15	17.4	18	5
WC 36	1.6	52	15	14.8	26	5	1.8	60	15	18.3	26	5
WC 41	1.9	48	17	14.9	32	3	1.2	50	12	15.6	16	5
WC 42	2.5	51	19	18.8	25	5	1.5	63	15	19.1	33	7
WC 44	1.7	53	15	13.9	17	4	2.2	60	14	16.9	35	10
WC 46	2.0	54	18	15.9	36	5	1.1	61	14	15.1	24	10
WC 48	1.9	51	16	16.9	25	4	2.1	55	17	17.4	11	7
WC 48A	2.0	47	14	15.0	29	4	1.4	55	14	18.6	21	8
WC 52	2.2	48	12	12.8	40	5	1.2	61	14	15.6	10	7
WC 53	1.8	50	15	15.4	23	6	1.3	59	15	17.0	21	10
WC 62	2.2	48	15	14.7	34	5	2.0	52	13	13.3	23	4
WC 63	2.1	45	18	17.0	20	4	1.5	58	12	15.5	25	5
WC 64	1.8	55	18	20.2	24	5	1.1	53	12	14.5	24	6
WC 66	1.7	49	15	14.1	26	4	1.1	54	15	15.4	13	6
WC 67	1.6	56	15	15.8	24	5	1.6	52	14	13.8	47	6
WC 67B	2.3	53	18	15.6	33	4	1.2	58	13	14.9	19	7
WC 68	2.3	47	16	14.5	29	5	2.0	59	16	17.9	46	8
WC 7	2.0	47	15	14.6	30	3	2.8	59	14	16.3	45	15
WC 8	2.2	52	16	15.1	30	4	1.8	59	13	14.3	31	5
MEAN	1.9	52	16	15.8	26	5	1.6	58	13	15.8	20	7
Max	2.8	57	19	21.1	44	7	2.9	68	17	19.5	49	15
Min	1.0	45	12	12.5	16	3	1.1	48	9	11.1	5	4
$LSD_{0.05}$	0.9	4	3	2.6	17	2	3.0	4	4	2.6	11	3

GY=Grain yield, DTF=Days to 50% flowering, No.SpP=Number of Seeds per Pod, PdL=Pod Length, Ped/Pt=Peduncles per Plant, No.Br=Number of Branches, $Lsd_{0.05}$=Least significant difference at probability level of 0.05, N=total number of genotypes evaluated, Max=Maximum Value and Min=Minimum Value.

Table 5: Correlations between rAUDPC, days to 50% flowering, number of branches, number of seeds per pod, pod length, peduncles per plant and grain yield of genotypes evaluated at MUARIK under natural infestation

Traits	DTF	No.Br	Ped/Pt	PdL	rAUDPC	No.SpP	GY
DTF							
No.Br	0.07						
Ped/Pt	-0.23	0.27					
PdL	0.05	0.08	-0.11				
rAUDPC	-0.11	0.11	-0.03	0.10			
No.SpP	-0.17	0.07	0.18	**0.60*** **	0.06		
GY	-0.05	**0.26***	0.20	0.02	0.10	0.08	

DTF=Days to 50% flowering, No.Br=Number of Branches, Ped/Pt=Peduncles per Plant, PdL=Pod Length, rAUDPC=Relative Area Under Disease Progress Curve, No.SpP=Number of Seeds per Pod, GY=Grain yield, and *, and ***=significance at Probability levels 0.05, and 0.001

the genetic materials evaluated in our study is possible. Earlier reports showed that cowpea genotypes varied in their resistance to cowpea bacterial blight disease and grain yield with its components (Manggoel *et al*., 2012). Cowpea bacterial blight disease is one of the major hindrances to cowpea production (Withanage, 2005) and the diversity attained will contribute to the pool of potential sources of parents that breeding programs can use in improving resistance to the disease.

The non-significant genotype-by-seasons interactions for rAUDPC and grain yield and some of its components implied that genotypes performed consistently across the two seasons. However, genotype-by-season interactions were significant for days to 50% flowering indicating an inconsistency in performance for this trait across the two seasons suggesting the need for multi-environment testing of genotypes to select

those with adaptation to specific areas as well as those with wider adaptations (Ajeigbe *et al.*, 2008). The differences in 50% flowering across the two seasons could be attributed to comparatively different disease pressures and rainfall amounts during season 1 and season 2.

The differences in CoBB response among the genotypes as revealed by rAUDPC values within seasons indicated that the majority of the genotypes were either moderately resistant or moderately susceptible. It was also noted that average performance for rAUDPC was higher for season 2 compared to season 1 indicating that most genotypes were susceptible or moderately susceptible to CoBB in season 2 compared to season 1. This could be attributed to the high disease pressure in season 2 since it was characterised by low temperatures, high relative humidity and rainfall at the podding stage than in season 1. Similarly, Bua *et al.* (1998) and Nema and Babber (2000) observed higher blight disease during heavy rains. This suggests that CoBB is more virulent under high moisture conditions as was recorded in season 2, and this season (September to December) could therefore be considered suitable for screening against CoBB.

Based on the results of this study, the genotypes evaluated therefore fell into four categories; resistant, moderately resistant, moderately susceptible and susceptible. Nearly similar results were reported by Withanage (2005) and Okechukwu *et al.* (2000) where cowpea genotypes were grouped into five categories with no genotype immune to the CoBB.

Correspondingly, the mean performances for days to 50% flowering, grain yield and related parameters followed the disease trend whereby; high rAUDP for CoBB during season 2 corresponded with low grain yield, number of seeds per pod, and number of peduncles per plant and high days to 50% flowering and number of branches (Table 3.4). Conversely, low rAUDPC for CoBB during season 1 corresponded with high grain yield, number of seeds per pod and number of peduncles per plant and low days to 50% flowering and number of branches. Irrespective of the disease trend in each of the two seasons at MUARIK, the pod length of genotypes recorded the same average of 15.8 cm (Table 4) indicating that pod length was not significantly influenced by CoBB.

It was observed from mean performances that, the resistant and moderately resistant genotypes during season 2 had averagely high grain yield and such genotypes included; WC 32 (1.7 t/ha), WC 4 (1.7 t/ha), WC 26 (1.9 t/ha) and WC 18 (1.9 t/ha). However, genotype WC 32A showed resistance at MUARIK 20B but moderate resistance at MUARIK 20A though its grain yield performance in both seasons was below the average. Genotype NE 40 was susceptible in both seasons but it still managed to yield high with 1.9 t/ha at MUARIK 20B and 2.0 t/ha at MUARIK 20A (Table 4).

The average grain yields of 1.9 and 1.6 t/ha for seasons 1 and 2 respectively indicated that the selected cowpeas comprised of high yielding genotypes. The high yield rankings registered in this study are in accordance with the cowpea yield rankings whereby yields of 1.6t/ha and above were considered high yielding (Bisikwa *et al.*, 2014). Among the genotypes in this study, there existed resistant or moderately resistant genotypes which exhibited high grain yield, pod length, early flowering, the high number of seeds per pod and the number of peduncles per plant. Withanage (2005) stated that the major yield components in cowpea are the number of peduncles per plant, the number of seeds per pod and pod length and that any change in yield is brought about by a change in one or more of the above components.

The average mean values recorded for the number of days to 50% flowering of 52 and 58 days during seasons 1 and 2 suggested that the genotypes were predominantly early to medium maturing. Low mean values for the number of days to 50% flowering are advantageous for the identification of early maturing varieties (Ddamulira *et al.*, 2017).

The highly significant positive correlation between pod length and the number of seeds per pod indicates that simultaneous selection for these two traits is achievable. However, the low positive significant correlation between the number of branches and grain yield suggests that the number of branches is not a more reliable predictor of yield. A highly significant and positive correlation between seeds per pod and pod length shows that with longer pods more space is provided for seeds which results in an increase in yield (Romanus *et al.*, 2008).

Among the biotic stresses, diseases such as CoBB have a negative effect on the cowpea yield (Atkinson & Urwin, 2012). Mundt (2014) noted that developing resistance against prevailing diseases of any crop through any of the breeding programmes would be much more effective and stable compared to other disease control methods. Therefore, screening diverse genotypes for diseases is effective to identify resistant varieties that can be utilized in further improvement of the prevailing susceptible varieties (Piquerez *et al.*, 2014). In the current study, 64 cowpea genotypes were screened against one of the major diseases, bacterial blight under prevailing environmental conditions. The overall judgment of the results in this study is that genetic variability for CoBB resistance exists. Genotypes were grouped according to their CoBB response and yielding ability. Finally, rAUDPC was found to be a useful index for screening for CoBB resistance because it enabled identification of CoBB resistant and high yielding genotypes.

CONCLUSIONS AND RECOMMENDATIONS

Of the 64 cowpea genotypes screened for resistance under field conditions, NE 32, WC 32A, NE 44 and WC 26 were the most consistent high yielding genotypes with moderate resistance to CoBB during season 1 and NE 32, WC 67B, and NE 44 exhibited high yield and resistance during season 2. Genotypes NE 40 and NE 31 were most susceptible to CoBB according to this study. This study, therefore, recommends genotypes NE 32, WC 32A, WC 26 and NE 44 as potential sources of CoBB resistance that should be exploited in cowpea breeding programmes to develop high-yielding resistant cultivars. These genotypes can further be included in multi environment field trials.

It is recommended to carry out further studies on the combining abilities of CoBB from this set of germplasm in Uganda. Also, it is recommended to carry out a pathogenicity study of the existing *Xanthomonas axonopodis* pv. *vignicola* (Burkh.) Dye strains in Uganda. Additional studies of these genotypes should focus on Genome Wise association mapping for CoBB.

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SUPPLEMENTARY TABLE

Table S1: Description of a Uganda collection of 100 cowpea genotypes screened for yield and resistance to CoBB

No.	Accession Name	Character state	Type
1	SECOW 1T x ACC 23	Early Maturity	Inbred lines
2	SECOW 2W x SECOW 1T	Early Maturity	Inbred lines
3	SECOW 2W x ACC 2	Early Maturity	Inbred lines
4	SECOW 4W x SECOW 5T	Early Maturity	Inbred lines
5	SECOW 5T x SECOW 3B	Early Maturity	Inbred lines
6	ACC 12 x SECOW 3B	Early Maturity	Inbred lines
7	ACC 2 x ACC 12	Early Maturity	Inbred lines
8	ACC 26 x SECOW 1T	Early Maturity	Inbred lines
9	ACC 26 x ACC 2	Early Maturity	Inbred lines
10	ALEGI x SECOW 3B	Early Maturity	Inbred lines
11	NE 31	Early Maturity	Landrace
12	NE 4	Early Maturity	Landrace
13	NE 49	Early Maturity	Landrace
14	NE 50	Early Maturity	Landrace
15	NE 53	Early Maturity	Landrace
16	NE 55	Early Maturity	Landrace
17	WC 48A	Early Maturity	Landrace
18	WC 62	Early Maturity	Landrace
19	WC 63	Early Maturity	Landrace
20	WC 68	Early Maturity	Landrace
21	NE 21	Late Maturity	Landrace
22	NE 36	Late Maturity	Landrace
23	NE 37	Late Maturity	Landrace
24	NE 40	Late Maturity	Landrace
25	NE 41	Late Maturity	Landrace
26	NE 46	Late Maturity	Landrace
27	NE 6	Late Maturity	Landrace
28	WC 29	Late Maturity	Landrace
29	WC 32	Late Maturity	Landrace
30	WC 32A	Late Maturity	Landrace
31	WC 33	Late Maturity	Landrace
32	WC 41	Late Maturity	Landrace
33	WC 46	Late Maturity	Landrace
34	WC 52	Late Maturity	Landrace
35	NE 18	Medium Maturity	Landrace
36	NE 23	Medium Maturity	Landrace
37	NE 30	Medium Maturity	Landrace
38	NE 32	Medium Maturity	Landrace
39	NE 44	Medium Maturity	Landrace
40	NE 5	Medium Maturity	Landrace
41	NE 70	Medium Maturity	Landrace
42	WC 17	Medium Maturity	Landrace
43	WC 18	Medium Maturity	Landrace

(Contd...)

Table S1: *(Continued)*

No.	Accession Name	Character state	Type
44	WC 21	Medium Maturity	Landrace
45	WC 26	Medium Maturity	Landrace
46	WC 35A	Medium Maturity	Landrace
47	WC 35B	Medium Maturity	Landrace
48	WC 36	Medium Maturity	Landrace
49	WC 42	Medium Maturity	Landrace
50	WC 44	Medium Maturity	Landrace
51	WC 48	Medium Maturity	Landrace
52	WC 53	Medium Maturity	Landrace
53	WC 64	Medium Maturity	Landrace
54	WC 66	Medium Maturity	Landrace
55	WC 67	Medium Maturity	Landrace
56	WC 67B	Medium Maturity	Landrace
57	WC 7	Medium Maturity	Landrace
58	WC 8	Medium Maturity	Landrace
59	ALEGI	Early Maturity	Landrace
60	SECOW 1T	Early Maturity	Improved varieties
61	SECOW 2W	Early Maturity	Improved varieties
62	SECOW 3B	Early Maturity	Improved varieties
63	SECOW 4W	Early Maturity	Improved varieties
64	SECOW 5T	Early Maturity	Improved varieties

ACC=Accession; NE=Northern and Eastern; WC=Western and Central; Inbred lines at F_7 generation.