



Investigating the Genetics of Scab Resistance and Yield Components in Cowpea (*Vigna unguiculata*)

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Authors' contributions

This work was carried out in collaboration among all authors. Authors EA and FK contributed to the conceptualization. Authors EA, SNTTA and PDL were involved in the investigation. Authors EA, FK, SNTTA and PAA handled data curation and analysis. Authors EA and MOA contributed to the writing. All authors contributed to the writing, review and editing. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/ijpss/2025/v37i55461>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/134389>

Original Research Article

Received: 25/02/2025

Accepted: 20/04/2025

Published: 14/05/2025

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ABSTRACT

Background: Economically important traits have complex inheritance and are environmentally influenced, thus making selection for such traits more difficult. Breeding efforts to develop varieties with resistance to the disease require an understanding of the genes that confer resistance to the disease in terms of their heritability and gene action in Ugandan germplasm.

Purpose: This study was conducted to determine the relative importance of GCA and SCA, and hence additive and non-additive effects in the inheritance of resistance to scab infections, and heritability of yield and yield-related traits in the new breeding populations.

Research Method: Eleven cowpea lines (four resistant, five moderately resistant and two susceptible) were selected as parents and crossed using a half diallel mating design to generate information on the genetics of control of scab disease resistance, yield and yield-related traits in cowpea (*Vigna unguiculata*). 55 F₂ progenies and their parents (11) were evaluated at two locations (Kabanyolo and Serere) using an 11 × 6 lattice design. Data were collected for grain yield and yield related traits such as 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 (g). Data were analysed using Griffing's method 4 model 1. Phenotypic correlation coefficients (rp) for scab disease incidence, severity, AUDPC, yield and yield-related traits were determined using IBM SPSS Statistics version 22.

Findings: Combined analysis of variance for the two locations revealed highly significant differences ($P < 0.001$ and $P < 0.01$) among the genotypes for all 12 traits studied but showed no significant genotype by location (G × L) interaction effect on any of the traits. Coefficient of genetic determination in the narrow and broad sense, analogous to narrow and broad sense heritability, respectively, were generally low, ranging from 1.23 % - 27.12% (h^2) and 7.4 % - 71.91 % (H^2). The low values of Baker's ratio (BR) (< 0.5) for most of the traits suggested that non-additive gene effects were more important except for number of pods per plant which indicated additive gene effects were more important (BR = 0.80) and number of seeds per pod (BR = 0.5) which indicated both additive and non-additive gene effects were important. Alegi, NE15 and NE48 were identified as parental lines with negative general combining ability (GCA) effects for improvement of scab disease resistance for both locations while SECOW5T was identified as the only parent with high positive GCA for improvement of both 100 seed weight (g) and grain yield (K/ha) of cowpea across the two locations. A cross between WC35B*WC66 had the best SCA effects for scab disease resistance.

Conclusion: The study confirmed earlier reports that additive gene effects were important for scab disease resistance. Six crosses, viz. Alegi*NE50, Alegi*WC36, ACC12.2W*SECOW5T, NE15*SECOW5T, NE48*WC36 and WC10*WC36 were identified as the best hybrids (crosses) for the improvement of cowpea yields across the locations.

Originality/Value: The study reveals potential parental lines and crosses for enhancing scab resistance and yield in cowpea, contributing to breeding strategies and crop improvement efforts.

Keywords: Coefficient of genetic determination; narrow sense; broad sense; diallel; phenotypic variability; genetic variability; combining ability.

1. INTRODUCTION

The cowpea plant (*Vigna unguiculata*) is a well-known legume plant because of its high nutritional content and adaptability as a food source. Diseases attack cowpea plants, just like they do all other crops, and hence stunt their development and reduce their yield (Megalingam et al., 2024). As a crop native to tropical regions, cowpeas exhibit sensitivity to low temperatures, so the time of sowing is key in order to reduce the incidence of disease (Kim et al., 2024; Afutu et al., 2016). Scab disease, caused by the

fungus *Sphaceloma* sp., is one of the most devastating diseases of cowpea, capable of causing 100% yield loss under severe infections (Mbong et al., 2012). When the disease is severe, the leaf spots coalesce to larger lesions, giving the affected area a rough, deformed appearance. In some cases, the centres of these older spots could later fall out, causing shot holes (Nakimera et al., 2024). None of the recently released varieties of the crop is resistant to the disease, and yet the disease is widespread in the country (Afutu et al., 2016a). Breeding efforts to develop varieties with resistance to the disease

require an understanding of the genes that confer resistance to the disease in terms of their heritability and gene action in Ugandan germplasm. Earlier studies on the subject were carried out by screening 80 cowpea lines for sources of resistance (Iceduna *et al.*, 1994), followed by Nakawuka and Adipala (1997) and Tumwegamire *et al.* (1998), who studied the inheritance and genetics of resistance to the scab disease. Recent studies to identify new sources of resistance showed that there were cowpea landraces in Uganda with wide horizontal resistance that could be used as parents in a breeding programme (Afutu *et al.*, 2016b; 2016c) to develop resistant varieties for farmers. There is, therefore, a need to understand the heritability and gene action within the identified populations.

Economically important traits have complex inheritance and are environmentally influenced, thus making selection for such traits more difficult (Smalley *et al.*, 2004). Heritability is based on the hypothesis that individuals more closely related are more likely to resemble one another than those less closely related (Falconer and MacKay, 1996) and can also be estimated in the broad sense (H^2) or narrow sense (h^2), but it is the narrow-sense heritability which depends on the additive portion of genetic variance that is used to predict how quickly selection can change the average phenotype of the population (Falconer, 1960). Heritability estimates help the breeder in determining the resource allocation necessary to effectively select for the trait of interest and to achieve maximum genetic gain with the use of minimum time and resources (Smalley *et al.*, 2004).

Nakawuka and Adipala (1997) suggested that general combining ability (GCA) effects were more important than specific combining ability (SCA) effects in the inheritance to scab disease resistance, however, Tumwegamire *et al.*, (1998) suggested both GCA and SCA effects were important for both foliar and pod resistance to scab infections as high estimates were obtained for both broad-sense and narrow-sense heritability for resistance to foliar ($H^2 = 93.8\%$; $h^2 = 79.8\%$) and pod ($H^2 = 97.0\%$; $h^2 = 84.5\%$) scab infections, thus, indicating both additive and non-additive gene actions were important to scab resistance. Broad sense heritability for traits such as pod length ($H^2 = 76.0\%$) (Roquib and Patnaik, 1990), the number of seeds per pod ($H^2 = 75.3\%$) and seed size measured as 100-seed weight ($H^2 = 94.4\%$) (Siddique and Gupta, 1991)

have been reported. Additive gene effects were reported to be more important than non-additive effects for pod length inheritance (Ogunbodede and Fatunla, 1985); however, additive, dominance and epistatic gene effects were observed to be of equal importance in conditioning inheritance for the number of seeds per pod (Drabo *et al.*, 1985). Any estimate of heritability is only relevant to a particular population in a particular set of environments, as different populations have different gene frequencies. This study was, therefore, conducted to determine the relative importance of GCA and SCA, and hence additive and non-additive effects in the inheritance of resistance to scab infections, and heritability of yield and yield-related traits in the new breeding populations.

2. MATERIALS AND METHODS

2.1 Experimental Materials

Following field evaluations of 100 cowpea lines carried out at the Makerere University Agricultural Research Institute – Kabanyolo (MUARIK) during the first raining season (April-July) of 2014 to identify sources of resistance (Afutu *et al.*, 2016b), 20 cowpea lines with varying levels of resistance were selected and later challenged in the screen house with five isolates of the scab fungus (*Sphaceloma* sp.) obtained from different districts and agroecological zones of Uganda to identify lines with wider horizontal resistance to the scab disease (Afutu *et al.*, 2016c). Subsequently, eleven cowpea lines (Table 1) comprising 4 resistant, 5 moderately resistant and 2 susceptible lines were selected based on their resistance levels and yield potential and used as parental lines.

2.2 Crossing and Advancing of F₁s to F₂

Crosses were made among the eleven selected parents in the screen house according to Griffing's (1956) diallel method 4 model 1 mating design. Flowers to be used as females were emasculated in the evening using a sterile scalpel blade regularly sterilised using alcohol (95%) and hand pollinated in the morning hours of the next day (Tumwegamire *et al.*, 1998). To ensure that enough successful crosses were obtained, flowers at all plant growth stages were used in crossing and tagged accordingly. In order for inferences from analysis to be limited to the parents themselves and the resultant crosses, the parents were considered as a fixed sample (Nakawuka and Adipala, 1997).

Table 1. List of selected parents and their resistance ratings

Genotype	Cultivar type	Resistance rating	Yield potential (t/ha)	Maturity
Acc 12*Sec 2W	Inbred line	Resistant	1.36	Early
NE 15	Landrace	Resistant	1.63	Medium
WC 35B	Landrace	Resistant	1.40	Medium
WC 66	Landrace	Resistant	1.43	Medium
Alegi	Local	Moderate	1.42	Early
NE 48	Landrace	Moderate	1.43	Medium
NE 50	Landrace	Moderate	1.45	Early
Secow 5T	Improved	Moderate	2.05	Early
WC 10	Landrace	Moderate	1.61	Medium
WC 36	Landrace	Susceptible	1.21	Medium
Sun shine	Introduction	Susceptible	0.72	Medium

Acc = Accession; Sec = Secow

At maturity, the F₁ seeds from successful crosses were harvested separately and were grown in the field at MUARIK together with the parents to advance F₁s to F₂. The F₁ seeds and the parents were planted in two rows, 1.5 m long and spaced 60 cm between rows and 30 cm within rows and the field was laid out in a randomised complete block design (RCBD) with three replications. A field previously cultivated with Sorghum (*Sorghum bicolor*) was selected in order to reduce the incidence of diseases and insect pests of cowpea. The experiment was weeded three times and sprayed with Roket @ 44 EC (Profenofos 40% + Cypermethrin 4%) insecticide at the rate of 30 ml to 15 L of water to control insect pests three times, one at four weeks after emergence, second at flower initiation stage and the third during pod setting. No fertiliser or fungicide was applied during the entire growing period.

2.3 Evaluation of F₂ Plants and Parents for Combining Ability Studies

The F₂ plants and their parents were evaluated in two locations, 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. The experiments were laid out in an 11× 6 alpha lattice design with 3 replications at each site. Each replication had 11 blocks, with each block having 6 plots. Each genotype was planted on a plot with an area of 1.5 m × 1.2 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 experiment was planted on fields previously cultivated with cowpea to create high disease pressure conditions in the field. Weed and insect

control were as described for advancing of F₁s to F₂s.

2.4 Data Collection and Analysis

Five plants were randomly selected from each plot and tagged at six weeks after planting, and scab disease incidence and severity data were collected at seven-day intervals (Mbong *et al.*, 2010a) for six consecutive weeks. Scab disease severity scores were determined 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 (Nakawuka and Adipala, 1997). Scab disease incidence was estimated by counting all individual plants with scab disease symptoms in each plot and expressed as a ratio over the total number of plants in each plot.

Data were collected for grain yield and yield related traits such as 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 (g). Yield (Kg ha⁻¹) was estimated from the yield per plot. The plot means for yield and yield-related traits, scab disease incidence and severity values were estimated using Microsoft Excel and the means were subjected to the analysis of variance (ANOVA) procedure using Genstat edition 14 (Payne *et al.*, 2011). Mean severity scores were used to estimate the area under disease progress curve (AUDPC) for both parental lines and F₂ plants, as according to Campbell and Madden (1990);

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

Where “t” is the time of each reading, “y” is the percentage of affected foliage at each reading and “n” is the number of readings. The variable “t” represents days after planting. Per cent incidence data were Arcsine transformed (Ezueh and Amusan, 1988) before being used for further analysis.

Means of scab disease incidence, severity, yield and yield related traits were analysed using restricted maximum likelihood (REML) procedure in GenStat® edition 14 (Payne et al., 2011) to determine the general and specific combining ability (GCA and SCA) effects using Griffing’s method 4 model 1 (Griffing, 1956) and the t-test was calculated and used to measure the significance of the GCA and SCA effects (Tumwegamire et al., 1998) using Microsoft Excel for Windows. The parents were considered as fixed and therefore, the model fitted was the fixed effects model of Singh and Chaudhary (2007):

$$Y_{ij} = \mu + GCA_i + GCA_j + SCA_{ij} + e_{ij}$$

Where: Y_{ij} = the observed mean; μ = overall population mean; GCA_i = effect of the i^{th} parent; GCA_j = effect of the j^{th} parent; SCA_{ij} = interaction effect of the i^{th} parent and j^{th} parent; and e_{ij} = experimental error.

The GCA effects for the parents, SCA effects for the crosses and their standard errors were calculated according to Kearsey and Pooni (1996). Coefficient of genetic determination in the narrow (CGD-NS) and broad sense (CGD-BS), analogues of the narrow sense (h^2) and broad sense heritability (H^2) respectively, were estimated using the variance component method as according to Ruming (2004), as follows:

$$CGD - NS \approx h^2 = \frac{(2 * \delta^2 GCA)}{(2 * \delta^2 GCA + \delta^2 SCA + \delta^2 e)}$$

$$CGD - BS \approx H^2 = \frac{(2 * \delta^2 GCA + \delta^2 SCA)}{(2 * \delta^2 GCA + \delta^2 SCA + \delta^2 e)}$$

Where; h^2 = narrow sense heritability; H^2 = broad sense heritability; $\delta^2 GCA$ = variance of general combining ability; $\delta^2 SCA$ = variance of specific combining ability of parents; $\delta^2 e$ = error variance.

The relative contribution of GCA and SCA were estimated using Baker’s ratio (BR) (Baker, 1978), computed as:

$$BR = \frac{(2 * \delta^2 GCA)}{(2 * \delta^2 GCA + \delta^2 SCA)}$$

Where; $\delta^2 GCA$ and $\delta^2 SCA$ are the variance components of GCA and SCA, respectively. Phenotypic correlation coefficients (rp) for scab disease incidence, severity, AUDPC, yield and yield-related traits were determined using data obtained from the 55 crosses alone (without parents) from the two locations using IBM SPSS Statistics version 22 (IBM Corporation, 2013).

3. RESULTS AND DISCUSSION

3.1 Phenotypic Variability

The results of analysis of variance for scab disease incidence, severity, yield and yield-related traits for Kabanyolo and Serere are shown in Table 2. Location-wise, in Kabanyolo, there were significant differences among the genotypes for scab disease incidence ($P < 0.01$), severity ($P < 0.001$), the number of pods per plant ($P < 0.05$), 100 seed weight ($P < 0.001$) and grain yield ($P < 0.05$) indicating significant diversity for these traits among lines evaluated. On the other hand, scab disease incidence was the only disease parameter that showed significant difference ($P < 0.05$) among the genotypes in Serere, attributable to the extreme drought conditions experienced at the location during the evaluation, thereby suppressing the growth and spread of the fungus compared to Kabanyolo (Table 3). The scab fungus has been reported to be more severe under wet conditions (Allan, 1983; Mbong et al., 2010b), thus explaining this observation. The genotypes also showed highly significant differences ($P < 0.001$) in grain yield (Kg/ha) and the days to flowering, significant differences ($P < 0.01$) for yield related traits such as the number of pods per plant and pod length (cm), while the number of pods per peduncle, number of branches and peduncles were shown to be significant at $P < 0.05$. These results imply a significant and wide diversity (Noubissie et al., 2011) in the yield and yield-related traits among the 66 lines evaluated, from which potentially high-yielding and early maturing lines could be selected in a breeding programme. According to Acquah (2007), response to selection and thus rapid genetic gain in breeding for a trait is enhanced when there is a wide diversity in the particular trait among the germplasm from which selections are to be made as the two (genetic gain and amount of variation within the population) are directly proportional.

Table 2. Analysis of variance for scab disease incidence, severity, yield and yield-related traits at different locations

Location	Source	Incidence	Severity ^a	AUDPC	Days to flowering	No. of Pods/peduncle	No. of branches	No. of Pods/plant	No. of seeds/pod	Pod length ^a	No. of peduncles	Seed weight (g)	Yield (Kg/ha)
Kabanyolo	Rep	(2) 5188.1***	(2) 1.37***	(2) 1286.97***	(2) 142.24***	(2) 0.11	(2) 5.11	(2) 72.5	(2) 51.25*	(2) 600.3	(2) 80.9	(2) 3.49	(2) 1331975*
	Block	(28) 190*	-	(29) 115.74*	(29) 19.96*	(28) 0.14	(28) 1.96	(29) 416.4	(28) 14.87	-	(29) 171.4	(29) 2.62*	(29) 643142**
	Genotype	(65) 356.04**	(65) 0.30***	(65) 106.09	(65) 19.37	(65) 0.11	(65) 1.33	(65) 450.36*	(65) 14.07	(65) 250.7	(65) 132.75	(65) 9.37***	(65) 554819.98*
	Residual	(102) 197.4	(130) 0.1296	(101) 82.86	(101) 14.29	(102) 0.12	(102) 1.75	(101) 294.6	(102) 12.44	(130) 246.1	(101) 126.3	(100) 1.64	(101) 317065
	LEE	(100) 195.62	-	(103) 88.4	(106) 15.25	(102) 0.12	(104) 1.80	(106) 314.94	(106) 12.90	-	(106) 134.10	(104) 1.80	(106) 357948.38
	SED	11.42	0.29	7.67	3.19	0.29	1.09	14.49	2.93	12.81	9.46	1.1	488.5
Serere	Rep	(2) 1717.1***	(2) 0.222*	(2) 325.75***	(2) 10.24**	(2) 1.47***	(2) 9.88***	(2) 38.67	(2) 47.29***	(2) 7.26	(2) 37.14	(2) 1.23	(2) 544658***
	Block	(29) 343.90*	-	(29) 60.29*	(30) 4.18***	(28) 0.17	(30) 1.35***	(30) 87.5***	(28) 6.82	(29) 4.40	(30) 38.57***	(28) 1.06	(30) 73700***
	Genotype	(65) 345.63*	(65) 0.07	(65) 53.43	(65) 3.88***	(65) 0.26*	(65) 0.95*	(65) 63.09**	(65) 6.61	(65) 6.47**	(65) 21.00*	(65) 14.07***	(65) 42928.90**
	Residual	(101) 215.6	(130) 0.07	(101) 42.28	(100) 1.53	(102) 0.17	(100) 0.51	(100) 28.89	(102) 6.02	(101) 3.22	(100) 11.78	(101) 0.91	(100) 20116
	LEE	(106) 235.13	-	(105) 45.28	(106) 1.789	(102) 0.17	(105) 0.59	(107) 34.10	(103) 6.18	(103) 3.42	(107) 14.00	(101) 0.95	(106) 24117.36
	SED	12.52	0.21	5.49	1.09	0.33	0.63	4.77	2.03	1.51	3.06	0.79	126.8

^a Empty spaces (i.e. no values) for block mean squares and Lattice effective error (LEE) implies blocking was not significant for the traits and therefore were analyzed using RCBD. Figures in brackets represent degrees of freedom; Values with *, ** and *** implies significant at P = .05, P < .01 and P < .001 respectively

Table 3. Mean values of scab disease indexes and Yield of parents and crosses grown at Kabanyolo and Serere in April-July, 2016

Genotype	Pedigree	Kabanyolo			Serere				
		Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)	Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)
SECOW5T	Parent	76.67 (65.00)	2.47	66.27	1429.64	59.67 (54.70)	2.00	42.00	687.04
SECOW5T*Sunshine	Cross	62.67 (52.90)	2.40	59.03	2155.57	53.67 (47.51)	2.00	44.10	731.49
SECOW5T*WC10	Cross	61.33 (55.76)	2.40	55.30	2029.65	90.67 (74.35)	2.00	51.57	638.89
SECOW5T*WC36	Cross	66.67 (55.30)	2.27	57.40	1077.79	80.00 (69.06)	2.00	49.35	435.19
ACC122W	Parent	40.00 (38.41)	2.20	59.03	1837.05	93.33 (78.55)	2.00	50.87	474.08
ACC122W*SECOW5T	Cross	70.00 (60.76)	2.33	49.70	2505.58	83.67 (69.15)	2.00	50.63	566.67
ACC122W*ALEGI	Cross	53.33 (47.53)	2.13	54.60	1025.93	68.33 (56.84)	2.00	49.00	490.75
ACC122W*NE15	Cross	86.67 (74.31)	2.40	60.43	1148.16	95.33 (80.10)	2.00	52.73	490.75
ACC122W*NE48	Cross	60.00 (51.24)	2.20	60.67	1775.94	66.67 (56.12)	2.00	52.03	512.97
ACC122W*NE50	Cross	63.33 (54.22)	2.33	60.43	1450.01	62.67 (53.59)	2.00	49.23	464.82
ACC122W*Sunshine	Cross	53.33 (47.21)	2.07	50.40	1687.05	45.33 (42.60)	2.33	53.90	672.23
ACC122W*WC10	Cross	66.67 (58.84)	2.33	62.53	1814.83	84.33 (69.87)	2.00	51.57	531.49
ACC122W*WC35B	Cross	73.33 (63.08)	2.60	62.53	1735.20	44.67 (42.18)	2.00	49.82	414.82
ACC122W*WC36	Cross	83.33 (68.94)	2.80	72.10	2044.46	74.33 (64.44)	2.00	49.23	427.78
ACC122W*WC66	Cross	96.67 (81.30)	2.80	66.73	1477.79	86.67 (72.82)	2.00	49.00	640.75
ALEGI	Parent	58.00 (51.13)	2.13	59.50	1172.23	64.00 (53.61)	2.00	47.95	435.19
ALEGI*SECOW5T	Cross	70.00 (60.85)	2.60	60.90	1951.87	79.00 (66.34)	2.00	50.40	527.78
ALEGI*NE48	Cross	93.35 (78.55)	2.27	59.03	1475.94	51.33 (46.04)	2.00	52.03	468.52
ALEGI*NE50	Cross	56.67 (49.13)	2.20	53.20	2925.95	95.33 (80.10)	2.00	52.50	392.60
ALEGI*Sunshine	Cross	86.67 (74.31)	2.87	69.07	1088.90	62.67 (52.79)	2.00	47.72	459.26
ALEGI*WC10	Cross	63.33 (56.91)	2.13	56.70	1114.82	79.67 (67.43)	2.00	50.63	546.30
ALEGI*WC36	Cross	57.00 (49.64)	2.33	57.87	2166.68	83.33 (72.38)	2.00	52.85	948.16
NE15	Parent	63.33 (56.91)	2.27	56.70	1485.20	96.67 (81.30)	2.00	50.17	559.26
NE15*SECOW5T	Cross	64.33 (57.45)	2.00	54.83	2316.69	93.33 (78.55)	2.00	53.67	929.64
NE15*ALEGI	Cross	90.33 (76.53)	2.33	61.83	1092.60	93.33 (78.55)	2.00	52.15	729.64
NE15*NE48	Cross	54.33 (47.81)	2.13	57.40	1672.24	71.33 (61.62)	2.00	45.97	429.63
NE15*NE50	Cross	53.33 (47.21)	2.13	57.40	1764.83	83.67 (69.15)	2.00	49.47	679.64
NE15*Sunshine	Cross	41.00 (40.05)	2.07	55.53	1062.97	71.00 (58.54)	2.00	51.10	490.75

Table 3. Continued

Genotype	Pedigree	Kabanyolo				Serere			
		Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)	Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)
NE15*WC10	Cross	90.00 (72.04)	2.73	67.90	1242.60	70.00 (60.76)	2.00	47.72	596.30
NE15*WC35B	Cross	76.33 (65.51)	2.40	61.60	2311.13	78.67 (66.15)	2.00	47.95	618.52
NE15*WC36	Cross	75.67 (62.18)	2.60	64.87	1231.49	80.00 (66.93)	2.00	47.02	775.93
NE15*WC66	Cross	50.00 (45.61)	2.27	56.47	1664.83	72.67 (59.13)	2.00	47.95	635.19
NE48	Parent	65.00 (54.23)	2.13	57.40	1785.20	75.00 (61.09)	2.00	48.07	412.97
NE48*SECOW5T	Cross	86.67 (71.69)	3.00	64.63	1655.57	75.00 (63.85)	2.33	56.93	637.04
NE48*NE50	Cross	46.67 (43.36)	2.00	56.00	2051.87	66.67 (58.86)	2.00	43.63	450.00
NE48*Sunshine	Cross	83.33 (72.38)	2.27	61.60	1346.31	80.00 (63.79)	2.00	45.03	666.67
NE48*WC10	Cross	70.00 (60.85)	2.53	66.97	1798.16	96.00 (80.68)	2.00	55.07	614.82
NE48*WC36	Cross	66.67 (55.30)	2.07	56.70	2409.28	52.33 (46.65)	2.00	46.90	687.04
NE50	Parent	86.67 (74.31)	2.73	66.50	966.67	72.00 (59.17)	2.00	48.07	494.45
NE50*SECOW5T	Cross	85.33 (73.53)	2.53	66.03	1761.13	70.00 (57.28)	2.00	49.93	622.23
NE50*Sunshine	Cross	75.33 (61.92)	2.47	63.23	1479.64	67.00 (55.29)	2.00	49.47	464.82
NE50*WC10	Cross	70.00 (60.85)	2.47	65.10	1251.86	63.00 (53.14)	2.00	50.17	405.56
NE50*WC36	Cross	56.00 (48.35)	2.87	67.90	1016.67	80.00 (70.46)	2.00	48.77	401.86
Sunshine	Parent	86.00 (71.07)	2.20	52.27	1270.38	80.00 (66.93)	2.00	53.20	468.52
WC10	Parent	48.33 (44.27)	2.00	56.00	1533.35	58.00 (50.30)	2.00	52.97	396.30
WC10*Sunshine	Cross	80.00 (63.79)	2.53	57.63	1996.31	70.00 (57.28)	2.00	49.00	477.78
WC10*WC36	Cross	56.67 (49.22)	2.20	58.57	2466.69	60.00 (54.91)	2.00	48.53	594.45
WC35B	Parent	76.67 (65.83)	2.87	66.50	1677.79	(71.67 (61.93)	2.33	54.37	761.12
WC35B*SECOW5T	Cross	90.00 (73.92)	2.87	66.50	1920.39	45.67 (42.68)	2.00	47.83	472.23
WC35B*ALEGI	Cross	70.00 (57.31)	2.40	58.80	2064.83	75.33 (64.63)	2.00	50.63	803.71
WC35B*NE48	Cross	65.33 (54.92)	2.20	50.17	1640.75	88.67 (72.66)	2.00	50.63	555.56
WC35B*NE50	Cross	90.33 (76.53)	3.27	77.93	1075.93	64.67 (54.63)	3.00	70.70	414.82
WC35B*Sunshine	Cross	90.00 (76.32)	3.13	73.03	2042.61	48.33 (44.45)	2.00	47.83	705.56
WC35B*WC10	Cross	83.33 (72.38)	2.60	64.63	1238.90	73.33 (62.77)	2.00	51.33	475.93
WC35B*WC36	Cross	76.67 (61.56)	2.40	61.37	2240.76	60.00 (54.91)	2.33	60.67	551.86
WC35B*WC66	Cross	50.00 (45.28)	2.07	56.00	1803.72	68.67 (59.98)	2.00	49.00	375.93

Table 3. Continued

Genotype	Pedigree	Kabanyolo				Serere			
		Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)	Final Incidence (%)	Final Severity	AUDPC	Yield (Kg/ha)
WC36	Parent	60.00 (51.45)	2.27	60.20	2592.61	56.33 (49.69)	2.00	47.13	640.75
WC36*Sunshine	Cross	70.00 (60.76)	2.33	59.27	1085.19	80.00 (66.71)	2.00	54.60	546.30
WC66	Parent	60.00 (54.99)	2.27	53.90	1851.87	71.00 (61.32)	2.00	48.30	640.75
WC66*SECOW5T	Cross	66.67 (55.39)	2.27	57.63	1925.94	77.67 (65.75)	2.00	47.37	683.34
WC66*ALEGI	Cross	60.00 (52.28)	2.13	54.83	1935.20	69.00 (60.23)	2.00	53.32	546.30
WC66*NE48	Cross	81.33 (65.06)	2.27	61.13	1364.83	63.67 (53.68)	2.00	47.83	727.78
WC66*NE50	Cross	66.37 (55.39)	2.33	59.50	1287.05	45.67 (42.86)	2.00	44.80	509.26
WC66*Sunshine	Cross	64.33 (54.12)	2.60	63.93	1588.90	88.00 (72.45)	2.00	50.17	729.64
WC66*WC10	Cross	96.67 (81.30)	3.53	80.03	1887.05	46.67 (43.36)	2.33	61.37	551.86
WC66*WC36	Cross	50.00 (45.02)	2.20	57.87	1983.35	71.33 (58.69)	2.00	48.07	661.12
LSD (0.05)		22.60	0.58	15.32	1011.50	25.31	0.42	11.00	294.10
CV (%)		23.50	14.90	15.60	37.30	25.60	12.80	13.50	32.00

Table 4. Combined analysis of variance for scab disease incidence, severity, yield and yield related traits across two locations

Source	Degrees of freedom	Incidence	Severity	AUDPC	Days to flower in g	No. of Pods/ peduncle	No. of branches	No. of Pods/ plant	No. of seeds/ pod	Pod length	No. of peduncles	Seed weight (g)	Yield (Kg/ha)
Location (L)	1	192.8	9.12	7084.26	1040.06	1.23	185.56	106857.04	990.39	1456.68	24239.44	157.41	81589856**
REP	4	6905.2***	1.59***	1612.72***	152.48***	1.58***	14.99***	111.17	98.54***	607.56***	118.04	4.73**	1876633***
Genotype (G)	65	215.2*	0.17**	67.60***	8.86***	0.15***	0.75**	191.12***	7.92***	85.74**	54.05***	13.35***	228772***
G x L	65	124.8	0.04	19.46	3.33	0.05	0.38	77.26	2.91	42.96	24.5	0.9879	82136
Pooled error	204 -260	215.95	0.1	66.63	8.52	0.14	1.19	173.86	9.54	3.42	73.77	1.378219	191032.9
SED		3.46	0.07	1.92	0.69	0.09	0.26	3.11	0.73	0.44	2.02	0.28	103.02
CV (%)		24.32	14.14	14.70	5.65	17.82	25.13	39.20	22.27	70.51	44.16	8.35	38.85

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

Results of analysis of variance for scab disease incidence, severity, yield and yield-related traits for the two locations combined are presented in Table 4. The results showed significant differences among the genotypes for all 12 traits studied. Traits such as the AUDPC, days to flowering, the number of pods per peduncle and per plant, number of peduncles, 100 seed weight and grain yield were shown to be highly significant ($P < 0.001$), scab disease severity, number of branches and pod length were significantly different ($P < 0.01$) suggesting that differences exist among the cowpea genotypes across the locations, indicating high variability. Disease incidence across the locations was also shown to be significantly different ($P < 0.05$). On the other hand, the data showed that there was no significant genotype by location ($G \times L$) interaction effects among the genotypes for any of the 12 traits studied, suggesting that the effects of the locations on the genotypes for the traits were negligible. This observation suggests that the genotypes (parents and crosses) performed consistently across the two locations, indicating that there would be no need to develop different cultivars for the two locations (Acquaah, 2007).

3.2 Genetic Variability, Heritability and Gene Action

The results of analysis of variance for combining ability of the 11 parents and resulting crosses for scab disease severity, yield and yield-related traits evaluated at the different locations are presented in Table 5. At MUARIK, general combining ability of the selected parents showed significant differences for only scab disease severity ($P < 0.05$) and 100 seed weight ($P < 0.001$) while the specific combining ability of the resultant crosses showed highly significant differences ($P < 0.001$) in disease severity and 100 seed weight, and significant differences ($P < 0.05$) for the number of pods per plant and grain yield (Kg/ha), indicating significant diversity among these traits. The results indicated a wide variation in these traits both among the parents and the resultant crosses, thus suggesting a high potential for selections among both the parents and crosses for improvement in these traits, especially 100 seed weight and grain yield. The coefficient of genetic determination values – narrow sense (h^2) were generally low ranging from 0.00 % (number of branches) to 25.12 % (100 seed weight) while the coefficient of genetic determination – broad sense (H^2) ranged between 0.00 % (number of branches) and 81.83

% (100 seed weight). Values of Baker's ratio estimated for all the traits in MUARIK were less than 0.5 ($BR < 0.5$), suggesting that the traits were under non-additive gene effects, implying that the heritability of the traits from the parents was not highly predictable, thus explaining the very low values obtained for the narrow sense heritability.

Evaluation at location two (Serere) showed that the general combining ability of the selected parents were highly significantly different ($P < 0.001$) for pod length (cm) and 100 seed weight (g) while GCA for traits such as number of pods per peduncle and per plant were significant at $P < 0.01$ with GCA for the number of peduncles and grain yield being significant at $P < 0.05$. On the other hand, the specific combining ability of the crosses showed highly significant difference ($P < 0.001$) for days to flowering and 100 seed weight (g), significant difference ($P < 0.01$) for grain yield (Kg/ha) while SCA for number of pods per plant and pod length were significant at $P < 0.05$. These results suggested the performance of parents (GCA) and progenies (SCA) was more variable at Serere than in Kabanyolo, suggesting a wider significant diversity among the genotypes, which could be attributed to the extremely harsh conditions experienced at Serere. Also, values for CGD narrow sense (h^2) were generally low, ranging from 0.00 for scab severity to 30.96 % for 100 seed weight, while CGD broad sense (H^2) was between 14.20 % (scab severity) and 94.40 % (100 seed weight). Apart from the number of pods per peduncle and pod length (cm) which had Baker's ratio greater than 0.5, all the remaining traits had BR values < 0.5 suggesting that additive gene action was more important for traits such as number of pods per plant and pod length indicating progress in breeding for these traits could be made through selection of parents with high GCA for the traits (Olweny, 2016).

The results of the analysis of variance for combining ability for the two locations are presented in Table 6. The results showed highly significant differences ($P < 0.001$) between the two locations for all the traits studied except for the number of pods per peduncle, which showed significance at $P < 0.01$, indicating significant variation between the two locations and thus the environments within which the lines were evaluated. GCA for the combined analysis showed significant differences for only three of the parameters, viz. 100 seed weight ($P < 0.001$), number of pods per peduncle ($P < 0.01$)

and scab severity ($P < 0.05$). On the other hand, SCA showed significant differences for only two parameters, 100 seed weight ($P < 0.001$) and scab severity ($P < 0.01$). These observations were particularly important as the main thrust of this study was towards identifying promising lines to be selected for improvement in yield and resistance to scab disease. GCA by location interaction (GCA \times L) effects were only significant ($P < 0.001$) for pod length while SCA by location interaction (SCA \times L) effects were highly significant ($P < 0.001$) for both pod length and 100 seed weight, and, the number of pods per plant showed a significant SCA \times L interaction effects at $P < 0.05$ suggesting that the performance of the parents (GCA) and crosses (SCA) were inconsistent in the two environments. This further suggests that for the selection of these traits, specific crosses (progenies) will have to be selected for the different environments to derive the benefits in the hybrids (progenies). The combined analysis also showed very low CGD narrow sense (h^2) (1.23 % - 27.12 %) and broad sense (H^2) between 7.4 % (number of peduncles) and 71.91 % (100 seed weight), suggesting that most of these traits studied were not highly predictable. This was confirmed by values of BR estimated for the combined locations, which suggested that all the traits had values < 0.5 except for number of seeds per pod (0.50) and number of pods per plant (0.80). The results further suggested that for a trait such as the number of seeds per pod, both additive and non-additive gene action are important while for a trait such as the number of pods per plant, additive gene action was more important than non-additive effects implying that heritability of the trait from the parents is very predictable.

3.3 Combining Ability Effects

Results of the general combining ability effects of the 11 selected parents for scab disease severity, yield and yield-related traits in Kabanyolo are shown in Table 7. The results showed that none of the parents had significant GCA effects for the number of pods per peduncle and branches. SECOW5T variety showed significant positive GCA effects for days to flowering.

(DTF) ($P < 0.05$), seeds per pod (SPP) ($P < 0.05$), grain yield ($P < 0.01$) and 100 seed weight ($P < 0.001$) suggesting that the cultivar performed far better in the crosses than predicted for these specific traits and therefore

could be selected as a good parent for breeding for high number of seeds per pod, high seed weight and grain yield. This was not surprising as SECOW5T is an improved cultivar released for cultivation in the country. On the other hand, ACC12.2W, Alegi, NE15 and Sunshine showed significant negative GCA effects for 100 seed weight suggesting that these three genotypes would not be good as parents for breeding to increase seed weight, but cultivar WC35B could be selected as it had a significant positive GCA effect for the trait. Among the parents which had negative GCA effects for scab disease severity, viz., ACC12.2W, Alegi, and WC36, only NE15 and NE48 had significant negative effects suggesting that these two parents were good combiners in reducing the severity of scab disease. These results implied that additive gene effects were important for this trait and significant breeding progress could be achieved through effective selection of good parents. Surprisingly, parents such as WC10 (moderately resistant) and WC35B (resistant line) had significant positive GCA effects on scab severity, suggesting that they were not good combiners for reducing scab disease severity.

The results of specific combining ability (SCA) effects for the crosses evaluated in MUARIK are presented in Table 8. A total of 35 crosses showed negative SCA effects for scab disease severity, out of which two (ACC12.2W*SS and WC35B*WC66) showed significant negative effects, suggesting that these crosses performed better than predicted and implying that the use of these crosses could result in a significant reduction in the severity of scab disease. On the other hand, eight crosses showed significant positive SCA effects for scab severity, an indication that these crosses were poor performers and could not be selected for resistance to the disease. Further, eight crosses had significant positive SCA effects ($P < 0.001$ to $P < 0.05$) for 100 seed weight, suggesting that these crosses could be selected for the improvement of seed weight. Crosses ACC12.2W*5T, ALEGI*NE50, NE48*WC36 and WC10*WC36 had significant positive SCA effects for grain yield (Kg/ha), which implied that the hybrid effects of these crosses could be harnessed to achieve high grain yields. Among the 55 crosses evaluated in MUARIK, only the cross between WC10*Sunshine showed significant negative SCA effects for days to flowering, signifying that this cross could be selected for the purpose of reducing the number of days to flowering in the location.

Table 5. Analysis of variance for combining ability studies with variance components and coefficient of genetic determination for scab disease severity, yield and yield-related traits at different locations

Location	Source	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
Kabanyolo	GCA	0.098*	5.796	0.047	0.513	189.8	5.546	88.8	48.51	4.329***	146138
	SCA	0.107***	6.261	0.036	0.496	158.9*	5.142	101.9	51.88	2.47***	195720*
	Residual	0.043	5.085	0.040	0.598	104.980	4.301	82.033	44.700	0.600	119316.130
	σ GCA	0.0061	0.079	0.001	0.000	9.424	0.138	0.752	0.423	0.414	2980.21
	σ SCA	0.0638	1.176	0	0.000	53.92	0.841	19.867	7.181	1.87	76403.88
	Baker's ratio	0.16	0.12	1.00	0.00	0.25	0.25	0.07	0.11	0.31	0.07
	CGDNS (%)	10.20	2.5	3.65	0.00	10.6	5.1	1.5	1.6	25.12	3
	CGDBS (%)	63.7	20.78	3.65	0.00	40.93	20.62	20.67	15.23	81.83	40.84
	GCA	0.018	0.836	0.153**	0.201	29.86**	2.65	4.469***	9.995*	8.16***	17257*
	SCA	0.027	1.265***	0.070	0.262	18.86*	2.280	1.755*	6.329	3.887***	14653**
Serere	Residual	0.023	0.596	0.056	0.197	11.370	2.060	1.142	4.667	0.315	8039.120
	σ GCA	0.000	0.027	0.011	0.001	2.055	0.066	0.37	0.592	0.872	1024.21
	σ SCA	0.004	0.669	0.015	0.064	7.493	0.221	0.613	1.662	3.572	6613.88
	Baker's ratio	0.00	0.07	0.59	0.03	0.35	0.37	0.55	0.42	0.33	0.24
	CGDNS (%)	0.00	4.04	23.45	0.69	17.89	5.45	29.64	15.76	30.96	12.26
	CGDBS (%)	14.20	54.77	39.52	25.12	50.51	14.6	54.24	37.89	94.4	51.87

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

Table 6. Combined analysis of variance for general and specific combining ability across two locations for scab disease severity, yield and yield related traits

Source	Df	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
Location (L)	1	4.134***	442.33***	0.416**	74.243***	43981.29***	410.225***	682.66***	10033.12***	73.48***	34977717***
GCA	10	0.087*	4.057	0.171**	0.417	152.348	5.628	47.41	39.72	11.69***	87754.1
SCA	44	0.089**	4.033	0.051	0.399	91.806	4.124	51.08	29.09	5.18***	126509.8
GCA*L	10	0.030	2.576	0.029	0.301	67.264	2.568	42.31***	18.79	0.8	75640.8
SCA*L	44	0.045	3.493	0.055	0.359	85.999*	3.297	53.39***	29.12	1.18***	83862.93
LEE	204- 260	0.033	2.841	0.048	0.397	57.954	3.180	1.14	24.59	0.46	63677.62
σ GCA		0.003	0.082	0.008	0.006	4.727	0.170	0.284	1.163	0.605	672.961
σ SCA		0.022	0.270	0.000	0.020	2.903	0.414	0.000	0.000	2.000	21323.432
σ GCA*L		0.000	0.000	0.000	0.000	1.034	0.000	4.574	0.000	0.037	1329.242
σ SCA*L		0.011	0.652	0.007	0.000	28.046	0.117	52.252	4.531	0.719	20185.309
Baker's ratio		0.23	0.40	1.00	0.40	0.80	0.50	1.00	1.00	0.40	0.10
CGDNS (%)		8.80	4.20	22.16	3.00	9.8	8.40	0.90	7.40	27.12	1.23
CGDBS (%)		39.00	11.06	22.16	7.60	12.30	18.61	0.90	7.40	71.91	20.76

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

Table 7. General combining ability (GCA) effects for scab disease severity, yield and yield-related traits in Kabanyolo

Parent	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ pod	Pod length	No. of peduncles	Seed weight	Grain yield (Kg)
SECOW5T	0.04	1.56*	0.07	0.14	1.00	1.54*	-0.97	2.16	1.47***	261**
ACC12.2W	-0.03	-0.77	-0.03	-0.31	2.59	-0.61	-2.68	1.64	-0.53*	0
ALEGI	-0.10	-0.49	0.11	0.00	4.52	-0.23	2.95	0.94	-0.71**	-58
NE15	-0.14*	1.04	0.07	0.34	7.70*	-0.36	-3.04	4.26*	-0.70**	-125
NE48	-0.15*	-0.20	0.07	0.35	2.79	0.01	-2.11	0.94	0.51*	-23
NE50	0.03	-0.86	-0.03	0.16	0.19	-0.83	3.02	-1.13	0.27	-92
Sunshine	0.05	-0.65	0.03	-0.23	-1.98	-0.07	-1.89	-0.12	-0.60**	-167
WC10	0.13*	0.74	-0.04	-0.11	0.72	-0.88	3.91	-0.92	-0.23	-28
WC35B	0.18**	-0.47	-0.08	-0.06	-5.55	0.41	5.44*	-3.58	0.75**	172
WC36	-0.03	-0.18	-0.10	0.08	-3.87	-0.22	-2.40	-0.91	-0.26	86
WC66	0.02	0.31	-0.07	-0.35	-8.08**	1.24*	-2.19	-3.29	0.03	-26
SE _{GCA}	0.07	0.72	0.06	0.25	3.26	0.66	2.88	2.12	0.25	109.78

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

Table 8. Specific combining ability (SCA) effects for scab disease severity, yield and yield related traits in Kabanyolo

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No of peduncles	Seed weight (g)	Grain yield (Kg/ha)
5T*SS	-0.11	-0.11	0.16	-0.74	1.66	-1.66	3.43	-0.64	0.82	291.88
5T*WC10	-0.20	6.67***	-0.10	-0.14	-9.89	-0.06	-2.02	-7.58	0.19	153.50
5T*WC36	-0.18	-2.08	-0.03	0.00	-1.79	-1.49	2.63	-0.52	1.59*	-943.19**
ACC12.2W*5T	-0.10	-1.96	0.23	-0.98	0.20	1.08	3.03	-6.07	0.30	651.40*
ACC12.2W*ALEGI	-0.16	1.41	-0.13	-0.50	-5.14	1.81	-2.77	1.08	-0.84	-460.63
ACC12.2W*NE15	0.15	-2.96	-0.10	-0.23	10.69	0.50	2.97	3.44	-0.23	-329.62
ACC12.2W*NE48	-0.04	-0.34	-0.11	0.42	6.15	-0.02	2.97	10.31	0.64	110.18
ACC12.2W*NE50	-0.10	-0.15	0.00	0.63	-9.36	-1.06	-4.23	-5.56	0.67	58.65
ACC12.2W*SS	-0.38*	-0.52	-0.06	0.12	-4.52	-0.52	2.87	-5.83	-0.40	215.05
ACC12.2W*WC10	-0.19	1.49	-0.01	-0.01	-1.01	-0.14	-4.10	-1.19	0.13	134.07
ACC12.2W*WC35B	0.02	1.87	0.04	0.22	-11.03	1.34	-2.27	-5.40	1.34*	-264.63
ACC12.2W*WC36	0.43*	0.63	0.08	0.12	8.81	-1.36	0.36	10.57	-0.40	182.75
ACC12.2W*WC66	0.38*	0.51	0.06	0.23	5.20	-1.62	1.17	-1.35	-1.20	-297.23
ALEGI*5T	0.23	-1.93	-0.23	-0.98	-16.06	-0.23	-2.49	-10.67	0.75	-17.91
ALEGI*NE48	0.09	0.93	0.43*	0.83	8.24	0.44	-3.11	0.56	-2.36***	-347.68
ALEGI*NE50	-0.16	0.81	-0.16	1.01	17.37*	0.86	42.07***	10.73	-0.65	1274.12***
ALEGI*SS	0.49**	-1.04	-0.22	-1.26*	-18.62*	0.40	-2.68	-8.22	2.73***	-284.91
ALEGI*WC10	-0.32	-1.94	0.22	0.61	7.23	-1.69	-9.54	6.53	0.59	-480.10
ALEGI*WC36	0.03	-1.00	0.24	0.05	10.97	-0.36	-4.26	4.54	0.44	379.13
NE15*5T	-0.33	0.44	0.12	0.74	26.60**	-1.37	1.90	22.25***	0.82	514.47
NE15*ALEGI	0.14	2.50	0.09	0.15	-10.04	0.01	-4.24	-6.36	1.72	-490.08

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE15*NE48	-0.01	4.19*	0.13	-0.16	18.54*	0.80	0.15	2.97	-3.14***	82.94
NE15*NE50	-0.19	-1.14	0.21	0.01	15.56	2.28	-3.17	2.72	-0.65	259.22
NE15*SS	-0.28	0.72	0.15	-0.27	-6.98	-0.77	1.49	-2.43	0.60	-196.09
NE15*WC10	0.31	-2.61	-0.43*	-0.01	-11.83	0.20	-4.22	-2.54	-1.15	-236.82
NE15*WC35B	-0.08	-1.41	-0.07	0.22	-3.56	-0.44	-3.98	0.38	0.21	554.42
NE15*WC36	0.33	3.35	-0.03	0.70	-13.30	0.26	4.13	-7.47	-0.85	-357.81
NE15*WC66	-0.04	-3.08	-0.07	-1.12	-25.67**	-1.46	4.95	-12.96*	2.68***	199.36
NE48*5T	0.68***	1.78	-0.23	-0.34	0.34	-2.74	2.19	-3.37	-0.44	-363.89

Table 8. Continued

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE48*NE50	-0.31	0.03	-0.11	-0.70	-12.27	1.25	-1.04	-3.79	3.71***	469.17
NE48*SS	-0.06	0.62	-0.19	0.78	0.42	1.33	3.08	4.78	0.54	-284.01
NE48*WC10	0.12	-1.99	0.20	-0.34	-3.32	-0.66	-2.90	-2.30	0.39	41.83
NE48*WC36	-0.18	-3.62	-0.02	-1.25*	-11.90	2.60	5.21	-5.58	3.27***	644.21*
NE50*5T	0.03	-1.87	-0.10	0.24	-6.07	-3.11	-4.02	-5.55	-2.23***	-206.52
NE50*SS	-0.05	1.45	0.27	0.28	11.11	0.80	-4.29	6.78	-1.72**	-192.99
NE50*WC10	-0.13	-2.86	0.01	0.50	10.96	-0.81	-12.15	5.35	-0.57	-404.25
NE50*WC36	0.43*	2.79	0.09	-1.04	-13.12	-0.69	-5.39	-8.17	-1.05	-624.38*
WC10*SS	-0.08	-4.21*	-0.07	-0.16	2.42	1.81	-3.37	-0.75	-1.07	430.12
WC10*WC36	-0.33	0.33	0.10	0.89	12.18	1.01	-4.50	6.91	-1.16	737.45*
WC35B*5T	0.22	2.10	0.26	0.47	2.93	-1.90	-5.25	2.06	-1.00	-119.88
WC35B*ALEGI	-0.11	-1.52	-0.12	0.26	8.57	0.69	-9.00	4.47	-0.78	320.61
WC35B*NE48	-0.26	-1.25	-0.06	0.58	-7.68	-1.90	-7.91	-2.81	-1.39*	-122.41
WC35B*NE50	0.63***	-1.79	-0.27	-0.28	-16.19	1.85	-6.18	-2.05	2.36***	-477.95
WC35B*SS	0.47*	1.68	-0.05	-0.17	-3.18	-0.07	-2.98	-3.02	0.24	350.72
WC35B*WC10	-0.14	4.81**	0.05	-0.36	5.06	0.08	42.96***	2.48	-0.32	-441.96
WC35B*WC36	-0.19	-1.41	0.12	-0.56	20.54*	0.59	-1.71	2.79	-0.81	209.65
WC35B*WC66	-0.56**	-3.08	0.10	-0.39	4.54	-0.23	-3.69	1.10	0.15	-8.56
WC36*SS	-0.12	-0.91	-0.31	0.67	-9.67	1.10	2.29	-3.81	-0.83	-417.83
WC66*5T	-0.22	-3.05	-0.07	1.74**	2.09	11.49***	0.60	10.10	-0.81	40.13
WC66*ALEGI	-0.22	1.78	-0.12	-0.16	-2.52	-1.93	-3.99	-2.67	-1.60*	107.45
WC66*NE48	-0.03	-0.35	-0.05	0.18	1.48	-1.11	1.35	-0.77	-1.23	-230.32
WC66*NE50	-0.14	2.74	0.05	-0.66	2.02	-1.36	-1.60	-0.45	0.15	-155.07
WC66*SS	0.10	2.32	0.32	0.76	27.37**	-2.40	0.15	13.15*	-0.91	88.06
WC66*WC10	0.95***	0.30	0.03	-0.98	-11.79	0.27	-0.16	-6.90	2.97***	66.17
WC66*WC36	-0.22	1.92	-0.25	0.41	-2.72	-1.65	1.22	0.75	-0.20	190.02
SE _{SCA}	0.19	2.02	0.18	0.69	9.16	1.85	8.10	5.98	0.69	308.95

5T = SECOW 5T; SS= Sunshine; Values with *, ** and *** implies significant at P = .05, P < .01 and P < .001 respectively

Table 9. General combining ability (GCA) effects for scab disease severity, yield and yield related traits in Serere

Parent	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ pod	Pod length	No. of peduncles	Seed weight	Grain yield
SECOW5T	-0.01	-0.04	0.09	0.13	0.08	-0.03	0.59	-0.37	2.13***	36.01
ACC12.2W	-0.01	-0.44	0.05	0.04	-1.51	0.28	0.05	-0.40	-0.29	-56.09*
ALEGI	-0.05	-0.39	0.27***	0.08	2.43*	-1.00*	-1.07**	1.5*	-0.94***	7.61
NE15	-0.05	0.47*	0.05	0.24	3.16**	0.24	-0.26	1.45*	-0.85***	34.31
NE48	-0.01	-0.25	0.09	-0.06	0.85	0.53	0.25	-0.16	0.68***	12.41
NE50	0.06	0.41	0.01	0.02	-2.09*	-0.26	-0.53	-0.99	-0.13	-91.89**
SS	-0.01	0.11	-0.02	0.05	-1.05	-0.18	0.08	-0.21	-0.19	16.71
WC10	-0.01	0.14	-0.17*	0.03	-0.25	-0.84*	-0.24	-0.63	-0.79***	-6.99
WC35B	0.10*	-0.07	-0.17*	-0.33*	-2.60*	0.74	1.50***	-1.85**	1.16***	-34.39
WC36	-0.01	-0.18	-0.09	-0.18	1.35	0.10	-0.77*	1.16	-0.23	41.11
WC66	-0.01	0.25	-0.10	-0.02	-0.33	0.41	0.41	0.50	-0.55**	41.21
SE _{GCA}	0.05	0.25	0.07	0.14	1.07	0.46	0.34	0.69	0.18	28.50

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

Table 10. Specific combining ability (SCA) effects for scab disease severity, yield and yield related traits in Serere

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
5T*SS	-0.02	0.64	-0.25	-0.63	-2.45	0.89	-1.51	0.27	2.60***	28.28
5T*WC10	-0.02	1.79**	-0.11	0.01	-3.07	0.46	1.81	-0.30	1.22*	18.46
5T*WC36	-0.02	0.36	-0.18	-0.48	-5.27	-1.77	0.64	-2.76	0.30	-217.38**
ACC12.2W*5T	-0.02	0.45	0.00	0.68	0.47	0.52	-0.27	-0.28	-1.59**	8.07
ACC12.2W*ALEGI	0.02	0.04	-0.18	-0.26	-4.21	1.67	0.99	-4.25*	0.81	-36.22
ACC12.2W*NE15	0.02	-2.81	-0.30	-0.41	-4.57	-0.13	1.52	-2.53	-0.02	-126.14
ACC12.2W*NE48	-0.03	-0.12	0.34	-0.10	-0.45	2.10	1.01	0.80	1.11*	31.92
ACC12.2W*NE50	-0.10	-1.33*	0.43*	0.44	1.07	-1.71	-1.68	0.47	-1.05*	88.97
ACC12.2W*SS	0.31*	0.03	-0.22	-0.22	5.6*	-1.82	-0.74	3.44	1.40**	179.51*
ACC12.2W*WC10	-0.01	0.00	-0.06	0.06	4.42	-0.05	0.14	2.15	0.57	10.87
ACC12.2W*WC35B	-0.14	-0.12	0.27	-0.02	-1.00	0.05	0.61	-0.52	1.01*	-84.87
ACC12.2W*WC36	-0.02	2.17**	-0.14	-0.46	-3.47	0.28	-0.96	-2.75	-0.58	-124.92
ACC12.2W*WC66	-0.02	1.69*	-0.14	0.29	2.07	-0.91	-0.61	3.47	-1.66***	52.83
ALEGI*5T	0.02	-0.89	-0.22	-0.25	-0.03	0.43	0.26	1.41	-0.96*	-103.08
ALEGI*NE48	0.01	-0.83	-0.22	0.00	-3.20	-0.33	0.62	-0.14	-1.23*	-203.49*
ALEGI*NE50	-0.06	0.91	-0.48*	-0.55	-2.50	0.19	-0.86	-0.27	0.58	-29.02
ALEGI*SS	0.01	-0.66	0.24	-0.21	-1.90	-2.05	-0.97	-1.28	-0.74	-169.39*
ALEGI*WC10	0.02	1.20	0.38	0.62	-0.10	-0.16	0.49	-1.76	0.67	-17.15
ALEGI*WC36	0.01	-0.20	0.30	0.30	8.66**	-0.03	-0.81	3.99*	0.56	322.46***
NE15*5T	0.01	-0.38	0.02	0.50	6.81*	0.22	0.05	0.59	-0.42	287.00***
NE15*ALEGI	0.05	1.08	0.49*	0.25	1.07	0.14	-0.05	-0.19	2.03***	93.48

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE15*NE48	0.02	0.29	-0.33	-0.13	-7.34*	-0.14	-1.86*	-2.57	-2.25***	-153.12*
NE15*NE50	-0.06	0.97	-0.26	1.29**	1.02	-0.59	0.12	0.00	-0.84	77.74
NE15*SS	0.02	2.21***	0.12	-0.15	-6.40*	-0.17	-0.51	-1.91	-1.41**	-114.01
NE15*WC10	0.01	-1.00	-0.07	-1.01*	1.27	-1.46	-1.67	1.67	0.48	-51.09
NE15*WC35B	-0.10	0.70	-0.07	-0.44	7.08*	1.69	1.37	-0.77	-0.74	8.73
NE15*WC36	0.02	-0.22	-0.14	0.31	3.91	1.78	1.37	6.99***	0.96*	71.43
NE15*WC66	0.02	-0.84	0.52*	-0.22	-2.85	-1.32	-0.35	-1.28	2.21***	-94.03
NE48*5T	0.31*	-1.79*	0.64**	-0.11	1.60	-1.19	-0.76	1.16	-0.27	-25.89

Table 10. Continued

Cross	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE48*NE50	-0.09	-0.09	0.05	-0.08	-0.32	-0.52	1.81*	-0.09	2.71***	40.96
NE48*SS	-0.02	0.56	-0.26	0.53	3.22	2.53*	2.09*	-2.60	1.01*	-19.75
NE48*WC10	-0.02	1.10	-0.11	0.24	6.00*	-1.10	-1.69	0.41	-1.69***	19.75
NE48*WC36	-0.02	-0.22	-0.18	-0.28	-6.74*	2.01	2.10*	-1.97	5.44***	119.02
NE50*5T	-0.10	0.15	0.04	0.17	3.02	-1.72	-1.58	0.62	-1.42**	74.82
NE50*SS	-0.10	-0.48	0.15	-1.02*	-0.27	0.51	0.39	1.46	-0.15	9.85
NE50*WC10	-0.10	-0.98	-0.03	-0.43	-2.07	-0.26	-0.44	0.03	-0.16	-31.12
NE50*WC36	-0.10	-0.39	0.23	0.53	0.70	0.84	-0.45	-0.52	-1.09*	-129.00
WC10*SS	-0.02	0.78	0.01	0.34	2.28	-1.33	0.21	2.60	-1.79***	-0.54
WC10*WC36	-0.02	-1.80**	0.08	-0.18	-3.53	0.34	-0.47	-1.76	-0.75	47.80
WC35B*5T	-0.13	-0.49	-0.11	0.08	-3.91	2.07	2.46**	-1.43	1.61**	-89.85
WC35B*ALEGI	-0.09	-0.91	0.05	0.30	6.38*	-2.00	-0.06	5.49**	-0.40	194.40**
WC35B*NE48	-0.13	1.42*	-0.11	-0.31	5.39	-0.67	-1.70	3.18	-4.30***	-22.43
WC35B*NE50	0.79***	0.94	-0.03	-0.88*	-2.35	0.28	0.89	-2.20	2.51***	-37.06
WC35B*SS	-0.13	-2.01**	0.01	1.10**	-5.10	0.54	-0.15	-3.09	2.54***	82.85
WC35B*WC10	-0.13	-0.04	0.16	0.46	-0.13	1.37	-1.03	1.30	-2.77***	56.22
WC35B*WC36	0.20	0.00	-0.25	0.30	-2.98	-2.49*	-0.91	-1.49	-1.76***	-14.86
WC35B*WC66	-0.13	0.51	0.08	-0.58	-3.40	-0.84	-1.47	-0.47	2.31***	-93.14
WC36*SS	-0.02	-0.03	0.27	0.12	3.32	0.82	0.19	-0.60	-1.73***	-72.19
WC66*5T	-0.02	0.17	0.16	0.03	2.84	0.09	-1.11	0.72	-1.06*	19.58
WC66*ALEGI	0.02	0.26	-0.36	-0.19	-4.17	2.15	0.40	-2.99	-1.32**	-51.97
WC66*NE48	-0.02	-0.32	0.16	0.24	1.84	-2.68*	-1.60	1.81	-0.52	213.02**
WC66*NE50	-0.10	0.28	-0.11	0.54	1.70	3.00*	1.81*	0.51	-1.09*	-66.14
WC66*SS	-0.02	-1.05	-0.07	0.14	1.63	0.09	0.99	1.71	-1.74***	75.39
WC66*WC10	0.31*	-1.03	-0.25	-0.10	-5.08	2.20	2.64**	-4.36*	4.23***	-53.20
WC66*WC36	-0.03	0.33	0.01	-0.16	5.41	-1.78	-0.70	0.88	-1.35**	-2.35
SE _{SCA}	0.14	0.69	0.21	0.40	3.02	1.28	0.96	1.93	0.50	80.20

5T = SECOW 5T; SS= Sunshine; Values with *, ** and *** implies significant at P = .05, P < .01 and P < .001 respectively

Table 11. General combining ability (GCA) effects for scab disease severity, yield and yield related traits for two locations combined

Parent	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ pod	Pod length	No. of peduncles	Seed weight	Grain yield
SECOW5T	0.01	0.76*	0.079	0.13	0.53	0.76*	-0.14	0.90	1.80***	148.46**
ACC12.2W	-0.02	-0.61	0.009	-0.14	0.54	-0.16	-1.28***	0.62	-0.41**	-28.04
ALEGI	-0.07*	-0.44	0.19***	0.04	3.47*	-0.61	0.85***	1.22	-0.83***	-25.14
NE15	-0.09*	0.75*	0.057	0.29*	5.43**	-0.06	-1.64***	2.86**	-0.77***	-45.44
NE48	-0.08*	-0.22	0.080	0.14	1.81	0.27	-0.93***	0.40	0.59***	-5.34
NE50	0.05	-0.23	-0.006	0.09	-0.96	-0.55	1.23***	-1.06	0.07	-91.84
SS	0.02	-0.27	0.004	-0.09	-1.52	-0.13	-0.98***	-0.16	-0.39**	-75.04
WC10	0.06	0.44	-0.11*	-0.04	0.23	-0.86*	1.83***	-0.77	-0.51***	-17.44
WC35B	0.14***	-0.27	-0.12*	-0.19	-4.08*	0.58	3.40***	-2.71**	0.95***	68.86
WC36	-0.02	-0.18	-0.10*	-0.05	-1.27	-0.06	-1.52***	0.13	-0.25	63.46
WC66	0.01	0.28	-0.083	-0.18	-4.21**	0.83*	-0.83***	-1.39	-0.26	7.46
SE _{GCA}	0.04	0.38	0.049	0.14	1.71	0.40	0.24	1.11	0.15	56.71

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

Table 12. Specific combining ability (SCA) effects for scab disease severity, yield and yield-related traits for two locations combined

Genotype	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
5T*SS	-0.07	0.26	-0.69	-0.40	-0.04	-0.39	0.96	-0.19	1.71***	160.08
5T*WC10	-0.11	4.23***	-0.07	-6.48	-0.11	0.20	-0.10	-3.94	0.70	85.98
5T*WC36	-0.10	-0.86	-0.24	-3.53	-0.10	-1.63	1.64*	-1.64	0.94*	-580.29***
ACC12.2W*5T	-0.06	-0.75	-0.15	0.34	0.11	0.80	1.38*	-3.17	-0.65	329.74*
ACC12.2W*ALEGI	-0.07	0.73	-0.38	-4.68	-0.15	1.74	-0.89	-1.59	-0.01	-248.43
ACC12.2W*NE15	0.08	-2.88**	-0.32	3.06	-0.20	0.18	2.25***	0.46	-0.13	-227.88
ACC12.2W*NE48	-0.03	-0.23	0.16	2.85	0.12	1.04	1.99**	5.56	0.87*	71.05
ACC12.2W*NE50	-0.10	-0.74	0.53	-4.15	0.21	-1.39	-2.95***	-2.55	-0.19	73.81
ACC12.2W*SS	-0.03	-0.24	-0.05	0.58	-0.14	-1.17	1.07	-1.20	0.50	197.28
ACC12.2W*WC10	-0.10	0.74	0.02	1.71	-0.03	-0.09	-1.98**	0.48	0.35	72.46
ACC12.2W*WC35B	-0.06	0.87	0.10	-6.01	0.15	0.69	-0.83	-2.96	1.17**	-174.75
ACC12.2W*WC36	0.20	1.40	-0.17	2.67	-0.03	-0.54	-0.30	3.91	-0.49	28.91
ACC12.2W*WC66	0.18	1.10	0.26	3.64	-0.04	-1.26	0.28	1.06	-1.43***	-122.20
ALEGI*5T	0.12	-1.41	-0.61	-8.05	-0.22	0.10	-1.12	-4.63	-0.10	-60.50
ALEGI*NE48	0.05	0.05	0.42	2.52	0.10	0.06	-1.25	0.21	-1.80***	-275.59
ALEGI*NE50	-0.11	0.86	0.23	7.43	-0.32*	0.52	20.61***	5.23	-0.04	622.55***
ALEGI*SS	0.25*	-0.85	-0.74*	-10.26*	0.01	-0.83	-1.83**	-4.75	1.00*	-227.15
ALEGI*WC10	-0.15	-0.37	0.61	3.56	0.30*	-0.93	-4.52***	2.39	0.63	-248.63
ALEGI*WC36	0.02	-0.60	0.17	9.81*	0.27*	-0.19	-2.53***	4.26	0.50	350.79*
NE15*5T	-0.16	0.03	0.62	16.70***	0.07	-0.58	0.98	11.42***	0.20	400.74*
NE15*ALEGI	0.10	1.79	0.20	-4.48	0.29*	0.07	-2.14***	-3.28	1.88***	-198.30

Genotype	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE15*NE48	0.00	2.24*	-0.15	5.60	-0.10	0.33	-0.86	0.20	-2.69***	-35.09
NE15*NE50	-0.13	-0.08	0.65	8.29	-0.02	0.84	-1.53*	1.36	-0.75	168.48
NE15*SS	-0.13	1.46	-0.21	-6.69	0.13	-0.47	0.49	-2.17	-0.41	-155.05
NE15*WC10	0.16	-1.81	-0.51	-5.28	-0.25	-0.63	-2.95***	-0.43	-0.34	-143.95
NE15*WC35B	-0.09	-0.36	-0.11	1.76	-0.07	0.63	-1.30*	-0.20	-0.27	281.58
NE15*WC36	0.17	1.56	0.50	-4.69	-0.08	1.02	2.75***	-0.24	0.06	-143.19
NE15*WC66	-0.01	-1.96*	-0.67	-14.26**	0.22	-1.39	2.30***	-7.12*	2.44***	52.66
NE48*5T	0.50***	0.00	-0.22	0.97	0.21	-1.97	0.71	-1.11	-0.36	-194.89

Table 12. Continued

Genotype	Severity	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ Pod	Pod length	No. of peduncles	Seed weight (g)	Grain yield (Kg/ha)
NE48*NE50	-0.20	-0.03	-0.39	-6.30	-0.03	0.36	0.38	-1.94	3.21***	255.06
NE48*SS	-0.04	0.59	0.66	1.82	-0.22	1.93	2.59***	1.09	0.78	-151.88
NE48*WC10	0.05	-0.44	-0.05	1.34	0.04	-0.88	-2.29***	-0.95	-0.65	30.79
NE48*WC36	-0.10	-1.92	-0.76*	-9.32*	-0.10	2.30*	3.66***	-3.78	4.35***	381.61*
NE50*5T	-0.03	-0.86	0.21	-1.53	-0.03	-2.42	-2.80***	-2.47	-1.83	-65.85
NE50*SS	-0.07	0.49	-0.37	5.42	0.21	0.66	-1.95**	4.12	-0.94*	-91.57
NE50*WC10	-0.11	-1.92	0.04	4.45	-0.01	-0.54	-6.29***	2.69	-0.37	-127.65
NE50*WC36	0.17	1.20	-0.26	-6.21	0.16	0.07	-2.92***	-4.35	-1.07**	-376.69*
WC10*SS	-0.05	-1.72	0.09	2.35	-0.03	0.24	-1.58*	0.93	-1.43***	214.79
WC10*WC36	-0.18	-0.74	0.35	4.33	0.09	0.68	-2.48***	2.57	-0.96*	392.63*
WC35B*5T	0.04	0.80	0.27	-0.49	0.07	0.08	-1.39	0.31	0.31	-104.86
WC35B*ALEGI	-0.10	-1.21	0.28	7.48	-0.04	-0.66	-4.53*	4.98	-0.59	257.51
WC35B*NE48	-0.20	0.09	0.14	-1.14	-0.08	-1.29	-4.81***	0.19	-2.84***	-72.42
WC35B*NE50	0.71***	-0.42	-0.58	-9.27*	-0.15	1.06	-2.65***	-2.12	2.43***	-257.50
WC35B*SS	0.17	-0.16	0.47	-4.14	-0.02	0.24	-1.56*	-3.05	1.39***	216.78
WC35B*WC10	-0.13	2.38*	0.05	2.47	0.11	0.72	20.96***	1.89	-1.54***	-192.87
WC35B*WC36	0.01	-0.70	-0.13	8.78*	-0.07	-0.95	-1.31*	0.65	-1.28**	97.39
WC35B*WC66	-0.35**	-1.28	-0.49	0.57	0.09	-0.53	-2.58***	0.31	1.23**	-50.85
WC36*SS	-0.07	-0.47	0.40	-3.18	-0.02	0.96	1.24	-2.21	-1.28**	-245.01
WC66*5T	-0.12	-1.44	0.88*	2.47	0.04	5.79***	-0.26	5.41	-0.93*	29.85
WC66*ALEGI	-0.10	1.02	-0.17	-3.35	-0.24	0.11	-1.79**	-2.83	-1.46***	27.74
WC66*NE48	-0.03	-0.33	0.21	1.66	0.05	-1.89	-0.12	0.52	-0.88*	-8.65
WC66*NE50	-0.12	1.51	-0.06	1.86	-0.03	0.82	0.10	0.03	-0.47	-110.60
WC66*SS	0.04	0.63	0.45	14.50**	0.13	-1.16	0.57	7.43*	-1.33**	81.73
WC66*WC10	0.63***	-0.36	-0.54	-8.44	-0.11	1.24	1.24	-5.63	3.60***	6.49
WC66*WC36	-0.12	1.13	0.13	1.35	-0.12	-1.72	0.26	0.82	-0.78	93.84
SE _{SCA}	0.12	1.07	0.40	4.81	0.14	1.13	0.68	3.14	0.43	159.60

5T = SECOW 5T; SS= Sunshine; Values with *, ** and *** implies significant at P = .05, P < .01 and P < .001 respectively

Table 13. Correlation of disease parameters, yield and yield-related traits of crosses (without parents) for two locations combined

Trait	Disease incidence	Severity	AUDPC	Days to flowering	Pods/ peduncle	No. of branches	Pods/ plant	Seeds/ pod	Pod length	No. of peduncles	Seed weight (g)	Yield (kg/ha)
Disease incidence	-											
Severity	0.390***	-										
AUDPC	0.409***	0.881***	-									
Days to flowering	0.187***	0.402***	0.417***	-								
Pods/ peduncle	0.007	-0.103*	-0.094*	-0.046	-							
No. of branches	-0.008	0.170***	0.221***	0.250***	-0.022	-						
Pods/ plant	-0.020	-0.272***	0.331***	0.402***	0.051	0.709***	-					
Seeds/ pod	-0.081	-0.202***	0.223***	0.291***	-0.099*	0.301***	0.325***	-				
Pod length	0.047	0.152**	0.133**	0.185***	-0.060	0.059	0.172**	0.132**	-			
No. of peduncles	-0.038	0.214***	0.266***	0.318***	-0.036	0.758***	0.919***	0.349***	0.159**	-		
Seed weight (g)	-0.087*	-0.241***	-0.185***	0.142**	-0.099*	0.130**	0.172**	0.257***	0.133**	0.174**	-	
Yield (kg/ha)	-0.105*	-0.250***	-0.263***	-0.308***	-0.048	0.488***	0.697***	0.442***	0.206***	0.651***	0.299***	-

Values with *, ** and *** implies significant at $P = .05$, $P < .01$ and $P < .001$ respectively. (N = 55 genotypes evaluated at two locations)

Results of general combining ability (GCA) effects for scab disease severity, yield and yield-related traits evaluated at Serere are shown in Table 9. Of the 11 parents, nine were shown to have negative GCA effects for scab disease severity, suggesting that these nine parents were good combiners for reducing scab severity in Serere and could therefore be selected for breeding for resistance to the disease. For 100 seed weight, four of the parents were shown to have positive GCA effects out of which three (SECOW5T, NE48 and WC35B) were highly significant ($P < 0.001$) positive effects indicating that these parents were good combiners and could therefore be selected for the purpose of breeding for increased seed weight. For grain yield (Kg/ha), two parents, ACC12.2W ($P < 0.05$) and NE50 ($P < 0.01$), had significant negative GCA effects, suggesting that they were generally bad combiners for the improvement of yield in Serere.

The results of specific combining ability (SCA) effects of the 55 crosses evaluated in Serere for scab disease severity, yield and yield-related traits are presented in Table 10. Out of the 55 crosses, 35 were shown to have negative SCA effects for scab disease severity, implying that these crosses could be selected among possible progenies for improvement of resistance to scab disease. 16 out of the 55 crosses showed significant ($P < 0.001$ to $P < 0.05$) positive SCA effects for 100 seed weight, suggesting that there was high potential for achieving significant gains in selecting among these crosses in Serere for improvement of seed weight. On the other hand, five crosses (ACC12.2W*SS, Alegi*WC36, NE15*SECOW5T, WC35B*Alegi and WC66*NE48) had significant ($P < 0.001$ to $P < 0.05$) positive SCA effects.

For grain yield, indicating high chances of improving the grain yield of cowpea when these crosses are selected for the location (Olweny, 2016). The results also indicated possibilities of selecting progenies when the target is to reduce the maturity period in the location, as four of the progenies (ACC12.2W*NE50, NE48*5T, WC10*WC36 and WC35B*SS) showed significant negative SCA effects for days to flowering.

The results of general combining ability (GCA) effects for scab disease severity, yield and yield related traits for the two locations combined (Table 11) indicated that out of the 11 parents, five had negative GCA effects for scab disease severity of which three (Alegi, NE15 and NE48)

were significant ($P < 0.05$) negative effects, suggesting that these three parents were good combiners and could be selected and used as parents in breeding for resistance to scab for across the two locations. For 100 seed weight, the combined analysis showed that four of the parents had positive GCA effects, out of which three (SECOW5T, NE48 and WC35B) had highly significant ($P < 0.001$) positive GCA effects suggesting that genes with additive effects were important and therefore, high chances of improving the seed weight of cowpea when these parents are selected. Of the 11 parents, four had positive GCA effects for grain yield (Kg/ha) of which only one (SECOW5T) had a significant ($P < 0.01$) positive GCA effect on yield. The desirable GCA effect associated with SECOW5T for high yield indicated that it combines well for increased grain yield and that genes with additive effects were more important for the trait. For pod length, four (Alegi, NE50, WC10 and WC35B) out of the 11 parents showed highly significant ($P < 0.001$) positive GCA effects, suggesting that they were good combiners and could be good parents for increasing the pod length of cowpea which could.

Lead to increased yields as pod length has been found to be highly correlated with grain yield in cowpea (Afutu et al., 2016b).

The results of specific combining ability effects for scab disease severity, yield and yield related traits for the two locations combined are presented in Table 12. Only one cross, WC35B*WC66, had significant ($P < 0.01$) negative effect for scab severity suggesting that the use of this hybrid (cross) could result in improved resistance to scab disease for the two locations. This was not surprising as the cross was from two parents both rated resistant to scab (Afutu et al., 2016b) suggesting that additive effects were important for scab disease resistance under the environments evaluated (Olweny, 2016). Six crosses, viz., Alegi*NE50 ($P < 0.001$), ACC12.2W*SECOW5T, Alegi*WC36, NE15*SECOW5T, NE48*WC36 and WC10*WC36 ($P < 0.05$) showed significant positive SCA effects for seed weight and grain yield suggesting high potential of selecting from among these lines for increased seed (100 seed weight) and grain yield across the two locations. Similarly, the combined analysis of the two locations showed that crosses such as ACC12.2W*NE15 and NE15*WC66 could be selected towards breeding for early maturity as these two hybrids had significant negative SCA

effects for days to flowering across the two locations.

3.4 Interrelationships among Disease Indexes, Yield and Yield-Related Traits for Crosses (Hybrids)

The results of correlation analysis for scab disease parameters, grain yield and yield-related traits of the 55 crosses for the two locations combined are presented in Table 13. The results indicated that scab disease incidence had highly significant ($P < 0.001$) positive correlations with disease severity (0.39) and AUDPC (0.41), suggesting that the scores of the two disease indices increased with disease incidence. Similar results were reported by Afutu *et al.* (2016b), in which scab disease incidence was shown to be significantly positively correlated with AUDPC (0.80, $P < 0.001$). Burdon (1987) suggested that as long as there was fresh new leaf tissue to be infected, the severity of polycyclic diseases such as scab would increase as the incidence increases. Further, the incidence of scab disease was reported to increase with plant age (Mbong *et al.*, 2010). On the other hand, as expected, scab disease incidence showed significant ($P < 0.05$) negative correlations with 100 seed weight (g) (-0.10) and grain yield (Kg/ha) (-0.11) as disease severity was also shown to be significantly ($P < 0.001$) negatively correlated with 100 seed weight (-0.24) and grain yield (-0.30) indicating that as the incidence and severity of scab increased, the 100 seed weight (g) and grain yields (Kg/ha) decreased significantly. Scab has significant negative effects on leaf area and reproductive parts of cowpea plants and this explains the significant negative correlations of scab severity with other traits such as the number of pods per peduncle (-0.10, $P < 0.05$), number of pods per plant (-0.30, $P < 0.001$) and number of seeds per pod (-0.20, $P < 0.001$). Yield related traits such as the number of branches (0.50), number of pods per plant (0.70), number of seeds per pod (0.44), pod length (0.21), number of peduncles (0.70) and 100 seed weight (0.30) were all shown to have highly significant ($P < 0.001$) positive correlations with grain yield (Kg/ha) implying that grain yield (Kg/ha) of these hybrids (crosses) was directly related to these traits and therefore, suggests that any factor that affects them would affect the grain yield of cowpea (Mbong *et al.*, 2012).

4. CONCLUSION

The study identified Alegi, NE15 and NE48 as parental lines with negative GCA effects for

improvement of scab disease resistance for both locations while SECOW5T was identified as the only parent with high positive GCA for improvement of both 100 seed weight (g) and grain yield (K/ha) of cowpea across the two locations. Cross WC35B*WC66 had the best SCA effects for reduction of scab disease severity. The study confirmed earlier reports that additive gene effects were important for scab disease resistance. Six crosses, viz. Alegi*NE50, Alegi*WC36, ACC12.2W*SECOW5T, NE15*SECOW5T, NE48*WC36 and WC10*WC36 were identified as the best hybrids (crosses) for the improvement of cowpea yields across the locations.

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ACKNOWLEDGEMENT

This study was funded by Carnegie Corporation of New York, the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM) (RU/2012/DRS/01) and the Cowpea Scab Project of the National Semi-Arid Resources Research Institute (NaSARRI), Serere – Uganda.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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