Journal of Agricultural Science; Vol. 6, No. 10; 2014
ISSN 1916-9752 E-ISSN 1916-9760
Published by Canadian Center of Science and Education

Evaluation of Cowpea Genotypes for Virus Resistance Under Natural Conditions in Uganda

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Received: June 3, 2014 Accepted: August 12, 2014 Online Published: September 15, 2014

doi:10.5539/jas.v6n10p176 URL: http://dx.doi.org/10.5539/jas.v6n10p176

Abstract

Cowpea (*Vigna unguiculata* L. Walp) is an important grain legume in most parts of Sub Saharan Africa. However, viral diseases are a major limiting production factor causing significant yield losses. An experiment was conducted to evaluate the reaction of 105 different cowpea genotypes to viral infection in different agro-ecological zones of Uganda. The aim was to identify genotypes that could serve as sources of resistance to virus infection. Virus infection in these experiments occurred naturally through insect vectors. Results showed that there were significant differences in disease reaction among genotypes within and among agro-ecological zones in terms of Area Under Disease Progress Curve (AUDPC) and incidence. Interactions of genotype by season (GXS), genotype by location (GXL) and genotype by location by season (GXLXS) also significantly affected reaction to viral infection among genotypes. Introduced cowpea genotypes exhibited a more susceptible viral disease reaction compared to the landraces over the two seasons in the three locations. A number of landraces such as WC32, WC18, NE43, NE15, WC35B consistently showed resistance to virus infection in the three locations and therefore could be good sources of resistance. Low disease pressure (AUDPC) was also recorded on SECOW2W (released variety) as reported by previous studies. The landraces also gave consistently higher grain yield values compared to the introduced genotypes. Overall, data from this study showed that locally adapted cowpea genotypes offer resistance to virus infection and may be desirable germplasm for Ugandan cowpea breeding programs.

Keywords: agroecological zone, AUDPC, cowpea, genotypes, incidence, natural, resistance, virus

1. Introduction

Cowpea (*Vigna unguiculata* L. Walp) is a grain legume crop with high protein, minerals and vitamins and is utilized as a fresh vegetable (pods and leaves), and as fodder. Cowpea is an early maturing crop and therefore helps reduce the "hunger period" that often occurs prior to harvest in farming communities (Singh et al., 2002; Timko et al., 2007a). It is an important source of income especially to the rural households after selling the grain and the fresh leaves (Isubikalu et al., 1999; Singh et al., 2002; Timko et al., 2007a). Cowpea curbs erosion through its rapid ground coverage and fixes atmospheric nitrogen thus improving soil fertility (Singh et al., 2002; Tarawali et al., 2002; Casky et al., 2002). In Uganda, cowpea is an important food security crop especially in the eastern and northern regions where up to 90% of the crop is grown (Adipala et al., 1999).

Wherever cowpea is grown, viral diseases are a major constraint to production and yield (Bashir & Hampton, 1996). More than 20 viruses affect cowpea production worldwide (Thottappilly & Rossel, 1985). Yield losses of almost 90% or even total crop failure have been reported (Kaiser & Mossahebi, 1975; Raheja & Leleji, 1974). In Uganda, the main viruses infecting cowpea are; *Cowpea aphid borne mosaic* (CABMV), *Cucumber mosaic virus* (CMV), *Cowpea mild mottle virus* (CPMMV) and *Cowpea severe mosaic virus* (CPSMV) (Amayo et al., 2012; Orawu et al., 2005; Edema et al., 1997). The seed-borne nature of these viruses renders them very destructive to emerging seedlings and insect vectors can spread these further (Ndiaye et al., 1993; Bashir et al., 2002). These viruses are transmitted by several insect species in a non persistent manner and therefore use of insecticides is not an effective method of control (Umaharan et al., 1997). Genetic resistance, therefore, is the best alternative in reducing crop losses due to these diseases.

To identify host resistance, it is important to evaluate different genotypes under field conditions in different environments (Goenaga et al., 2011; Maphosa et al., 2013; Oloka et al., 2008). This study was therefore undertaken to study the reaction of 105 cowpea genotypes to natural virus infection to identify sources of resistance for breeding.

2. Materials and Methods

2.1 Experimental Sites and Their Characteristics

The study was conducted in 2012 during two seasons, herein referred as 2012A and 2012B, at three locations in Uganda that are known to grow cowpeas extensively (Table 1). These locations have differing edaphic characteristics, land use types and cropping systems, and climatic conditions that influence crop growth, vector populations and virus disease development.

Table 1. Altitude and climatic data at three experimental sites in Uganda

Site	*AEZ	Altitude (m.a.s.l)	[4]Average Minimum Annual Temperature (°C)	[4]Average Maximum Annual Temperature (°C)	[4]Annual Mean Rainfall (mm)
Serere	NMF1	1,110	17.7	30.1	1,357
Budaka	SELKB2	1,142	16.8	29.3	1,198
Tororo	LVIC 3	1,204	16.0	28.7	1,484

*Agroecological zone, [1]Northern Moist Farmlands, [2]Southern and Eastern Lake Kyoga Basin, [3]Lake Victoria Crescent and Mbale Farmlands.

Source: [4]Meteorological stations at the experimental sites in 2012 and *AEZ delineation according to Wortmann and Eledu (1999).

2.2 Genotypes and Experimental Design

A total of 105 cowpea genotypes that included landraces (82), commercially released varieties (1) and introductions (22). The introductions were provided by the International Institute of Tropical Agriculture (IITA) (Table 2). The landraces were collected from the northern and eastern regions (NE), western and central regions (WC) of Uganda.

At all sites, the fields were ploughed twice before harrowing to prepare a fine seedbed before planting. Each genotype was planted in two rows measuring 4 m long with spacing of 60 cm between rows and 30 cm between plants within rows. The experimental design was α-design (incomplete block design) as described by Patterson and Williams (1976a) generated using the ALPHA program (http://www.designcomputing.net/gendex) with three replicates. In each season, experimental plots were kept free of weed by hoeing. Fertilizers and /or supplementary water through irrigation were not applied during the trials. Post flowering pests such as flower thrips (*Megalurothrips sjostedti* Trybom), pod borer (*Maruca vitrata* Fabricius) and pod sucking bugs were controlled by 3-4 sprays using Roket 44 EC (Profenofos 40% and Cypermethrin 4%) starting from the budding stage.

Table 2. Description of cowpea genotypes used in the study

Genotype	Source	Type
WC4	WC	Landrace
WC41	WC	Landrace
WC42	WC	Landrace
WC44	WC	Landrace
WC48	WC	Landrace
WC5	WC	Landrace
WC51	WC	Landrace
WC52	WC	Landrace
WC53	WC	Landrace
WC55	WC	Landrace
WC6	WC	Landrace
WC62	WC	Landrace
WC63	WC	Landrace
WC64	WC	Landrace
WC65	WC	Landrace
WC66	WC	Landrace
WC67	WC	Landrace
WC67A	WC	Landrace
WC68	WC	Landrace
WC69	WC	Landrace
WC7	WC	Landrace
MU20	MAK	Landrace
NE53	NE	Landrace
WC39	WC	Landrace

NE = Northern and Eastern, Uganda; WC = Western and Central, Uganda; MAK = Makerere University, Uganda; IITA = International Institute of Tropical Agriculture, Nigeria.

Table 2 continued. Description of cowpea genotypes used in the study

Genotype	Source	Type	Genotype	Source	Type	Genotype	Source	Type
EBELAT	NE	Landrace	MU20B	MAK	Landrace	NE55	NE	Landrace
IT00K-835-45	IITA	Introduction	MU9	MAK	Landrace	NE6	NE	Landrace
IT03K-124	IITA	Introduction	NE13	NE	Landrace	NE67	NE	Landrace
IT04K-219-2	IITA	Introduction	NE15	NE	Landrace	NE70	NE	Landrace
IT04K-221-1	IITA	Introduction	NE17	NE	Landrace	NE71	NE	Landrace
IT04K-227-4	IITA	Introduction	NE18	NE	Landrace	SECOW2W	NE	Cultivar
IT06K-121	IITA	Introduction	NE19	NE	Landrace	WC1	WC	Landrace
IT06K-123-1	IITA	Introduction	NE23	NE	Landrace	WC10	WC	Landrace
IT06K-124	IITA	Introduction	NE30	NE	Landrace	WC11	WC	Landrace
IT06K-147-1	IITA	Introduction	NE31	NE	Landrace	WC12	WC	Landrace
IT06K-154-1	IITA	Introduction	NE32	NE	Landrace	WC13	WC	Landrace

IT06K-281-1	IITA	Introduction	NE36	NE	Landrace	WC15	WC	Landrace
IT06K-91-11-1	IITA	Introduction	NE37	NE	Landrace	WC16	WC	Landrace
IT07K-187-24	IITA	Introduction	NE39	NE	Landrace	WC17	WC	Landrace
IT07K-188-49	IITA	Introduction	NE4	NE	Landrace	WC18	WC	Landrace
IT07K-211-1-8	IITA	Introduction	NE40	NE	Landrace	WC2	WC	Landrace
IT07K-243-1-5	IITA	Introduction	NE41	NE	Landrace	WC21	WC	Landrace
IT07K-292-10	IITA	Introduction	NE42	NE	Landrace	WC26	WC	Landrace
IT07K-299-4	IITA	Introduction	NE43	NE	Landrace	WC27	WC	Landrace
IT07K-300-12	IITA	Introduction	NE44	NE	Landrace	WC29	WC	Landrace
IT89KD-288	IITA	Introduction	NE45	NE	Landrace	WC30	WC	Landrace
IT97K-499-35	IITA	Introduction	NE46	NE	Landrace	WC32	WC	Landrace
IT98K-503-1	IITA	Introduction	NE48	NE	Landrace	WC33	WC	Landrace
MU09B	MAK	Landrace	NE49	NE	Landrace	WC35A	WC	Landrace
MU15	MAK	Landrace	NE5	NE	Landrace	WC35B	WC	Landrace
MU17	MAK	Landrace	NE50	NE	Landrace	WC35C	WC	Landrace
MU19	MAK	Landrace	NE51	NE	Landrace	WC36	WC	Landrace

NE = Northern and Eastern, Uganda; WC = Western and Central, Uganda; MAK = Makerere University, Uganda; IITA = International Institute of Tropical Agriculture, Nigeria.

2.3 Data Collection Method

For each trial, data were collected at 14-days interval starting three weeks after planting (WAP) until the appearance of the first ripe pods. Viral disease incidence was recorded on all plants per plot while severity was recorded on ten randomly selected plants in a plot. Disease severity was based on visual estimation of the diseased plants as manifested by the different symptoms on a modified scale of 1-5 where 1 = no symptoms on all leaves, 2 = slight symptoms (1 to 25% of the leaves infected), 3 = moderate symptoms (26 to 50 % leaves infected), 4 = prominent symptoms with stunting (51 to 75% of leaves infected), 5 = highly severe symptoms with stunting (> 75% of leaves infected) (Gumedzoe et al., 1997).

2.4 Statistical Analysis

Disease severity data were used to compute area under disease progress curve (AUDPC) as described by Campbell and Madden (1990).

$$\text{AUDPC} = \sum_{i=1}^{n-1} \left(\frac{Y_i + Y_{i+1}}{2}\right)(t_{i+1} - t_i) \quad (1)$$

where; n = number of successive readings, Y_i = disease severity at time i, t_i = number of days after the first observation on assessment date i. Data were also recorded on number of days to 50% flowering (midbloom), number of days to maturity and yield. Data was subjected to analysis of variance (ANOVA) using the linear mixed models (REML) in Genstat discovery Edition 4 (http://discovery.genstat.co.uk) and R version 3.1.0 (R core team, 2014). Mean AUDPC and incidence per genotype were computed per location as well as per season and genotype.

3. Results

Area under disease progress and disease incidence were high in Budaka and lowest in Tororo over the two seasons (Table 3). In the first season (2012A), lowerAUDPC and disease incidence were recorded than in the second season (2012B). Overall, mean AUDPC was lower in 2012A than in 2012B, with Budaka 12A recording the highest values followed by Tororo12A and then Serere12A. In 2012B, Budaka12B had the highest disease severity followed by Serere 12B and lastly Tororo12B. Based on genotype source, cowpea genotypes from IITA had higher AUDPC and disease incidence values than genotypes from Uganda (Table 4). Among the Ugandan genotypes, accessions from the western and central regions of the country had lower disease levels (Table 4).

Table 3. Mean AUDPC and mean disease incidence across locations

Location	Season	AUDPC	Incidence
Budaka	2012A	34.8	28
Budaka	2012B	79.9	62.6
Serere	2012A	31.1	25.4
Serere	2012B	78.2	61.2
Tororo	2012A	31.5	28.5
Tororo	2012B	65.0	34.9

Table 4. Mean AUDPC and mean disease incidence according to source of planting material

Source	Location	AUDPC	Incidence
IITA	Budaka	77.3	66.9
MAK	Budaka	58.9	45.0
NE	Budaka	54.5	42.1
WC	Budaka	50.9	38.6
IITA	Serere	65.2	61.3
MAK	Serere	53.9	48.2
NE	Serere	55.0	44.7
WC	Serere	51.2	37.7
IITA	Tororo	54.1	46.8
MAK	Tororo	49.5	39.5
NE	Tororo	45.6	28.1
WC	Tororo	45.5	25.9

NE = Northern and Eastern; WC = Western and Central; MAK = Makerere University collection; IITA = International Institute of Tropical Agriculture, Nigeria.

Analysis of variance showed significant differences among genotypes, seasons and locations for AUDPC. The site x season, site x genotype, season x genotype and site x season x genotype interactions were also highly significant (Table 5).

Table 5. Analysis of variance for area under disease progress curve among cowpea genotypes evaluated for two seasons

Source of variation	d.f.	Mean squares
Site	2	135.7***
Season	1	8074.3***
Genotype	104	1569.1***
Site xSeason	2	155.9***
Site x Genotype	208	427***
Season x Genotype	104	373.9***
Site x Season x Genotype	208	268.9**

*** = significant at 0.001 and 0.003 respectively.

Among locations, analysis of variance indicated that there were significant genotype, season and genotype x season interaction for AUDPC and disease incidence (Table 6). However, seasonal differences had the strongest effects on both AUDPC and disease incidence. The effects of genotype and genotype x season on AUDPC were greater in Budaka than for Serere and Tororo.

Table 6. Variation of AUDPC and incidence across experimental locations

Source of variation	df	AUDPC Mean squares			Incidence Mean squares		
		Budaka	Serere	Tororo	Budaka	Serere	Tororo
Genotype	104	1158.8***	352.9***	518.3***	1313.4***	780.1***	890.1***
Season	1	307183.2***	330899.6***	183031.3***	183902.1***	223977.4***	6659.1***
Genotypex season	104	298.1***	78.4**	245.6***	253.3**	256.5***	264.2***
Residual	300	129.3	59.8	116.4	193.4	140.7	166.7

*** = significant at 0.001 level, ** = significant at 0.05 level.

Mean AUDPC for the 105 genotypes screened for reaction under natural infestation are shown in Table 7. Average AUDPC across the three locations over the two seasons, ranged from 39.4 (on genotype WC48) to 94.9 (genotype NE46). It is evident from the table that none of the genotypes evaluated were immune. The introduced germplasm from IITA exhibited more susceptible reaction than the local accessions (Table 7 and Figure 1). Among the local genotypes, the accessions WC48, MU19 and NE43 from the western and central region, Makerere University and Northern and Eastern Uganda respectively had the lower AUDPC. A range of typical virus symptoms were also observed on most genotypes during evaluation such as; leaf mosaic, necrosis, chlorosis, vein clearing, vein banding, purpling, leaf curling, leaf deformation, and blotching.

Table 7. Overall Cowpea genotype reaction based on AUDPC

Location				Location			
Genotype	Budaka	Serere	Tororo	Genotype	Budaka	Serere	Tororo
EBELAT	62.7	59.1	51.9	MU20	92.6	61.3	67.6
IT00K-835-45	62.3	63.8	41.2	MU20B	60.8	51.9	43.4
IT03K-124	71.2	62.8	54.4	MU9	42.9	52.3	42.8
IT04K-219-2	63.8	67.2	54.5	NE13	52.4	56.4	44.0
IT04K-221-1	61.8	63.5	72.3	NE15	46.6	48.8	31.0
IT04K-227-4	68.4	68.2	41.4	NE17	48.5	50.5	37.1
IT06K-121	86.5	67.9	68.0	NE18	48.9	52.4	43.4
IT06K-123-1	73.1	66.3	61.1	NE19	68.7	53.9	56.6
IT06K-124	70.5	56.6	56.5	NE23	52.2	52.1	37.8
IT06K-147-1	76.2	55.9	67.5	NE30	48.6	53.4	45.8
IT06K-154-1	79.9	58.8	42.4	NE31	57.8	53.5	50.8
IT06K-281-1	69.2	62.2	47.3	NE32	48.5	51.9	38.8
IT06K-91-11-1	85.0	82.2	80.7	NE36	46.0	51.4	51.4
IT07K-187-24	74.6	72.6	50.8	NE37	47.8	46.2	44.3
IT07K-188-49	76.2	69.6	69.2	NE39	46.7	53.6	45.4
IT07K-211-1-8	60.2	57.8	62.4	NE4	59.7	52.7	54.4
IT07K-243-1-5	65.1	63.8	48.8	NE40	61.0	57.1	44.1
IT07K-292-10	81.8	47.0	66.0	NE41	49.0	52.4	47.5

IT07K-299-4	77.1	65.6	44.2	NE42	52.4	53.8	41.3
IT07K-300-12	75.2	66.7	52.9	NE43	48.9	47.6	30.7
IT89KD-288	70.7	60.8	59.8	NE44	52.9	51.7	40.4
IT97K-499-35	80.6	66.1	39.5	NE45	54.9	50.8	46.0
IT98K-503-1	69.8	59.9	53.1	NE46	101.7	92.4	90.5
MU09B	43.8	57.4	49.5	NE48	48.9	48.8	42.5
MU15	47.0	51.4	55.5	NE49	56.5	57.3	52.0
MU17	59.5	55.1	52.6	NE5	50.5	52.2	43.9
MU19	44.6	47.6	41.3	NE50	42.3	56.2	41.2
NE51	51.5	47.7	48.9	NE70	55.0	59.0	44.2
NE53	53.9	51.8	47.3	NE71	65.0	52.0	58.4
NE55	63.6	52.8	43.5	SECOW2W	46.6	48.3	39.6
NE6	56.1	47.6	43.4	WC1	43.4	50.8	52.5
NE67	48.8	50.8	44.1	WC10	57.2	49.4	50.1

Table 7 continued. Overall Cowpea genotype reaction based on AUDPC

Location				Location			
Genotype	Budaka	Serere	Tororo	Genotype	Budaka	Serere	Tororo
WC11	48.3	53.0	49.7	WC4	48.5	53.8	48.5
WC12	42.1	55.3	42.2	WC41	50.8	51.4	48.1
WC13	62.7	55.0	42.0	WC42	51.2	54.2	51.7
WC15	57.6	51.4	46.5	WC44	49.2	50.5	48.8
WC16	57.9	50.5	58.8	WC48	42.5	45.6	30.0
WC17	55.2	48.5	44.8	WC5	56.3	55.1	52.5
WC18	42.7	49.6	42.2	WC51	51.8	48.9	39.2
WC2	48.4	45.7	43.2	WC52	62.8	46.3	54.6
WC21	46.2	48.7	44.0	WC53	46.9	47.4	44.0
WC26	48.0	53.1	44.7	WC55	59.1	48.5	41.7
WC27	44.9	51.1	47.3	WC6	61.2	54.2	48.3
WC29	49.4	47.6	42.4	WC62	60.9	50.2	47.8
WC30	47.6	53.5	51.2	WC63	43.5	50.9	42.7
WC32	44.4	54.3	38.0	WC64	55.9	48.8	50.0
WC33	41.4	46.9	52.6	WC65	48.1	53.2	45.2
WC35A	39.5	51.1	42.9	WC66	47.7	50.7	47.5
WC35B	54.0	49.7	33.0	WC67	49.8	53.1	51.3
WC35C	40.4	50.3	44.5	WC67A	46.0	54.6	42.0
WC36	60.5	51.4	47.5	WC68	54.9	49.4	54.1
WC39	44.6	50.3	42.5	WC69	60.3	51.4	47.5
				WC7	67.0	52.5	59.6

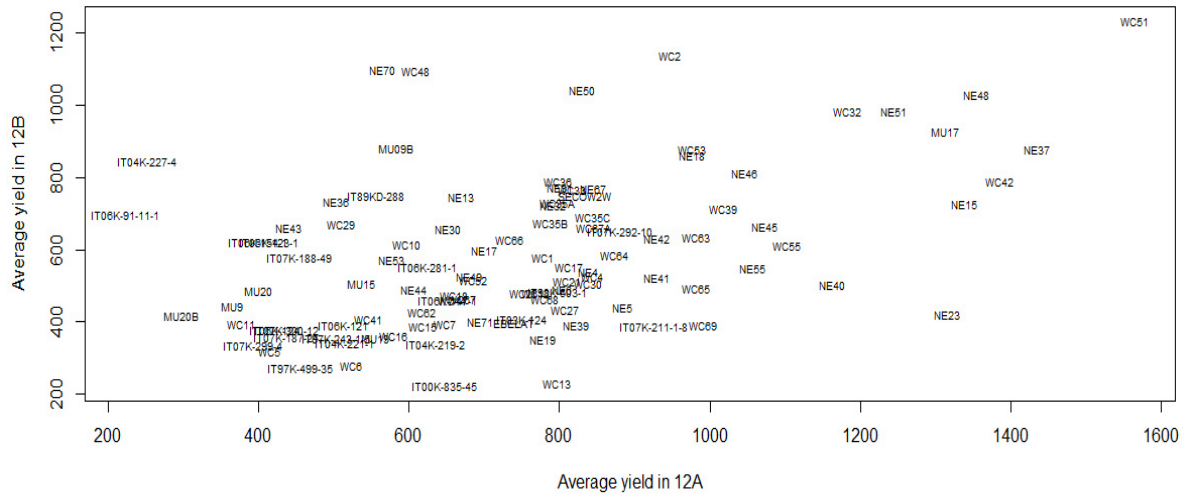

Figure 1. Relationship of mean yield (kg/ha) by genotypes across 2012A and 2012B

Number of days to 50% flowering over the two seasons ranged from 45 days to 73 days in Budaka, 39 days to 63 days in Serere and 42 days to 67 days in Tororo. The average number of days to 50% flowering in 2012A was 57 days, 44 days and 53 days for Budaka12A, Serere12A and Tororo12A respectively. In 2012B, the average number of days to 50% flowering was 52 days, 54days and 52 days in Budaka12B, Serere12B and Tororo12B respectively (Table 8).

Table 8. Average number of days to 50%flowering, maturity and average yield across study sites in 2012A and 2012B

Season	Site	Mean number of days to Midbloom	Mean number of days to Maturity	Mean Yield (kg/ha)
12A	Budaka	56.9	88.6	1529.3
12A	Serere	43.6	81.2	187.3
12A	Tororo	53.3	85.2	565.9
12B	Budaka	51.9	73.5	522.6
12B	Serere	53.5	80.5	899.4
12B	Tororo	52.1	88.5	344.8

Number of days to maturity across the two seasons ranged from 69 days to 101 days in Budaka, 71 days to 88 days in Serere and 67 days to 99 days in Tororo. Average number of days to maturity in 2012A was 87 days in Budaka, 81 days in Serere and 85 days in Tororo while in 2012B, the average number of days to maturity was 74 days, 81 days and 89 days respectively in Budaka, Serere and Tororo respectively (Table 8).

Yield over the two seasons ranged from 25 kg/ha to 3000 kg/ha in Budaka, 8.3 kg/ha to 2650 kg/ha in Serere and 25 kg/ha to 2708 kg/ha in Tororo. In Budaka, higher average yields were recorded in 2012A (1529 kg/ha) compared to 523 kg/ha obtained in 2012B. In Serere, there were higher yields in 2012B (899 kg/ha) compared to 187 kg/ha in 2012A while in Tororo, higher yields were obtained in 2012A (566 kg/ha) compared to 345 kg/ha in 2012B (Table 8). A plot of yield by genotypes across the two seasons showed that there were huge season to season differences for among genotypes (Figure 2). From the plot, some genotypes were consistently high yielding across the two seasons such as WC51, NE48, WC32, NE51 and MU17 while some were consistently low yielding such as IT07K-299-4 and WC5. Some genotypes performed better in 12A such as NE23, NE40 and NE15 while IT04K-227-4 and 1T06K-91-11-1 were better in 12B than 12A.

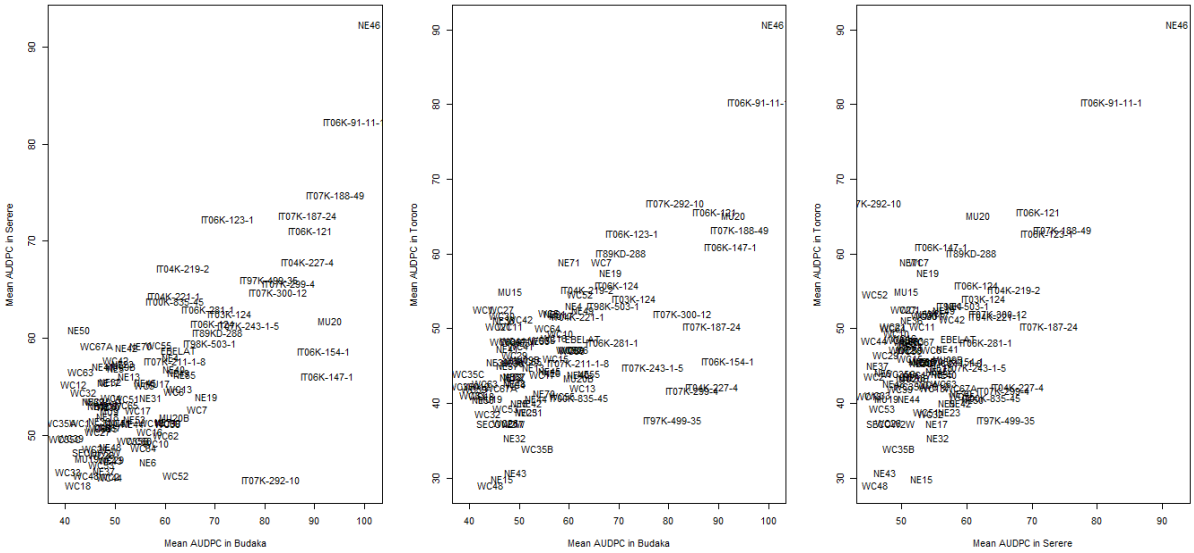

Figure 2. Variation of AUDPC by genotypes across study sites

Across the three study sites, local genotypes WC51, and NE48 gave consistently higher mean yield values while introduced genotypes such as IT97K-499-35, IT00K-835-45, and IT07K-299-4 were consistently low yielding (Figure 3). There was also yield variability among genotypes when two sites were compared for instance genotypes WC51, NE50, NE48, SECOW2W and WC2 gave higher yields both in Budaka and Serere while genotypes IT97K-499-35, IT04K-219-2, MU20B, WC13 and IT07K-300-12 gave consistently low yields in both locations. Comparing Budaka and Tororo, genotypes WC32, MU17, NE48 and WC42 registered higher yields while IT04K-221-1, IT97K-499-35, MU20, IT07K-187-24 and IT07K-299-4 gave low yields in both locations. For Serere and Tororo, higher yields were obtained from WC51 and NE51 genotypes while lower yield values were obtained from IT04K-221-1 and IT97K-499-35.

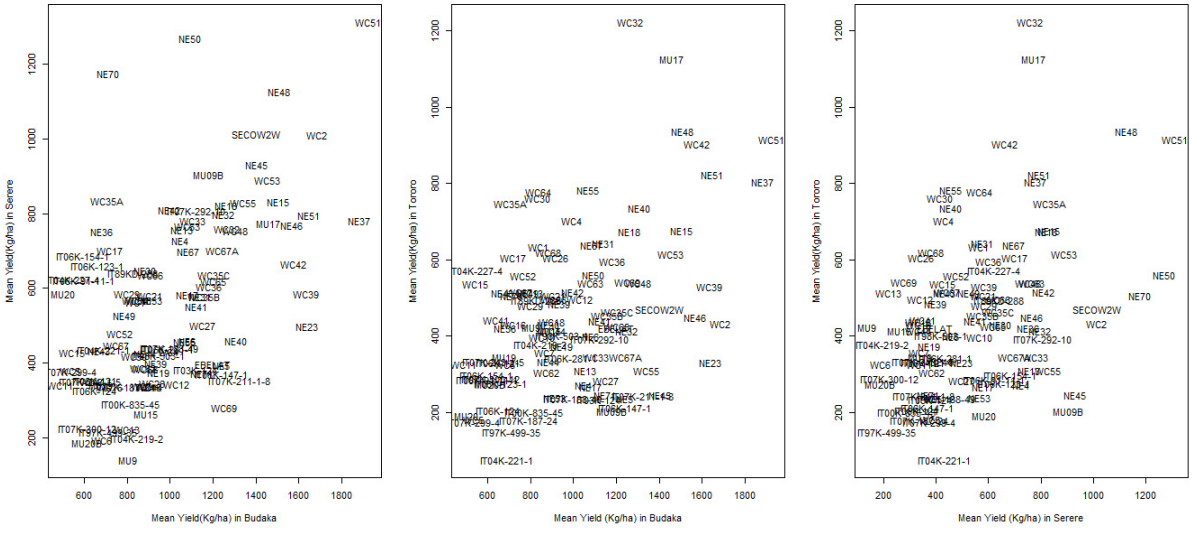

Figure 3. Relationship of mean yield (kg/ha) by genotypes across study sites

4. Discussion

There was variation in disease pressure across sites and seasons with higher AUDPC recorded in 2012B than in 2012A. These differences can be attributed to the influence of environmental conditions such as rainfall, temperature and relative humidity (Kaisser & Mossahebi, 1975; Edema et al., 1997). Edema et al. (1997)

however reported higher disease incidence in the first (wet season) than in the dry season. In our study, this could be attributed to rapid symptom development that normally occurs in dry conditions (Schuerger & Hammer, 1995). Also under dry conditions, cowpea plants do not show considerable plasticity and recovery growth and hence are severely affected by viral infections (Booker et al., 2005).

During the trials at the three sites, the genotypes expressed a range of symptoms some appearing on the primary leaves shortly after germination. The symptoms ranged from leaf mosaic, necrosis, chlorosis, vein clearing, vein banding, purpling, leaf curling, leaf deformation, and blotching. It has been reported that symptom expression depends on the virus type or strain, genotype, species and plant age, time of the year and environmental conditions and some viruses cause similar or related symptoms (Shoyinka et al., 1997). Some symptoms such as mosaic, necrosis, chlorosis, vein banding, stunted growth, leaf deformation, and mottling are associated with viruses such as *Cowpea aphid borne mosaic virus* (CABMV), *Blackeye cowpea mosaic virus* (BICMV), *Cowpea yellow mosaic virus* (CYMV) (Aliyu et al., 2012; Orawu, 2007).

Results from this study also show that with the exception of genotype NE46, most of the landraces and the released variety (SECOW2W) were either resistant or moderately resistant compared to the introduced genotypes. However, Orawu et al. (2012) found Ebelat (landrace) to be susceptible especially to *Cowpea aphid borne mosaic virus* (CABMV). In this study, the cowpea genotypes were screened for resistance to field viruses and therefore, genotypes such as WC32, WC18, NE43, NE15, WC35B and SECOW2W with low disease severity may offer multiple virus resistance. Breeding for disease resistance in cowpea is a complex problem because of the occurrence of multiple virus infections in a single field/plant (Amayo et al., 2012; Orawu et al., 2012; Shoyinka et al., 1997). However, most of these viruses are transmitted by the same vectors which offers an opportunity to utilize horizontal resistance to vector transmission in breeding programmes (Shoyinka *et al*., 1997). The development of resistant varieties would be the most effective and environmentally friendly means of controlling these viral diseases. In the course of developing varieties that are resistant to a particular disease, the breeder has to select a resistant individual as a parent. The gene(s) conferring resistance can then be transferred to a cultivated variety in order to obtain improved lines (Ogundiwin et al., 2002). There is no ecological restriction to viruses affecting cowpea and therefore screening of genotypes under natural field conditions in different agro-ecological conditions is critical for identifying resistant genotypes (Shoyinka et al., 1997). The introduced genotypes were more susceptible compared to the local genotypes. Differential response of genotypes is common in disease resistance screening and can be attributed to differences in environmental conditions, pathogen variability and virulence (Gremillion et al., 2011).

5. Conclusion

Overall, results from this study identified a number of local landraces in addition to the released variety (SECOW2W) as useful sources of resistance to cowpea viruses that can be used in the local breeding program. These include; WC32, WC18, NE43, NE15, WC35B. Follow up studies both in the field and green house involving high virus innoculum levels (by artificial inoculation) need to be undertaken to confirm the levels of resistance in these genotypes. This study also showed consistency among genotypes in reaction to virus infection in the three locations over the two seasons. These study sites are therefore ideal for future screening of genotypes for resistance or susceptibility to virus infection.

Acknowledgements

We are grateful to the McKnight Foundation for funding this study through the Collaborative Crop Research Program (CCRP). We are thankful to the Centre Managers of Tororo DATIC and Ikiki DATIC in Budaka district for offering land over the two seasons to conduct field experiments.

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