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Evaluation of Ugandan Cowpea Germplasm for Yield and Resistance to Scab Disease

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Authors' contributions

This work was carried out in collaboration between all authors. Author EA designed the study, carried out the experiment and wrote the first draft of the manuscript. Authors TLO, MB and PRR reviewed the experimental design and all drafts of the manuscript. Authors EA, KEM and TLO performed the statistical analysis. Authors EA and KEM managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Aims: This study was conducted to identify cowpea (*Vigna unguiculata*) cultivars with high yield potential and resistance to scab disease caused by *Sphaceloma* sp. in Uganda. 100 cowpea genotypes were evaluated at two locations (Kabanyolo and Serere) in Uganda between April and July, 2014 using a 10 × 10 alpha lattice design.

Place and Duration of Study: Makerere University Agriculture Research Institute - Kabanyolo (MUARIK) and the National Semi Arid Resources Research Institute (NaSARRI) – Serere between April to July, 2014.

Study Design and Methodology: Hundred cowpea lines (69 landraces, 25 inbred lines at F7, 1 local and 5 improved cultivars) were grown at each location in a 10 × 10 alpha lattice design with 3 replications to assess their reaction to the scab disease and yield potential (grain yield and yield related traits).

Results: The cowpea lines differed significantly (*P* = .05) in their response to natural disease

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pressure as determined by disease incidence, apparent infection rate (r) and severity indicated by area under disease progress curve (AUDPC). Analysis of variance showed that there was highly significant differences (P < .001) in genotypes, locations, AUDPC and other traits and genotype by location (G×L) interaction on AUDPC. The correlation analysis revealed a positive relationship of scab disease incidence with AUDPC (0.8; P < .001) but a significant (P < .001) negative relationship with grain yield (-0.8), number of pods per plant (-0.5), number of seeds per pod (-0.5) and 100 seed weight (-0.5). Cluster analysis based on only scab disease indexes produced 4 main clusters while cluster analysis based on disease and yield traits produced 3 main clusters. However, the two different clusters revealed similar grouping patterns in which cowpea lines with similar resistance ratings were shown to form unique clusters. R-mode principal component analysis yielded 4 principal components explaining 62.28% of the variation observed.

Conclusion: The study revealed that the use of apparent infection rate "r" alone as an index for rating a genotype for scab reaction was not decisive. One line (NE 15) was found to be resistant to the scab disease at both locations and high yielding and could be used in the cowpea improvement programme to breed for resistance to the scab disease.

Keywords: Sphaceloma sp.; severity; AUDPC; apparent infection rate; cluster analysis.

1. INTRODUCTION

Cowpea (*Vigna unguiculata*) is an important component of subsistence agriculture particularly in the dry savannas of sub-Saharan Africa (SSA) [1]. This is due to its drought tolerance, quick growth and rapid ground cover to check soil erosion [2] and unique ability to fix atmospheric nitrogen [3]. Its ability to tolerate shade makes it compatible as an intercrop with maize, millet, sorghum, cotton and several plantation crops [4]. Though cowpea is the most economically important indigenous African legume crop [5] grown in more than 60 countries either as a food crop or cash crop [6], its yields are generally low. Mean yield in Uganda is less than 400 kg ha^{-1} [7]. The annual production in the country is estimated to be at 20,000 t/yr, with Northern and Eastern regions accounting for most of the production in the country [8]. It is the third most important legume food crop in Uganda after the common beans (*Phaseolus vulgaris* L.) and groundnuts (*Arachis hypogea* L.) [9]. Rusoke and Rubaihayo [10] reported that a yield potential of 3000 kg ha^{-1} was achievable. According to Ajeigbe and Singh [11], the low yields recorded were due to a number of constraints including insect pests, diseases, parasitic weeds, low soil fertility, drought and lack of inputs among others.

Scab (*Sphaceloma* sp.) is one of the major and common diseases of cowpea [12]. It is widespread in Tropical Africa and very damaging in Savannah areas [13], capable of causing yield losses of up to 100% [14]. The disease affects all the above ground parts of cowpea [15]. Cowpea improvement programme in Uganda was initiated in the late 1960s at Makerere University with the collection of local and exotic accessions, which were screened for yield potential [16]. The promising selections were evaluated under different management practices for control of diseases [17] and insect pests [18,19]. Nakawuka and Adipala [20] screened 75 cowpea lines against scab of which 10 were resistant and observed that in general, local lines were less infected than introductions. These were then used to study the genetics of resistance to scab by using a half-diallel cross set [21].

There is currently a surge in the occurrence of the scab disease in the country [22] suggesting that over the years, the fungus has developed variability in its patho-types. None of the five recently released varieties (SECOW 1T, SECOW 5T, SECOW 2W, SECOW 4W and SECOW 3B) is resistant to the disease. Following screening of 70 lines done by the National Semi Arid Resources Research Institute (NaSARRI) in Serere, some promising lines were identified but there is the need to screen a wider collection and at different locations in the country to ensure selection of stable parents both in terms of yield and resistance to scab.

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 [23]. In contrast, resistant varieties are easily adopted resulting in boosting production dramatically with a positive impact on the farmers' livelihoods. Mbong et al. [24] suggested the use of resistant varieties would help in disease management and improve the yield of the crop. According to Rusoke and Rubaihayo [10], the use of host resistant varieties is the most practical control measure available to farmers, and it is environmentally friendly. This study was conducted to screen a wide range of cowpea lines available in Uganda at two locations to identify sources of host resistance and yield potential that could be used in the breeding programmes for the purpose of developing improved resistant varieties to scab.

2. MATERIALS AND METHODS

2.1 Experimental Materials

100 cowpea lines (Table 1) consisting of 69 landraces, 25 inbred lines at F_7, 1 local and 5 improved cultivars recently released by the National Semi Arid Resources Research Institute (NaSARRI) Serere, Uganda were used in the study.

2.2 Experimental Sites

The screening experiments were conducted at two locations, Makerere University Agriculture Research Institute - Kabanyolo (MUARIK) (0°28'N and 32°37'E; 1200 m above sea level) in the Central part of Uganda and the National Semi Arid Resources Research Institute (NaSARRI) in Serere (1°39'N and 33°27'E; 1038 m above sea level), Eastern part of Uganda during the first rainy season (April-July) of 2014. The average rainfall and relative humidity recorded during the period in kabanyolo were 162.8 mm and 69-87% respectively while Serere recorded 136.3 mm and 61-73% for rainfall and relative humidity respectively for the same period.

2.3 Experimental Design

A 10 × 10 alpha lattice design with 3 replications at each site was used to conduct the evaluation. Each replication had 10 blocks with each block having 10 plots. Each genotype was planted on a plot with an area of 3 m × 3 m with a spacing of 1 m between plots and between replications. A spacing of 60 cm between rows and 30 cm within rows was used. The fields were weeded three times and insecticide application was done twice, one just before flowering and the second during pod setting. No fertilizer or fungicide were applied during the entire growing period.

2.4 Data Collection and Analysis

Six weeks after planting, five plants were randomly selected in each plot, tagged and severity ratings done visually at seven days intervals [23] for six consecutive weeks. Disease scoring was done using a scale of 1-5, where 1 = no symptoms, 2 = less than 10% infection, 3 = 10 to 20% infection, 4 = 20 to 50% infection, and 5 = more than 50% infection [20]. Incidence was estimated by counting all the individual plants with scab disease symptoms in each plot and expressing the number as a ratio over the total number of plants in the plot.

Data on yield and yield components including number of days to 50% flowering, number of branches per plant, number of peduncles per plant, number of pods per peduncle, number of pods per plant, pod length (cm), seeds per pod, and 100 seed weight (grams) were recorded. Grain yield (tons ha^{-1}) was estimated from yield per plot.

Mean severity scores were estimated using Microsoft Excel and the means obtained were used to calculate Area under the Disease Progress Curve (AUDPC) for each of the cowpea lines in Microsoft Excel using the following formula of Campbell and Madden [25]:

$$AUDPC = \sum_{i=1}^{n-1} \left(\frac{y_i + y_{i+1}}{2}\right) (t_{i+1} - t_i)$$

Where "t" is the time of each reading, "y" is the percent of affected foliage at each reading and "n" is the number of readings. The variable "t" represents days after planting. The AUDPC as a resistance measurement calculated from the estimated percentages of leaf area affected recorded on weekly basis, was used to measure resistance [26] of the cowpea lines. Percentage incidence data were Arcsine transformed [27] and used to estimate the Apparent Infection Rate (r) in Microsoft Excel using van der Plank's equation [28]:

$$r = \frac{1}{t_2 - t_1} \, log_e \left[\frac{x_2\,(1-x_1)}{x_1\,(1-x_2)}\right]$$

Where: "t_1" = initial time of disease assessment (i.e. days after planting – DAP); "t_2" = final time of disease assessment (DAP); "x_1" and "x_2" represent amounts of disease present at "t_1" and "t_2" respectively.

Table 1. Description of a Uganda collection of 100 cowpea lines screened for yield and resistance to scab disease

No.	Name	Cultivar type	Maturity	Disease reaction[a]	No.	Name	Cultivar type	Maturity	Disease reaction[a]
1	WC 62	Landrace	Early	Moderate	51	WC52	Landrace	Late	Unknown
2	NE4	Landrace	Early	Unknown	52	NE41	Landrace	Late	Unknown
3	NE49	Landrace	Early	Moderate	53	NE6	Landrace	Late	Moderate
4	WC68	Landrace	Early	Unknown	54	NE46	Landrace	Late	Unknown
5	WC48A	Landrace	Early	Moderate	55	WC5	Landrace	Late	Moderate
6	NE55	Landrace	Early	Moderate	56	WC2	Landrace	Late	Unknown
7	WC15	Landrace	Early	Moderate	57	NE20	Landrace	Late	Susceptible
8	NE31	Landrace	Early	Unknown	58	WC55	Landrace	Late	Unknown
9	NE50	Landrace	Early	Moderate	59	NE71	Landrace	Late	Resistant
10	WC63	Landrace	Early	Resistant	60	NE36	Landrace	Late	Moderate
11	NE53	Landrace	Early	Unknown	61	WC20	Landrace	Late	Unknown
12	WC16	Landrace	Early	Moderate	62	NE19	Landrace	Late	Resistant
13	NE44	Landrace	Medium	Moderate	63	WC33	Landrace	Late	Unknown
14	WC30	Landrace	Medium	Unknown	64	WC29	Landrace	Late	Susceptible
15	WC21	Landrace	Medium	Unknown	65	WC58	Landrace	Late	Moderate
16	NE18	Landrace	Medium	Unknown	66	NE21	Landrace	Late	Unknown
17	WC7	Landrace	Medium	Unknown	67	NE40	Landrace	Late	Moderate
18	WC42	Landrace	Medium	Resistant	68	WC32A	Landrace	Late	Unknown
19	NE5	Landrace	Medium	Unknown	69	WC46	Landrace	Late	Unknown
20	NE70	Landrace	Medium	Unknown	70	ACC23 × SECOW4W	Inbred line	Early	Susceptible
21	WC53	Landrace	Medium	Unknown	71	ACC26 × ACC2	Inbred line	Early	Susceptible
22	WC67	Landrace	Medium	Resistant	72	ACC23 × SECOW2W	Inbred line	Early	Moderate
23	WC35A	Landrace	Medium	Unknown	73	ALEGI × SECOW3B	Inbred line	Early	Resistant
24	WC35B	Landrace	Medium	Unknown	74	ACC23 × SECOW3B	Inbred line	Early	Moderate
25	WC44	Landrace	Medium	Moderate	75	ALEGI × SECOW5T	Inbred line	Early	Susceptible
26	WC26	Landrace	Medium	Moderate	76	ALEGI × ACC12	Inbred line	Early	Moderate
27	NE23	Landrace	Medium	Unknown	77	SECOW5T × SECOW3B	Inbred line	Early	Moderate
28	WC64	Landrace	Medium	Unknown	78	SECOW5T × ACC12	Inbred line	Early	Moderate
29	WC18	Landrace	Medium	Susceptible	79	ACC23 × ACC12	Inbred line	Early	Moderate
30	WC27	Landrace	Medium	Susceptible	80	ALEGI × SECOW4W	Inbred line	Early	Moderate
31	WC8	Landrace	Medium	Susceptible	81	ACC12 × SECOW3B	Inbred line	Early	Susceptible

No.	Name	Cultivar type	Maturity	Disease reaction[a]	No.	Name	Cultivar type	Maturity	Disease reaction[a]
32	WC37	Landrace	Medium	Moderate	82	SECOW1T × ALEGI	Inbred line	Early	Susceptible
33	WC66	Landrace	Medium	Moderate	83	ACC12 × SECOW5T	Inbred line	Early	Susceptible
34	NE30	Landrace	Medium	Resistant	84	SECOW2W × ACC2	Inbred line	Early	Resistant
35	WC36	Landrace	Medium	Susceptible	85	ALEGI × ACC2	Inbred line	Early	Susceptible
36	WC17	Landrace	Medium	Unknown	86	ACC2 × SECOW1T	Inbred line	Early	Susceptible
37	NE15	Landrace	Medium	Resistant	87	ACC12 × SECOW2W	Inbred line	Early	Resistant
38	NE13	Landrace	Medium	Unknown	88	SECOW3B × SECOW2W	Inbred line	Early	Moderate
39	WC48	Landrace	Medium	Moderate	89	ACC2 × ACC12	Inbred line	Early	Resistant
40	WC69	Landrace	Medium	Susceptible	90	SECOW1T × ACC23	Inbred line	Early	Moderate
41	NE51	Landrace	Medium	Unknown	91	ACC26 × SECOW1T	Inbred line	Early	Moderate
42	NE32	Landrace	Medium	Resistant	92	SECOW4W × SECOW5T	Inbred line	Early	Moderate
43	NE39	Landrace	Medium	Moderate	93	SECOW5T × SECOW4W	Inbred line	Early	Moderate
44	NE48	Landrace	Medium	Moderate	94	SECOW2W × SECOW1T	Inbred line	Early	Moderate
45	WC35C	Landrace	Medium	Susceptible	95	ALEGI	Local	Early	Moderate
46	WC10	Landrace	Medium	Moderate	96	SECOW1T	Improved	Early	Susceptible
47	WC67B	Landrace	Medium	Susceptible	97	SECOW2W	Improved	Early	Moderate
48	WC41	Landrace	Late	Unknown	98	SECOW3B	Improved	Early	Moderate
49	WC32	Landrace	Late	Resistant	99	SECOW4W	Improved	Early	Susceptible
50	NE37	Landrace	Late	Unknown	100	SECOW5T	Improved	Early	Susceptible

[a] = Disease reaction as described by NaSARRI; ACC = Accession; NE = Northern and Eastern; WC = Western and Central; Inbred lines at F_7 generation

Plot means for yield, yield components and scab incidence and severity values were subjected to analysis of variance (ANOVA) using R statistical package for Windows v.3.1.2. Correlation among traits and Principal component analysis (PCA) were calculated using IBM SPSS Statistics version 22 [29]. The PCA was performed using varimax rotation method which is generally considered superior to other orthogonal factor rotation methods in achieving a simplified factor structure [30]. Hierarchical cluster analysis was performed using R statistical package for windows v.3.1.2 based on Ward's [31] method [32].

3. RESULTS AND DISCUSSION

3.1 Phenotypic Variability

The results of analysis of variance for agronomic traits, scab disease incidence, apparent infection rate and AUDPC evaluated at the two locations are presented in Table 2. The results showed highly significant differences (P < .001) among genotypes for AUDPC, yield traits (P < .01) and grain yield (P = .05). This indicates the presence of sufficient variability in the lines [33] for these traits. This could in part be explained by the highly significant differences (P < .001) in the AUDPC observed since each of the traits is affected by scab disease [15]. Similar findings were reported by Sharawy and El-Fiky [34]. The traits, including incidence of the disease showed highly significant differences (P < .001) between locations suggesting different disease pressures in the locations. There were highly significant (P < .001) genotype by location (G×L) interaction effects on AUDPC, days to 50% flowering and 100 seed weight suggesting inconsistent performance in the two locations. The results also suggested that for the purpose of breeding, different cultivars have to be developed for different locations [35].

3.2 Interrelationships among Disease Indexes, Yield and Yield Traits

The results of correlation analysis among the traits studied are presented in Table 3. Scab disease incidence was shown to be significantly correlated (P < .001) with AUDPC (0.8) suggesting that the severity of scab disease increased with incidence. This was expected since scab is a polycyclic epidemic disease and thus, as long as there is fresh new leaf tissues to be infected, the severity of polycyclic diseases will increase as the incidence increases [36]. Mbong et al. [23] also reported that the incidence of scab disease increased with plant age. Scab disease incidence and AUDPC showed a significant (P < .001) negative correlation with grain yield. This means that as the incidence and severity of the disease increased, the grain yield decreased significantly through the significant negative effects of scab disease on both the morphological and reproductive growth of cowpea plants [15]. The incidence of scab also showed a significant negative correlation (-0.5; P < .001) with the number of pods per plant, number of seeds per pod and 100 seed weight implying that there was significant reduction in these yield traits as the incidence of scab increased. Grain yield was found to be significantly positively correlated (0.5; P < .001) with the number of pods per plant, number of seeds per pod and 100 seed weight which were negatively affected by severity of scab disease indicating that yield was directly related to these traits and any factor affecting them would affect the grain yield [24].

3.3 Disease Intensity, Resistance and Yield Potential

Mean values of final scab disease incidence (FI), severity (FS), area under disease progress curve (AUDPC), yield, apparent infection rate (r) and host resistance (HR) of the cowpea lines grown at Kabanyolo and Serere are presented in Table 4. In all cases, scab disease incidence, severity, AUDPC and apparent infection rate (r) were more severe under conditions of lower rainfall (136.3 mm in Serere) than of higher rainfall (162.8 mm in Kabanyolo). This suggests that the scab fungus is more virulent under relatively low moisture conditions as was recorded. However, earlier reports suggested that scab was more severe under wet conditions [13,23]. Final scab disease incidence at Kabanyolo ranged between 0 – 43 % while mean final severity ranged between 1.0 – 5.0 and final scab disease incidence at Serere was 100% with mean final severity ranging from 2.1 – 5.0. The range of values for the final scab disease incidence and severity recorded at Kabanyolo indicated that the disease pressure was lower compared to Serere (Table 4) suggesting that the environmental conditions in Serere were more favourable to the scab fungus attack and thus overcame the defense system of the plants [37].

Table 2. Mean sum of squares for scab disease incidence, AUDPC and agronomic traits of 100 cowpea lines

Sources of variation	Df	Disease incidence	Apparent infection rate (r)	AUDPC	Days to flowering	No. of branches	Peduncles / plant	Pods/ peduncle	Pods/ plant	Pod length (cm)	Seeds/ pod	100 seed weight (g)	Grain yield (t/ha)
Genotype (G)	99	174	0.0005	989***	19.6***	2.241***	85	0.1221***	22.1***	43.71	5.3**	22.0***	0.27*
Location (L)	1	599747***	0.0311***	333926***	1872.7***	14.107***	9149***	1.2150***	2488.8***	307.81**	970.3***	1513.4***	291.50***
G×L	99	177	0.0005	1056***	17.8***	1.309	80	0.0466	6.1	43.77	3.6	6.8***	0.25
Error	400	139	0.0005	609	7.5	1.195	77	0.0650	6.3	37.34	3.7	1.7	0.20

*Df = Degrees of freedom; *** = Significant at .001; ** = Significant at .01; * = Significant at .05*

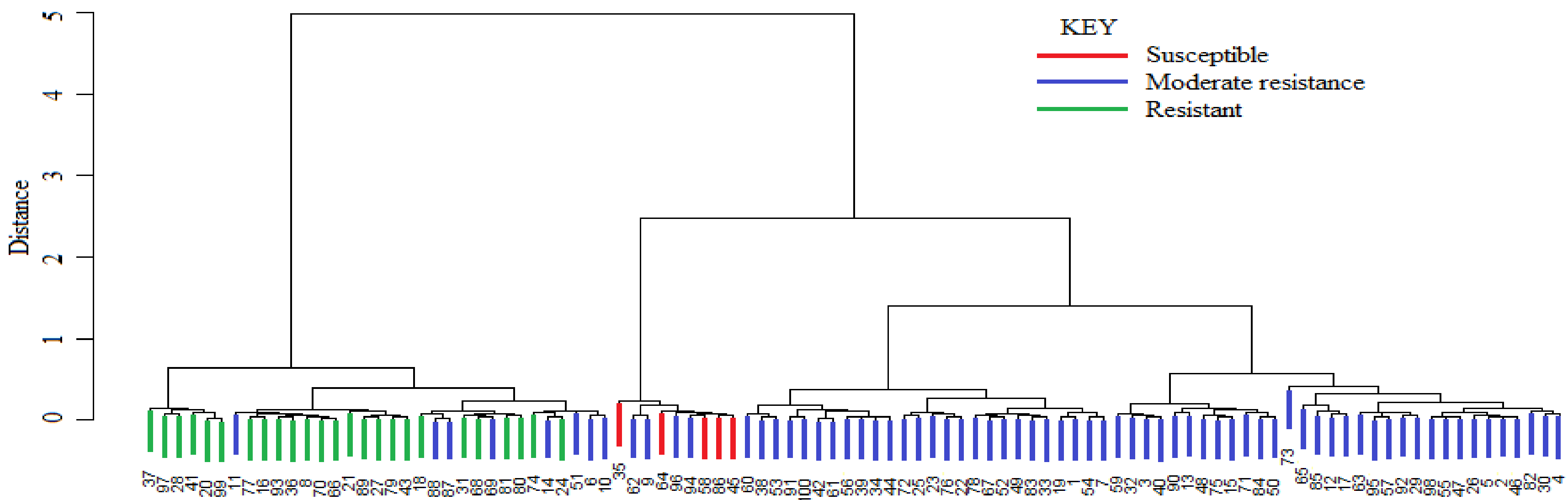

Fig. 1. Ward's cluster dendogram of the 100 cowpea lines based on 13 traits

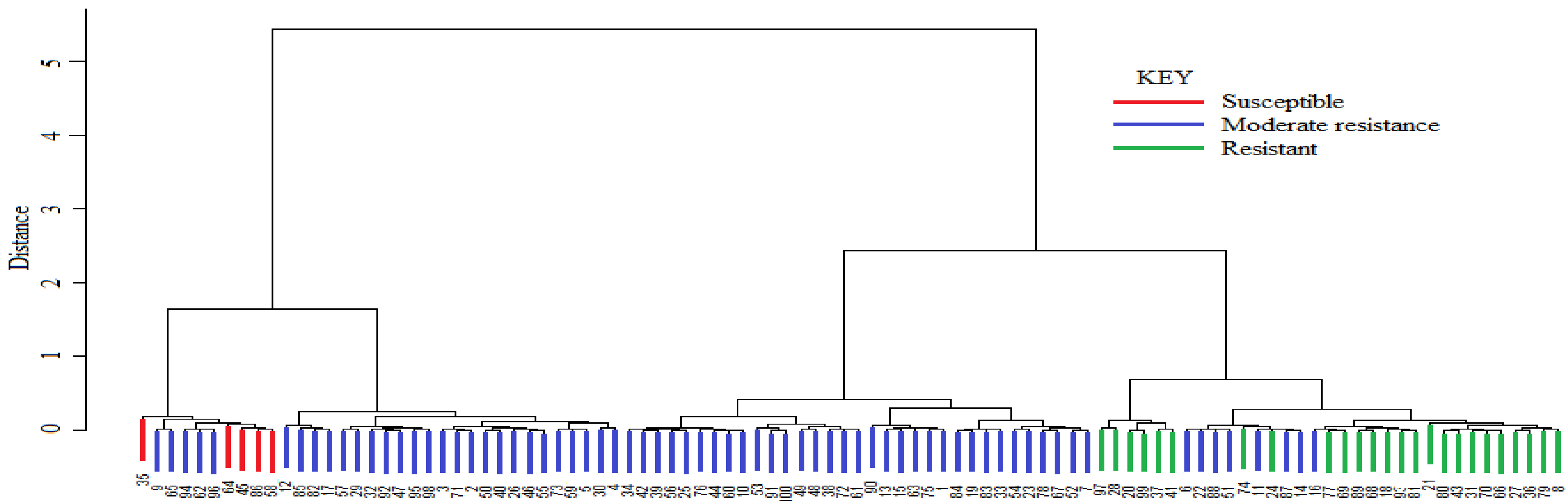

Fig. 2. Ward's cluster dendogram of the 100 cowpea lines based on 4 disease indexes

Table 3. Correlation of disease incidence, apparent infection rate, AUDPC and agronomic traits

Traits	Disease Incidence	Apparent infection rate	AUDPC	Days to flowering	No. of branches	Peduncles/ plant	Pods/ peduncle	Pods/ plant	Pod length (cm)	Seeds/ pod	100 seed weight (g)	Grain yield (t/ha)
Disease Incidence	-											
Apparent infection rate	0.197***	-										
AUDPC	0.814***	0.146***	-									
Days to flowering	-0.435***	-0.075	-0.290***	-								
No. of branches	-0.106**	-0.037	-0.066*	0.112*	-							
Peduncles/ plant	-0.389***	-0.072	-0.326***	0.087*	0.399***	-						
Pods/ peduncle	-0.155***	-0.039	-0.118**	-0.038	0.133***	0.208***	-					
Pods/ plant	-0.547***	-0.066	-0.408***	0.287***	0.125***	0.327***	0.172***	-				
Pod length (cm)	-0.116**	-0.053	-0.097*	0.113	0.136***	0.050	-0.006	0.042	-			
Seeds/ pod	-0.522***	-0.103*	-0.384***	0.260***	0.062	0.176***	0.059	0.392***	0.154***	-		
100 seed weight (g)	-0.505***	-0.256***	-0.327***	0.326***	0.063	0.156***	0.031	0.321***	0.193***	0.386***	-	
Grain yield (t/ha)	-0.793***	-0.288***	-0.591***	0.361***	0.142***	0.419***	0.165***	0.481***	0.069*	0.466***	0.525***	-

*Values with *, ** and *** implies significant at P = .05, P < .01 and P < .001 respectively*

Table 4. Mean values of FI, FS, AUDPC, Yield, r and HR for the 100 cowpea lines grown at Kabanyolo and Serere, Uganda, in 2014

Line	Kabanyolo						Serere					
	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)
SEC1T × ACC23	11.14 (17.54)	0.038	2.33	49.00	R	1.333	100.00 (85.93)	0.000	4.27	112.93	S	0.773
SEC1T × Alegi	15.43 (19.63)	0.006	3.00	77.00	MR	2.074	100.00 (85.93)	0.030	4.40	112.70	S	1.016
SEC2W × SEC1T	23.52 (29.13)	0.032	4.00	91.00	MR	1.889	100.00 (85.93)	0.011	4.07	115.97	S	0.599
SEC2W × ACC2	0.00 (4.05)	0.000	1.00	35.00	R	2.111	100.00 (85.93)	0.007	4.47	131.83	S	1.129
SEC3B × SEC2W	3.33 (9.00)	0.016	1.67	42.00	R	2.074	100.00 (85.93)	0.036	3.67	102.43	MR	0.722
SEC4W × SEC5T	2.78 (8.46)	0.015	1.33	38.50	R	1.815	100.00 (85.93)	0.003	4.73	138.37	S	0.874
SEC5T × SEC3B	1.69 (7.26)	0.002	1.67	51.33	R	2.148	100.00 (85.93)	0.036	3.20	87.97	MR	0.672
SEC5T × SEC4W	2.22 (7.88)	0.007	1.67	49.00	R	2.370	100.00 (85.93)	0.042	2.67	88.43	MR	0.694
SEC5T × ACC12	2.23 (7.88)	0.000	1.67	57.17	R	2.037	100.00 (85.93)	0.037	3.67	104.30	MR	0.738
ACC12 × SEC2W	0.00 (4.05)	0.000	1.00	35.00	R	2.148	100.00 (85.93)	0.023	3.60	106.63	S	0.571
ACC12 × SEC3B	2.78 (4.86)	0.015	1.67	44.33	R	2.481	100.00 (85.93)	0.043	2.93	91.70	MR	0.725
ACC12 × SEC5T	0.57 (5.56)	0.008	1.33	40.83	R	2.593	100.00 (85.93)	0.018	4.20	125.53	S	0.508
ACC2 × SEC1T	28.00 (28.46)	0.009	3.67	86.33	MR	1.519	100.00 (85.93)	0.023	4.13	127.17	S	0.611
ACC2 × ACC12	0.00 (4.05)	0.000	1.00	35.00	R	1.556	100.00 (85.93)	0.038	3.33	98.47	MR	0.651
ACC23 × SEC2W	8.31 (14.51)	0.013	2.33	59.50	R	1.667	100.00 (85.93)	0.020	3.00	93.10	MR	0.630
ACC23 × SEC3B	5.61 (12.74)	0.017	1.33	45.50	R	1.667	100.00 (85.93)	0.020	3.27	94.03	MR	0.910
ACC23 × SEC4W	5.00 (10.43)	0.002	2.00	54.83	R	1.593	100.00 (85.93)	0.038	2.93	82.60	MR	1.043
ACC23 × ACC12	0.00 (4.05)	0.000	1.00	35.00	R	1.963	100.00 (85.93)	0.019	3.20	96.83	MR	0.680
ACC26 × SEC1T	9.68 (16.55)	0.024	2.33	60.67	R	1.926	100.00 (85.93)	0.012	2.93	89.60	MR	1.011
ACC26 × ACC2	0.00 (4.05)	0.000	1.00	35.00	R	1.741	100.00 (85.93)	0.007	5.00	142.33	S	0.598
Alegi	9.14 (15.94)	0.020	2.33	61.83	R	1.963	100.00 (85.93)	0.009	3.73	116.67	S	0.875
Alegi × SEC3B	14.17 (16.36)	0.007	2.33	71.17	MR	1.815	100.00 (85.93)	0.019	3.73	112.23	S	0.563
Alegi × SEC4W	6.67 (11.68)	0.010	2.00	54.83	R	2.259	100.00 (85.93)	0.040	2.93	80.27	MR	0.513
Alegi × SEC5T	3.90 (9.51)	0.003	1.67	50.17	R	2.444	100.00 (85.93)	0.009	3.73	115.27	S	0.886
Alegi × ACC12	7.33 (14.23)	0.014	2.33	56.00	R	1.704	100.00 (85.93)	0.044	2.93	94.97	MR	1.494
Alegi × ACC2	15.03 (16.86)	0.004	2.33	64.17	R	2.000	100.00 (85.93)	0.011	4.40	123.90	S	1.333

Line	Kabanyolo						Serere					
	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)
NE13	3.33 (9.00)	0.009	1.67	49.00	R	1.593	100.00 (85.93)	0.012	3.60	107.33	S	0.708
NE15	0.00 (4.05)	0.000	1.00	35.00	R	2.222	100.00 (85.93)	0.052	2.13	70.40	R	1.044
NE18	3.89 (9.51)	0.017	1.67	44.33	R	2.000	100.00 (85.93)	0.043	3.07	97.53	MR	0.985
NE19	32.43 (31.02)	0.008	3.33	94.50	MR	1.111	100.00 (85.93)	0.019	3.67	108.97	S	0.750
NE20	15.86 (20.52)	0.021	3.00	73.50	MR	2.259	100.00 (85.93)	0.020	3.13	98.93	MR	0.777
NE21	1.69 (7.26)	0.013	1.67	44.33	R	2.333	100.00 (85.93)	0.031	3.20	92.87	MR	0.844
NE23	0.00 (4.05)	0.000	1.00	35.00	R	1.815	100.00 (85.93)	0.029	2.80	95.43	MR	0.800
NE30	0.00 (4.05)	0.000	1.00	35.00	R	1.407	100.00 (85.93)	0.015	4.20	119.47	S	0.995
NE31	0.00 (4.05)	0.000	1.00	35.00	R	1.778	100.00 (85.93)	0.024	3.40	96.37	MR	1.144
NE39	4.44 (11.41)	0.027	2.00	47.83	R	1.778	100.00 (85.93)	0.038	3.20	86.10	MR	0.610
NE4	12.88 (18.95)	0.008	3.00	81.67	MR	1.852	100.00 (85.93)	0.037	3.27	96.60	MR	0.686
NE40	12.00 (15.09)	0.025	2.00	45.50	R	1.630	100.00 (85.93)	0.047	3.87	115.97	S	0.789
NE41	1.67 (7.22)	0.012	1.33	38.50	R	1.333	100.00 (85.93)	0.028	4.13	125.30	S	0.818
NE44	14.66 (20.19)	0.028	2.67	57.17	R	1.926	100.00 (85.93)	0.020	3.67	105.00	MR	0.830
NE46	3.45 (9.11)	0.006	2.00	58.33	R	2.444	100.00 (85.93)	0.035	3.00	99.87	MR	0.834
NE48	9.33 (13.46)	0.004	2.33	66.50	R	2.037	100.00 (85.93)	0.034	2.73	84.70	MR	0.818
NE49	19.59 (22.35)	0.008	3.00	89.83	MR	1.852	100.00 (85.93)	0.048	3.00	86.33	MR	1.031
NE5	1.15 (6.52)	0.003	1.33	45.50	R	2.667	100.00 (85.93)	0.015	4.20	122.97	S	0.805
NE50	11.67 (17.99)	0.023	2.67	64.17	R	2.148	100.00 (85.93)	0.013	4.87	140.47	S	0.751
NE51	0.00 (4.05)	0.000	1.00	35.00	R	2.778	100.00 (85.93)	0.046	2.40	73.27	MR	0.893
NE53	3.89 (10.48)	0.016	2.00	52.50	R	1.704	100.00 (85.93)	0.027	3.13	90.30	MR	0.738
NE55	2.22 (7.88)	0.014	1.67	46.67	R	1.852	100.00 (85.93)	0.031	3.73	99.87	MR	1.141
NE6	3.89 (9.50)	0.017	1.67	39.67	R	1.741	100.00 (85.93)	0.000	4.07	116.90	S	0.881
NE70	0.00 (4.05)	0.000	1.00	35.00	R	1.630	100.00 (85.93)	0.030	2.53	81.67	MR	0.863
NE71	20.41 (22.49)	0.022	2.67	74.67	MR	1.185	100.00 (85.93)	0.036	3.73	106.87	S	0.653
SECOW1T	23.10 (28.86)	0.046	4.00	87.50	MR	1.926	100.00 (85.93)	0.014	3.93	118.07	S	1.246
SECOW2W	0.56 (5.53)	0.007	1.33	36.17	R	2.222	100.00 (85.93)	0.055	2.87	86.33	MR	0.878
SECOW3B	18.82 (24.19)	0.023	4.00	85.17	MR	1.963	100.00 (85.93)	0.028	3.07	95.43	MR	0.941

Line	Kabanyolo						Serere					
	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)
SECOW4W	2.78 (8.46)	0.015	1.33	38.50	R	2.259	100.00 (85.93)	0.040	2.53	76.77	MR	1.000
SECOW5T	5.55 (12.87)	0.023	2.33	53.67	R	2.741	100.00 (85.93)	0.007	3.27	97.53	MR	1.359
WC10	13.61 (17.80)	0.005	3.00	70.00	R	2.370	100.00 (85.93)	0.028	3.47	106.87	S	0.855
WC15	4.67 (11.87)	0.016	2.00	56.00	R	2.000	100.00 (85.93)	0.033	3.67	107.33	S	0.990
WC16	28.82 (32.11)	0.014	4.33	105.00	MR	1.444	100.00 (85.93)	0.025	2.73	82.37	MR	0.735
WC17	0.00 (4.05)	0.000	1.00	35.00	R	1.481	100.00 (85.93)	0.033	3.40	96.60	MR	0.853
WC18	19.84 (19.63)	0.003	2.33	63.00	R	1.926	100.00 (85.93)	0.014	3.93	112.47	S	0.801
WC2	6.67 (11.68)	0.004	2.00	58.33	R	2.444	100.00 (85.93)	0.025	3.27	95.67	MR	0.694
WC20	8.47 (12.90)	0.006	2.00	57.17	R	2.704	100.00 (85.93)	0.022	3.47	94.27	MR	0.937
WC21	9.60 (14.74)	0.002	2.33	67.67	R	2.000	100.00 (85.93)	0.015	3.20	95.67	MR	1.174
WC26	11.30 (16.81)	0.022	2.33	56.00	R	1.630	100.00 (85.93)	0.025	3.73	118.77	S	0.793
WC27	9.76 (16.62)	0.023	2.67	72.33	MR	2.333	100.00 (85.93)	0.044	3.47	108.03	S	0.874
WC29	42.84 (41.01)	0.039	5.00	116.67	S	1.041	100.00 (85.93)	0.017	3.60	103.60	MR	0.737
WC30	0.00 (4.05)	0.000	1.00	35.00	R	1.667	100.00 (85.93)	0.022	3.40	106.87	S	0.885
WC32	5.00 (10.43)	0.019	1.00	35.00	R	1.778	100.00 (85.93)	0.023	4.27	125.07	S	0.628
WC32A	5.00 (10.43)	0.019	1.67	39.67	R	2.333	100.00 (85.93)	0.047	3.13	94.73	MR	0.744
WC33	2.78 (8.46)	0.015	1.67	44.33	R	1.963	100.00 (85.93)	0.000	4.13	124.37	S	0.761
WC35A	3.09 (8.77)	0.003	1.67	49.00	R	2.111	100.00 (85.93)	0.032	3.73	107.80	S	0.640
WC35B	0.00 (4.05)	0.000	1.00	35.00	R	2.037	100.00 (85.93)	0.020	3.33	105.93	S	0.770
WC35C	23.71 (28.64)	0.008	4.33	105.00	MR	2.037	100.00 (85.93)	0.010	3.87	112.47	S	0.820
WC36	32.18 (34.32)	0.012	4.67	128.33	S	1.630	100.00 (85.93)	0.043	3.27	105.47	MR	0.786
WC37	16.19 (17.52)	0.005	2.33	60.67	R	1.556	100.00 (85.93)	0.016	4.27	116.20	S	0.641
WC41	22.23 (21.05)	0.022	1.67	53.67	R	2.296	100.00 (85.93)	0.010	3.73	106.87	S	0.758
WC42	0.00 (4.05)	0.000	1.00	35.00	R	2.481	100.00 (85.93)	0.039	3.47	103.83	MR	0.779
WC44	13.46 (15.95)	0.015	2.33	64.17	R	1.667	100.00 (85.93)	0.035	3.00	89.83	MR	0.550
WC46	14.44 (20.06)	0.028	2.33	53.67	R	1.963	100.00 (85.93)	0.059	2.73	84.47	MR	0.694
WC48	0.00 (4.05)	0.000	1.33	40.83	R	1.963	100.00 (85.93)	0.010	3.33	110.83	S	0.981
WC48A	14.53 (16.57)	0.004	2.33	64.17	R	1.926	100.00 (85.93)	0.028	4.00	119.23	S	0.669

Line	Kabanyolo						Serere					
	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)	FI[a] (%)	r	FS[b]	AUDPC	HR	Yield (t/ha)
WC5	14.52 (19.97)	0.022	3.00	72.33	MR	1.778	100.00 (85.93)	0.029	3.73	104.77	MR	0.816
WC52	5.77 (11.02)	0.020	1.67	46.67	R	2.148	100.00 (85.93)	0.041	3.53	101.03	MR	0.820
WC53	7.84 (14.99)	0.034	2.00	43.17	R	1.815	100.00 (85.93)	0.023	2.60	84.00	MR	0.612
WC55	13.34 (21.34)	0.016	3.33	82.83	MR	1.370	100.00 (85.93)	0.000	4.33	127.63	S	0.873
WC58	24.62 (28.26)	0.014	4.33	112.00	S	2.185	100.00 (85.93)	0.039	3.13	94.73	MR	1.106
WC62	15.08 (20.38)	0.023	3.00	73.50	MR	2.148	100.00 (85.93)	0.035	3.00	93.33	MR	0.702
WC63	4.24 (9.81)	0.007	2.00	50.17	R	2.111	100.00 (85.93)	0.024	3.13	99.63	MR	0.867
WC64	0.00 (4.05)	0.000	1.00	35.00	R	2.148	100.00 (85.93)	0.048	3.27	94.03	MR	0.855
WC66	0.00 (4.05)	0.000	1.00	35.00	R	2.074	100.00 (85.93)	0.013	4.60	129.73	S	0.793
WC67	0.00 (4.05)	0.000	1.00	35.00	R	1.963	100.00 (85.93)	0.019	4.00	110.83	S	0.870
WC67B	17.97 (22.41)	0.031	3.33	81.67	MR	1.593	100.00 (85.93)	0.029	3.07	96.60	MR	1.210
WC68	14.05 (22.22)	0.031	3.00	78.17	MR	2.259	100.00 (85.93)	0.059	3.47	107.80	S	0.897
WC69	2.87 (8.56)	0.015	1.67	44.33	R	1.481	100.00 (85.93)	0.012	4.13	128.33	S	0.723
WC7	19.77 (23.33)	0.008	3.33	93.33	MR	1.963	100.00 (85.93)	0.031	3.20	99.17	MR	0.637
WC8	1.82 (7.41)	0.013	1.33	36.17	R	2.148	100.00 (85.93)	0.029	3.27	100.57	S	0.778
LSD (0.05)	18.12	0.032	2.03	44.98		0.921	0.00	0.035	1.10	29.90		0.370
CV (%)	56.50	85.70	49.80	39.10		29.40	0.00	61.80	20.00	17.80		41.70

FI = Final incidence, FS = Final severity, AUDPC = Area under disease progress curve, r = Apparent infection rate and HR = Host resistance ratings. [a] = Incidence at 81 days after planting; Figures in parenthesis = arcsine transformed values; [b] = Severity at 81 days after planting; AUDPC (35-70) = severity (1.0-2.0); AUDPC (71-105) = severity (2.1-3.0) and AUDPC (> 105) = severity (> 3.0); SEC = Secow; ACC = Accession; R = Resistant; MR = Moderately resistant; and S = Susceptible

The apparent rate of infection (r) in Kabanyolo was between 0.000 - 0.046 while Serere recorded between 0.000 - 0.059. The smaller range of ‘r’ recorded in Kabanyolo compared to Serere was suggestive of disease incidence being lower in Kabanyolo and with a more steady progression in infection compared to Serere. Nagesha and Nargund [38] reported a wide variation in apparent infection rate (r) in sunflower while Mbong et al. [23] reported similar findings in cowpea with the values varying among genotypes and attributed these observations to the differences in sowing dates and the effect of the scab disease on the genotypes. According to Parry [39], the more resistant a variety is, the smaller the ‘r’ value. Since the initial incidence of the disease in Serere was high (mean incidence = 81.26%) and almost all the genotypes were affected by the end of the evaluation with incidence reaching 100% for most of the genotypes, the difference between the final and initial incidence recorded in Serere were of a narrow range. These results did not delineate genotypes as being resistant or susceptible based on the use of the ‘r’ alone since a lower ‘r’ value recorded in Serere did not reflect more resistance. This suggests that the use of ‘r’ alone as an index to measure resistance to disease may not yield useful results. The ‘r’ estimated was suggested to quantify the rate of disease development and estimate cultivar resistance [28], and to evaluate the effectiveness of fungicide application [26].

The values for AUDPC and hence resistance rating showed that the genotypes behaved differently at the two locations with Serere recording a higher range of AUDPC and thus, showing most of the lines to be susceptible to the disease. Lines such as WC 29, WC 36 and WC 58 were found to be susceptible (AUDPC > 105 which is equivalent to a mean severity score > 3.0) at Kabanyolo but were moderately resistant (AUDPC 104, 105 and 95 respectively) to scab at Serere. On the other hand, cowpea lines such as ACC12 × Secow 2W, ACC26 ×ACC2, Alegi, Alegi × ACC2, NE 50, WC 10 and WC 66 rated as resistant (AUDPC 35-70) to scab disease in Kabanyolo were found to be susceptible to scab in Serere (AUDPC > 105 i.e. mean severity score > 3.0). The variability in responses of these lines to scab where lines which were resistant in one location were found to be susceptible in the other location suggested the existence of different pathotypes of the fungus (Afutu et al., unpublished) at the two sites. A significant G×L interaction observed could be explained in part by the different levels of disease pressure in the two locations and the existence of different biotypes of the fungus (Afutu et al., unpublished). On the other hand, 11 lines were found to have shown a consistent reaction to the scab disease at both locations. These were Secow 3B, NE 4, NE 20, NE 32, NE 49, WC 5, WC 7, WC 16, WC 62, and WC 67B which were moderately resistant at both locations and NE 15 which was rated as resistant at both locations. The stability in both locations suggested that these 11 lines could serve as good parents for resistance breeding to scab disease.

Mean cowpea yield recorded in Kabanyolo was between 1.0 (WC 29) to 2.8 (NE 51) t/ha while mean yields recorded at Serere were between 0.5 (ACC 12 × Secow 5T) and 1.63 (Alegi × ACC2) t/ha (Table 4) but none of the lines was found to be stable in yield in the two locations which was attributable to the significant difference in the disease pressure in the two locations and the significant negative effect of scab disease on the genotypes [15]. There was significant negative correlation between both disease incidence and AUDPC with yield (-0.8 and -0.6 respectively) (Table 3) suggesting that Serere would have lower yields than Kabanyolo due to the high disease incidence and AUDPC recorded in Serere. According to Ali et al. [40], the loss of active leaf area results in less photosynthetic available region during grain filling stage which eventually results in lower yield.

3.4 Principal Component Analysis (PCA)

Principal component analysis was used to analyze the structure of the interrelationships among the 100 genotypes and to explain these genotypes in terms of their common underlying dimensions. The results of the R-mode principal component analysis (PCA) are presented in Table 5. Four principal components were obtained based on components with Eigen values greater than 1 [41], and factor loadings of ±0.3 [30] explaining 62.28% of the total variance. The first principal component (PC1) explained 35.34% of the total variance observed and this was mainly due to the high negative factor loadings of disease incidence, severity and AUDPC and high positive factor loadings of days to 50% flowering, pods per plant, seeds per pod, 100 seed weight and grain yield. The second principal component (PC2) was primarily positively correlated with the number of branches per plant, peduncles per plant and pods per peduncle. These together explained 10.50% of the total variation observed and was due to the high positive factor loadings of the yield traits. Principal components 3 and 4 were weighted on pod length (cm) and apparent infection rate (r) respectively. These were due to the high positive factor loadings of pod length and apparent infection rate (r) respectively with each explaining 8.66% and 7.78% respectively, of the total variation in the cowpea lines. Chiorato et al. [42] suggested that the greatest loading coefficient in the last component indicated a redundancy of the descriptor (trait) associated to the component and therefore, the apparent infection rate (r) may be described as redundant descriptor in the description and characterization of the lines evaluated.

3.5 Cluster Analysis (CA)

The results of cluster analysis constructed using Ward's method based on all 13 traits are presented in Fig. 1. The 100 lines were grouped into three major clusters when the dendogram was cut at a distance of 1.5 (k = 3). Cluster 1 was the heaviest weighted comprising 58 lines which were all moderately resistant to the scab disease. Cluster 2 comprised 9 cowpea lines consisting of 5 susceptible and 4 moderately resistant lines. The third Cluster comprised 33 lines which were made up of 24 resistant lines and 9 moderately resistant lines. Cluster analysis performed based on the 4 disease indexes alone i.e. scab disease incidence, severity, AUDPC and apparent infection rate (r) (Fig. 2) produced clusters with similar patterns to the clusters produced based on 13 traits. The dendogram was cut at a distance of 1.5 (k = 4). Cluster 1 consisted 33 lines while cluster 2 was made up of 24 lines, with both clusters consisting lines which were moderately resistant to scab. Cluster 3 was made up of 10 lines comprising 5 susceptible lines and 5 moderately resistant lines while cluster 4 consisted 33 lines comprising 24 resistant and 9 moderately resistant lines. Both figures showed clear patterns of grouping of the lines, where lines with close resistance ratings were clustered together suggesting that the disease indexes had a significant effect on most of the other traits. Thus, even in cluster 3 (Fig. 1) and cluster 4 (Fig. 2) where there was a mix of resistant and moderately resistant lines, unique and clearly distinct sub clustering of lines based on resistance levels was observed. The same phenomenon was observed in the pattern of clustering comparing cluster 2 (Fig. 1) and cluster 3 (Fig. 2) which had a mix of susceptible and moderately resistant lines implying that for the purposes of screening and categorization of cowpea lines based on resistance to scab, cluster analysis based on scab disease indexes alone generated reliable information comparable to information that was generated by disease indexes together with yield and yield parameters involved in the analysis.

Table 5. Rotated component matrix of four factor model explaining 62.28% of the total variance for traits

Disease and agronomic trait	PC1	PC2	PC3	PC4	Communalities
Disease incidence	**-0.91**	-0.16	0.02	0.12	0.87
Disease severity	**-0.72**	-0.10	0.02	0.10	0.55
Apparent infection rate (r)	-0.10	-0.04	-0.03	**0.93**	0.88
AUDPC	**-0.78**	-0.13	0.06	0.06	0.63
Days to 50% flowering	**0.53**	-0.12	0.37	0.09	0.44
No. of branches	-0.02	**0.74**	0.41	0.05	0.72
Peduncles/ plant	0.32	**0.74**	0.02	0.01	0.65
Pods/ peduncle	0.08	**0.57**	-0.32	-0.13	0.45
Pods/ plant	**0.67**	0.23	-0.04	0.10	0.52
Pod length (cm)	0.05	-0.07	**0.79**	-0.08	0.64
Seeds/ pod	**0.64**	-0.02	0.19	-0.02	0.45
100 seed weight (g)	**0.55**	-0.05	0.32	-0.38	0.56
Grain yield (t/ha)	**0.78**	0.22	0.02	-0.28	0.74
Eigen values	4.59	1.37	1.13	1.01	
Percentage of total variance	35.34	10.50	8.66	7.78	
Cumulative percentage of variance	35.34	45.84	54.50	62.28	

4. CONCLUSION

There was variation in the traits among the 100 lines which could be used in selecting parental lines for improving yields and resistance to the cowpea scab disease. One line (NE15) was found to be resistant to the disease at both locations and high yielding and could be used in the cowpea improvement programme to breed for resistance to the scab disease.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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