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RESPONSE OF THE MAGIC POPULATION OF COWPEA TO SCAB DISEASE RESISTANCE AND GRAIN YIELD

RÉPONSE DE LA POPULATION MAGIC DU NIÉBÉ À LA RÉSISTANCE À LA GALE ET
AU RENDEMENT EN GRAIN

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ABSTRACT

Scab disease, caused by *Sphaceloma* spp., is a major constraint to cowpea (*Vigna unguiculata* L. Walp) production in sub-Saharan Africa (SSA), with yield losses of up to 100% under severe infection. Currently, no scab-resistant cowpea varieties have been developed or identified. The objective of this study was to identify novel sources of resistance by evaluating the response of the cowpea Multiparent Advanced Generation Inter-Cross (MAGIC) population to natural scab pressure. A total of 208 cowpea genotypes, including MAGIC varieties, were evaluated across two locations at Kabanyolo and Arapai, in Uganda, during the 2023 cropping seasons. Significant genotypic variation in disease response was observed, with the highest severity recorded at Kabanyolo, likely due to elevated precipitation of the 2023B rainy seasons. Pearson correlation analysis revealed negative associations between scab severity (week 10 and AUDPC) and days to 50% maturity, with a significant correlation at 10 WAP ($r = -0.14$, $P < 0.05$). Scab severity at 10 WAP was also negatively correlated with yield traits ($r = -0.01$ to -0.14). Five lines, MAGIC 064, MAGIC 254, NAROCOWPEA 2, NAROCOWPEA 3 and MAGIC 062,

were found to be resistant. Overall, NAROCOWPEA 3 combined resistance with high yield (1,562 kg ha⁻¹), making it a strong parent for Scab resistance and grain yield breeding.

Key Words: AUDPC, *Sphaceloma* spp., *Vigna unguiculata*

RÉSUMÉ

La gale, causée par *Sphaceloma* spp., constitue une contrainte majeure à la production du niébé (*Vigna unguiculata* L. Walp) en Afrique subsaharienne (ASS), entraînant des pertes de rendement pouvant atteindre 100 % en cas d'infection sévère. Actuellement, aucune variété de niébé résistante à la gale n'a été développée ou identifiée. L'objectif de cette étude était d'identifier de nouvelles sources de résistance en évaluant la réponse de la population MAGIC (*Multiparent Advanced Generation Inter-Cross*) du niébé à une pression naturelle de gale. Un total de 208 génotypes de niébé, incluant des variétés MAGIC, ont été évalués sur deux sites, Kabanyolo et Arapai, en Ouganda, au cours des saisons culturales de 2023. Une variation génotypique significative de la réponse à la maladie a été observée, avec une sévérité maximale enregistrée à Kabanyolo, probablement en raison des précipitations élevées de la saison des pluies 2023B. L'analyse de corrélation de Pearson a révélé des associations négatives entre la sévérité de la gale (semaine 10 et AUDPC) et le nombre de jours jusqu'à 50 % de maturité, avec une corrélation significative à 10 semaines après plantation ($r = -0,14$, $P < 0,05$). La sévérité de la gale à 10 semaines était également négativement corrélée aux caractères de rendement ($r = -0,01$ à $-0,14$). Cinq lignées, MAGIC 064, MAGIC 254, NAROCOWPEA 2, NAROCOWPEA 3 et MAGIC 062, se sont révélées résistantes. Globalement, NAROCOWPEA 3 a combiné résistance et haut rendement (1 562 kg ha⁻¹), ce qui en fait un parent prometteur pour l'amélioration génétique de la résistance à la gale et du rendement en grain.

Mots Clés: AUDPC, *Sphaceloma* spp., *Vigna unguiculata*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is an annual leguminous crop cultivated globally, primarily in low input production systems across arid and tropical regions (Xiong *et al.*, 2018). It is grown on more than 15 million hectares worldwide, with total production estimates of 9.8 million metric tonnes of grain. Africa accounts for the majority of this output, contributing 96.8%, followed by Asia (2.3%), America (0.7%), and Europe (0.2%) (FAOSTAT, 2023). Within Africa, Uganda ranks as the 8th largest producer of cowpea (Ronner and Giller, 2015).

In Uganda, cowpea is the fourth most widely grown legume after common bean, groundnut and soy-bean (Ronner and Giller, 2015), and is cultivated by an estimated 2.2 million smallholder farmers, primarily in the Eastern and Northern regions of the country

(Nabirye *et al.*, 2003; Orawu *et al.*, 2013; Ddungu *et al.*, 2015). The crop is vital for both food and nutrition security in SSA, being valued for its multiple edible parts, including dry grain, immature pods, seeds and the leaves, which are consumed as vegetables. Consumption of cowpea-based dishes provides 37% Magnesium, 26% Protein, 30% folate, 42% fibre, 15% energy and more than 15% zinc and potassium (Akissoé *et al.*, 2023). This makes it a key contributor to dietary quality in regions where nutrient deficiency is prevalent (Carvalho *et al.*, 2017).

Beyond its nutritional value, cowpea contributes significantly to the livelihoods of millions of smallholder farmers who rely on it for economic and nutritional well-being (Bolarinwa *et al.*, 2022). In Uganda, the crop is consumed by over 90% of population in the Eastern region (Mundua, 2010). In this region, cowpea leaves are consumed during the early

stages of the growing season to mitigate hunger and bridge food shortages (Isubikalu *et al.*, 2000).

Cowpea is tolerant to low annual rainfall of 500 mm, but grows best in rainfall ranges of 750 to 1100 mm and temperatures ranging from 25 to 35° C (Madamba *et al.*, 2006; Abebe and Alemayehu, 2022). Although cowpea is reported to be resilient to abiotic constraints, the crop remains susceptible to a range of biotic stresses, especially insect pests in Uganda (Karungi *et al.*, 2000) and Nigeria (Tazerouni *et al.*, 2019) which pose a significant challenge to its productivity (Afutu *et al.*, 2017). This is evident in the reduced average yields of the crop across many African countries, with West African nations producing about 600 kg ha⁻¹ (Kamara *et al.*, 2018); while in Uganda an average of around 400 kg ha⁻¹ is produced. Cowpea production is also affected by a range of diseases (Tazerouni *et al.*, 2019). According to Allen (1983), cowpea is affected by more than 40 species of fungal pathogens.

Scab, a fungal disease caused by *Sphaceloma* sp is among the most devastating fungal diseases of cowpea (Mbong *et al.*, 2012). The disease affects all above ground parts of the plant, including the leaves, stems, peduncles, flower cushions and pods; causing yield losses of over 60%, and up to 100% in severe, unmanaged fields (Emechebe, 1980). The disease thrives in moderate temperatures (23-28 °C), which aligns closely with the climatic conditions of East and Southern Africa (Afutu *et al.*, 2017). In Uganda, high incidence and severity of scab disease is linked to several factors, such as the continuous cultivation of susceptible cultivars, which promote pathogen adaptation, and planting at altitudes above 1200 meters above sea level, where cooler temperatures and high humidity prevail, thus favouring the disease development and sporulation (Afutu *et al.*, 2017).

Cultural and chemical methods are popularly recommended in the management of scab disease pathogen in the cowpea growing countries in Africa. However, an earlier study

by Edema and Adipala (1996) reported that controlling scab with fungicidal spray was costly for the small-scale farmers, who rely on this crop. Consequently the use of host resistant varieties has been advocated for as a more practical, cost effective and environmentally friendly measure to control the disease (Rusoke and Rubaihayo, 1994; Mbong *et al.*, 2012). According to Xiong *et al.* (2018), developing highly outstanding and high performing genotypes requires a systematic exploration and evaluation of available cowpea germplasm to identify and select suitable genotypes with desirable phenotypic traits to use in improvement programmes. In Uganda, several studies have identified potential sources of resistance to scab in different cowpea accessions. These cowpea genotypes include accession Number (No.) 46, No. 39, KVu/175 and IT82D- 1321 (Iceduna *et al.*, 1994; Nakawuka and Adipala, 1997; Tumwegamire *et al.*, 1998). Further research by Afutu *et al.* (2016; 2017) identified additional sources of resistance. Afutu *et al.* (2016; 2017) identified cowpea line NE 15 as high yielding and resistant against scab in Kabanyolo and Serere locations; while lines NE 31 and NE 70, showed wide resistance against different *Sphaceloma* spp. isolates collected from different Agro-ecological zones in the country. These resistant genotypes are being used as parents in cowpea improvement for scab resistance in Uganda and across Africa.

Recent research has shown that cowpea scab is still increasing in cowpea growing areas in Uganda (Afutu *et al.*, 2016). This could be partly attributed to the use of elite genotypes, and bi-parental crosses of the elite cultivars in cowpea improvement programmes (Boukar *et al.*, 2016). Elite genotypes have a narrow genetic base (Li *et al.*, 2001; Boukar *et al.*, 2016), with fixed essential alleles for desirable end-use agronomic traits; in comparison with the native land races from which they were crossed (Falk, 2010). It is important to use genetically diverse crop germplasm in development of improved

cultivars, as this increases genetic gain of agronomic traits thus promoting successful breeding programme (Salgotra and Chauhan, 2023; Dieng *et al.*, 2024; Nakimera *et al.*, 2024). Multi-parental populations, such as the multi-parent advanced generation inter-cross (MAGIC) and nested association mapping (NAM) possess increased diversity than biparentals, thus they offer power in detection of genotypes with desirable traits (Olatoye *et al.*, 2019). The objective of this study was to identify novel sources of resistance by evaluating the response of the cowpea Multiparent Advanced Generation Inter-Cross (MAGIC) population to natural scab pressure and assessing grain yield performance.

MATERIALS AND METHODS

Genetic material. A total of 208 cowpea genotypes comprising 198 cowpea MAGIC lines, 7 checks and 3 varieties recently released by the National Agricultural Research Organisation (NARO) with sufficient seeds, were used in this study. The germplasm was sourced from Makerere University Regional Centre for Crop Improvement (MaRCCI), genebank in Uganda. The list of checks is presented in Table 1. The cowpea MAGIC population used in this study was developed from eight genetically diverse founder parents, carrying abiotic and biotic stress resistance, seed quality and agronomic traits relevant to

TABLE 1. List of the founder parents used in MAGIC population development, along with the check varieties and their desirable attributes

Name	Source	Resistance / tolerance trait
IT89KD-288	IITA	Root-knot nematode resistant
IT84S-2049	IITA	Resistant to aphid, bacterial blight, viruses, root-knot nematode
CB27	UCR	Heat tolerant, resistant to root knot nematode, Fusarium wilt and foliar thrips
IT82E-18	IITA	Broadly adapted, resistant to root-knot nematode
SuVita 2	INERA	Drought tolerant, resistant to Striga, foliar thrips and <i>Macrophomina</i> disease
IT00K-1263	IITA	Resistant to Striga, aphid, fusarium wilt, root-knot nematode
IT84S-2246	IITA	Resistant to aphid, bacterial blight, viruses, root-knot nematode
IT93K-503-1	IITA	Drought tolerant, resistant to nematodes, Fusarium wilt, and <i>Macrophomina</i>

Checks used in the study

NE15*	Uganda	Resistant to scab
NE70*	Uganda	Resistant to scab
NE 50*	Uganda	Moderately resistant to scab
SECOW 5T*	Uganda	Moderately resistant to scab
SUNSHINE*		Susceptible to scab
WC 10*		Moderately susceptible to scab
WC 29*		Susceptible to scab

IITA = International Institute of Tropical Agriculture, Nigeria, UCR = University of California-Riverside, CA; INERA = Institute de l'Environnement et des Recherches, Burkina Faso; * List of checks used in this research (Afutu *et al.*, 2017)

cowpea improvement SSA (Huynh *et al.*, 2019a).

The eight parents were intercrossed using structured mating to ensure balanced representation of populations from each parent. This was followed by single -seed descent, which resulted in 305 F_8 recombinant inbred lines (RILs) each of which carries a mosaic of genome blocks contributed by all founder parents. Due to this broadened genetic base and wide phenotypic variation, the cowpea MAGIC population promises enhancement of breeding populations and variety release through increase in genetic gain and identification of Quantitative Trait Loci (QTL) for desired genes (Huynh *et al.*, 2019a).

Experimental site and cropping seasons. A field experiment was conducted at two sites; at Makerere University Agricultural Research Institute MUARIK, Kabanyolo, located in Wakiso district in the Central part of Uganda (latitude “0° 27' 46.1” N and longitude “32° 36' 44” E); and Arapai, in Soroti district the Eastern part of Uganda (latitude “1° 47' 34.8” N and longitude “33° 37' 35.7” E), during the first rainy season of April – August 2023, (named 2023A) and second season rains in September - January 2023 (named 2023B). These locations are hotspots for scab disease (Afutu *et al.*, 2016), and therefore provided sufficient scab disease inoculum. Table 2 shows the environmental conditions during the study.

Experimental design and management. At the two trial sites, the genotypes were planted in an alpha lattice design of 13 blocks by 16 plots with two replications, spaced at 1 m between plots, 1.5 m between blocks and 2 m between replicates to avoid inter-plot and inter-block plant competition. Each genotype was planted in a three-row plot with spacing of 75 cm between rows and 30 cm within rows. In each hole, two seeds were sown and thinned to 1 plant per hole, 3 weeks after planting.

After 2 weeks of germination, each plot was tagged with the genotype name, to ease identification during data collection. Hand hoe weeding was done thrice and no fertiliser was applied. To manage pest damages, the experimental plots were sprayed twice using Rokat 44 EC (Profenofos 40% + Cypermethrin 4%) one just before flowering and the second during pod setting.

Data collection

Assessment of disease severity. Foliar scab disease severity on the cowpea plants was visually assessed and rated at six weeks after planting, and thereafter, at 7 days intervals for 4 weeks after planting, using a scale of 1 to 5, where: 1 = 0% infection (no visible symptoms on either foliage); 2 = less than 10% scab infection (scattered lesions on either foliage); 3 = 10 to 20% infection (extensive spotting of young stems and branches); 4 = 20 to 50% infection (stem lesions coalescing, covering

TABLE 2. Environmental conditions of the experimental sites used in the study

Environment	Latitude	Longitude	Altitude m.a.s.l	Average rainfall mm day ⁻¹	Average temperature ° C	Soil type
Kabanyolo-2023 A	“0° 27' 46.1” N	“32° 36' 44” E	1,172	481.4	22.4	Sandy clay loam
Arapai- 2023 A	“1° 47' 34.8” N	“33° 37' 35.7” E	1,136	244.9	25.2	Clay
Kabanyolo-2023 B	“0° 27' 49.9” N	“32° 36' 2.6” E	1,192	680.2	22.3	Sandy loam
Arapai- 2023 B	“1° 47' 34.8” N	“33° 37' 35.7” E	1,136	198.3	25.6	Clay

Abbreviation: m.a.s.l, meters above seas level

half the plants); and 5 = 50% or greater infection (foliage severely damaged) (Nakawuka and Adipala, 1997). Based on this scale, the disease rating for each genotype was given a score of 1-5. Scab disease symptoms begin appearing on the cowpea leaves at six weeks after planting, for susceptible genotypes. The last disease assessments and rating were taken as final severity and presumed to be at full disease development (Nakawuka and Adipala, 1997). With the use of the final severity disease score at 10 weeks after plant (10 WAP), the cowpea lines with score of less than 2, 2.1 to 3.0, and greater than 3.0 (3.1-5.0), were classified into resistant (R), moderately resistant (MR) and susceptible (S), respectively (Nakawuka and Adipala, 1997).

Assessment of yield performance. The genotypes were also assessed for their yield performance as follows:

For each line, calendar days to flowering (D50FLO) were determined when 50% of plants in the plot have flowered. Fifty percent maturity (D50MAT) was determined when 50% of pods in the plot have matured. Other yield components measured included: plant stand (PSD), number of peduncles per plant (PDC/PLT), number of pods per plant (PD/PLT), number of pods per peduncle (PD/PDC) and seeds per pod (SD/PD).

Calculation of grain yield. Total dry yield of the seeds (g per plot) was recorded and converted to the kilogramme per hectare (kg ha⁻¹) using Equation 1:

$$\text{Grain yield } \left(\frac{\text{kg}}{\text{ha}} \right) = \frac{\text{Yield per plot (kg)}}{\text{plot area (m}^2\text{)}} \times 10000$$

..... Equation 1

Area under the disease progress curve (AUDPC). Mean disease severity scores were used to calculate the area under the disease progress curve (AUDPC) in order to study the

plant-pathogen interaction over time, using the formula below described by Campbell and Madden (1990).

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

Where:

y_i is a scab disease score for each genotype, at the i^{th} observation, t_i is time (in weeks) at the i^{th} observation, and n is the total number of observations.

Data analysis. The data were subjected to analysis of variance (ANOVA), using the Linear Mixed Model, with the *lmer()* function under the *lmer4* package (Bates *et al.*, 2015) in R software Version 4.3.3 (R Core Team, 2021). The analysis considered genotype effects as fixed; whereas replication and blocks effects were considered random. The locations and seasons combination were treated as unique environments (Acquaah, 2012).

Two step data analysis was undertaken: this involved the single site analysis and the combined analysis across seasons and locations (environments). The single site analysis for the disease and agronomic traits data were performed using the linear mixed model (3):

$$y_{ijk} = \mu + \rho_i + b_{k(j)} + \varepsilon_{ijk} \dots \dots \dots \text{Equation 3}$$

Where:

μ = Grand mean; y_{ijk} is the response of the genotype 'i' in the k^{th} block in l^{th} replication; ρ_i is the i^{th} genotype effect (considered fixed effect); $b_{k(j)}$ is the effect of k^{th} block nested within the j^{th} replication (considered as random); and ε_{ijk} is the random error.

The combined analysis across environments was done using the linear mixed model (2):

$$y_{ijkl} = \mu + \rho_i + e_l + b_{j(kl)} + \rho e_{ij} + \varepsilon_{ijkl}$$

..... Equation 4

Where:

y_{ijkl} is the response of the genotype “i” in the j^{th} block, in the k^{th} replication at the l^{th} environment; μ is the overall mean of the responses; ρ_i is the i^{th} genotype effect; e_l is the l^{th} environment effect; $b_{j(kl)}$ is the block effect “j” in the k^{th} replication in “l”th environment; ρe_{ij} is the interaction effect of genotype “i”; and environment “l” ε_{ijkl} is the random error

Where the F -values for each trait indicated significance ($P = 0.05$), the predicted genotype mean performance was separated using Fisher’s Protected Least Significant Difference (LSD) at 5% significance level. The mixed model (2) fitted using the R package *lme4* (Bates *et al.*, 2015) was used to estimate: (i) the predicted estimated means for each genotype in the combined datasets. These predicted means were used to compute the Pearson’s correlation coefficients among the traits studied so as to understand the relationships between the disease scores and yield parameters using *corr* function in R. (ii) Variance components and the best linear unbiased prediction (BLUP) of the MAGIC lines for all the traits evaluated. All variables in models 1 and 2 were treated as random effects. Comparative analysis for Scab resistance among genotypes was based on scores captured at 10 WAP, when the disease was presumed to be at full disease development, with distinct phenotypic differentiation among genotypes and the Area Under Disease Progress Curve (AUDPC) (Nakawuka and Adipala, 1997).

Heritability. Variance components for individual locations were estimated using Model 1 and used to calculate the entry based broad-sense heritability using Equation 5 (Johnson *et al.*, 1955). Model 2 was used to

calculate the variance components of the combined datasets. The variances of genotype (G) were signified by σ_g^2 , for Genotype x Location (G x L) is σ_{gl}^2 , for Genotype x Season (G x S) is σ_{gs}^2 , Genotype x Season x Location (G x S x L) is σ_{gsl}^2 and error term, σ_e^2 and Equation 6 was used for calculating across season and location broad sense heritability, H^2 .

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + (\sigma_e^2/n)} \dots \dots \dots \text{Equation 5}$$

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gs}^2}{s} + \frac{\sigma_{gls}^2}{l*s} + \frac{\sigma_e^2}{l*s*r}} \dots \dots \dots \text{Equation 6}$$

RESULTS

Response of genotypes of cowpea MAGIC lines to scab disease

Disease severity across environments. Combined analysis of variance for 208 genotypes in four environments revealed significant differences ($P < 0.001$) for genotypes effects and genotype-by-environment interaction effects for the disease traits (Table 3). Comparison of genotypes’ variability to scab resistance was based on the 10 weeks after planting (WAP) time-point, because at this time, the disease is assumed to be fully developed. The last disease severity ratings were taken at this time-point. Genotype-by-environment interaction effects were significant ($P < 0.001$) for scab severity at 10 weeks after planting (10 WAP) and AUDPC (Table 3). Environment effects showed significant differences ($P < 0.05$) among the genotypes for scab severity at week 10 and AUDPC. For the combined analysis of variance for the four environments, severity ratings at this time-point ranged from 2 to 5, with a mean of 3.74, and AUDPC ranged from 57.75 to 147.00, with a mean of 94.01.

TABLE 3. Analysis of Variance for Scab disease severity at 10 weeks after planting (WAP) and AUDPC for cowpea genotypes screened for two seasons in 2023 in Kabanyolo and Arapai

Mean squares				
Combined analysis	SOV	Df	10 WAP	AUDPC
	Genotype	207	0.87***	409.90***
	Env	3	10.18**	3349.30**
	Genotype*Env	619	0.58***	256.70***
	Residual		0.32	145.22
	H ²		34.13	39.11
Individual environments				
KAB 2023A	Genotype	207	1.18***	310.98.***
	Residual	183	0.38	122.2
	Mean		2.75	77.51
	LSD		1.2	21.81
	CV%		22.43	14.26
	H ²		78	74
KAB 2023B	Genotype	207	0.53***	293.00***
	Residual	183	0.22	101.1
	Mean		4.33	105.2
	LSD		0.93	19.84
	CV%		10.84	9.56
	H ²		74	79
ARAP 2023A	Genotype	205	0.59	306
	Residual	151	0.5	273.4
	Mean		3.57	98.64
	LSD		1.48	34.59
	CV%		19.82	16.76
	H ²		15.03	14.25
ARAP 2023B	Genotype	207	0.34***	265.70***
	Residual	183	0.2	104.8
	Mean		4.28	96.07
	LSD		0.88	20.2
	CV%		10.44	10.66
	H ²		58	75

*** = significant at 0.001; ** = significant at 0.01; * = significant at 0.05, KAB 2023A, KAB 2023B, ARAP 2023A and ARAP 2023B refer to environments (Kabanyolo 2023A, Kabanyolo 2023B, Arapai 2023A and Arapai 2023B); Rep= Replication, Env = Environment, LSD = Least Significant Difference, CV = Coefficient of Variation, H²=Broad sense heritability, SOV = Source of Variation, Df = Degrees of freedom, WAP = Weeks after planting, AUDPC = Area under disease progress curve

Disease severity in Kabanyolo environments. During season 1 (Kabanyolo 2023A), there was a significant difference among the genotypes for all the four disease traits ($P < 0.001$) (Table 3). The final scab severity scored at 10 WAP in this location ranged from 1.81 to 5 with a mean of 2.75; forty-eight genotypes were rated resistant with scores ranging from 1.0 - 2.0, 113 genotypes were moderately resistant (2.1-3.0) and 47 were susceptible (3.1-5.0). Eight genotypes had very low severity scores at 10 WAP (1.81 – 1.89) (Table 4). Four genotypes (MAGIC075, MAGIC089, MAGIC180 and MAGIC202), had the highest severity score of 5, at 10 WAP, therefore rated susceptible (Table 4).

In season 2 (Kabanyolo 2023B), genotypes showed significant differences ($P < 0.001$) in their response to scab, with the final severity rating ranging from 2.34 to 5, with a mean of 4.33 (Fig. 1). None of the genotypes was rated resistant (score < 2) (Table 4). However, seven genotypes were moderately resistant with their mean severity at 10 WAP ranging from 2.34 to 3.07. Two hundred one genotypes were rated susceptible with final severity at 10 WAP ranging from 3.14 to 5. MAGIC068 had the highest Scab severity rating of 5 and AUDPC of 140.2. Based on AUDPC values, Kabanyolo 2023A (mean of 77.1) had lower scab disease intensity than in Kabanyolo 2023B (mean AUDPC of 105.2). Lines MAGIC153, MAGIC086 and NAROCOWPEA 2 maintained low resistance in both season in this location (Table 4).

Disease severity in Arapai environments. For Arapai 2023A, the mean values of the scab disease traits showed that there were no significant differences ($P > 0.05$) among the genotypes. Final scores of scab severity were taken at 10 WAP and ranged from 1.98 to 5 with a mean score of 3.57. Two genotypes, MAGIC064 and MAGIC147 had the lowest severity scores of 1.98 and 2.05, respectively; and were classified as resistant (Table 4). In Arapai 2023B, genotype effects were significantly different in all disease severity

traits ($P < 0.001$). At 10 WAP, scab severity ranged from 2.94 to 5 with a mean of 4.28. There was virtually no resistant genotype (Table 4). However, 3 genotypes were moderately resistant with scab severity at 10 weeks ranging from 2.1 to 3.0 and 205 rated susceptible (score = 3.38 to 5) (Table 4). ARAPAI 2023B showed slightly lower disease pressure with AUDPC ranging from 58.4 to 136.7 and mean of 96.07 than in ARAPAI 2023A; where AUDPC ranged from 63.2 to 151 with a mean of 98.64. Lines MAGIC254, MAGIC064, MAGIC083 and MAGIC120 maintained low resistance in both season in this location (Table 4). On the whole, the average AUDPC of Arapai 2023A and 2023B, (AUDPC = 194.71), and that of Kabanyolo 2023A and 2023B, (AUDPC = 182.6) showed that Arapai had higher disease pressure than Kabanyolo (Fig. 1). Overall, there was no genotype with no scab symptoms.

According to the rating of the means of scab severity scores for the combined data at 10 WAP for the four environments, lines MAGIC064, MAGIC254, NAROCOWPEA 2, NAROCOWPEA 3 and MAGIC062, had the least scab severity and were rated resistant (Table 4). The most susceptible were MAGIC331, ITOOK-1263, MAGIC180, MAGIC336. Among the resistant checks, it was observed that NE15 had the lowest AUDPC of 70, compared to these genotypes with the least severity.

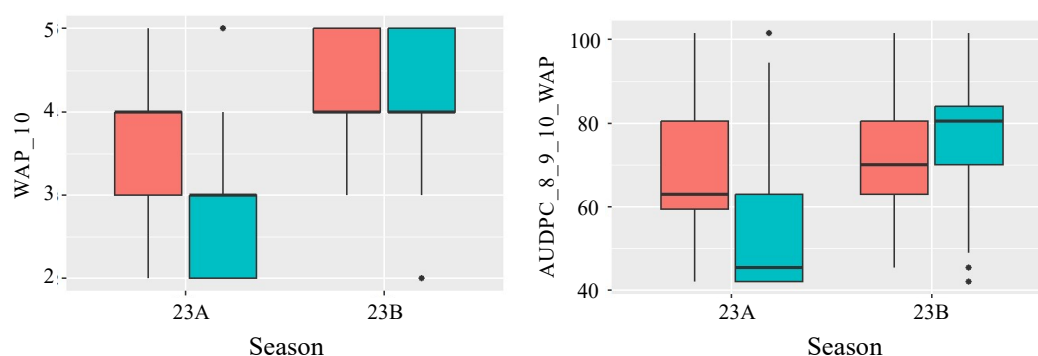
MAGIC population to grain yield and yield components

Yield components. For yield components, the study focused on data collected from three environments (Kabanyolo 2023A, Kabanyolo 2023B and Arapai 2023A). Yield data for Arapai 2023B was not included in the analysis due to its damage by grazing livestock. Across environments, the Analysis of Variance for the combined environment analysis of the yield components showed significant differences ($P < 0.001$) among the genotypes and genotype by environment interaction effects, for grain

TABLE 4. Top 20 most resistant and the 20 most susceptible cowpea genotypes in Kabanyolo 2023A and 2023B, Arapai 2023A and 2023B and the overall combined reaction across four environments

Genotype	KAB23A			KAB23B			ARAP 23A			ARAP 23B			Overall		
	10 WAP	R.S	Genotype	10 WAP	R.S	Genotype	10 WAP	R.S	Genotype	10 WAP	R.S	Genotype	10 WAP	R.S	Genotype
IT82E-18	1.8	R	MAGIC337	2.3	MR	MAGIC064	2.0	R	MAGIC120	2.9	MR	MAGIC062	3.0	MR	MAGIC062
MAGIC066	1.8	R	MAGIC153	2.5	MR	MAGIC147	2.1	R	MAGIC117	3.0	MR	MAGIC064	3.0	MR	MAGIC064
MAGIC126	1.9	R	MAGIC064	3.0	MR	MAGIC324	2.1	MR	MAGIC335	3.1	MR	MAGIC254	3.0	MR	MAGIC254
NE 50	1.9	R	MAGIC320	3.0	MR	MAGIC001	2.5	MR	MAGIC225	3.4	S	NAROCowpea 2	3.0	MR	NAROCowpea 2
MAGIC001	1.9	R	MAGIC086	3.1	MR	NAROCowpea 3	2.5	MR	MAGIC083	3.4	S	NAROCowpea 3	3.0	MR	NAROCowpea 3
MAGIC335	1.9	R	MAGIC083	3.1	MR	MAGIC028	2.5	MR	MAGIC254	3.4	S	MAGIC001	3.1	S	MAGIC001
MAGIC003	1.9	R	MAGIC226	3.1	MR	MAGIC062	2.5	MR	MAGIC298	3.5	S	MAGIC226	3.1	S	MAGIC226
MAGIC019	1.9	R	MAGIC216	3.1	S	MAGIC115	2.5	MR	MAGIC232	3.5	S	MAGIC302	3.1	S	MAGIC302
MAGIC157	1.9	R	NAROCowpea 2	3.2	S	MAGIC266	2.5	MR	MAGIC245	3.5	S	WC 29	3.1	S	WC 29
NAROCowpea 2	1.9	R	MAGIC044	3.2	S	MAGIC041	2.6	MR	MAGIC292	3.5	S	MAGIC083	3.1	S	MAGIC083
WC 10	1.9	R	MAGIC313	3.3	S	MAGIC087	2.6	MR	MAGIC119	3.6	S	MAGIC216	3.1	S	MAGIC216
MAGIC105	1.9	R	SUNSHINE	3.4	S	MAGIC015	2.6	MR	MAGIC296	3.6	S	MAGIC153	3.2	S	MAGIC153
MAGIC301	1.9	R	MAGIC091	3.4	S	MAGIC085	2.6	MR	MAGIC320	3.6	S	MAGIC086	3.3	S	MAGIC086
MAGIC060	1.9	R	MAGIC302	3.4	S	MAGIC254	2.6	MR	MAGIC250	3.6	S	MAGIC104	3.3	S	MAGIC104
MAGIC107	1.9	R	MAGIC116	3.5	S	MAGIC083	2.9	MR	MAGIC024	3.9	S	MAGIC115	3.3	S	MAGIC115
MAGIC027	2.0	R	MAGIC273	3.5	S	MAGIC120	2.9	MR	IT89KD-288	3.9	S	MAGIC192	3.3	S	MAGIC192
MAGIC086	2.0	R	NAROCowpea 3	3.5	S	MAGIC098	2.9	MR	MAGIC064	3.9	S	MAGIC225	3.3	S	MAGIC225
MAGIC153	2.0	R	MAGIC327	3.5	S	MAGIC231	2.9	MR	MAGIC020	3.9	S	MAGIC284	3.3	S	MAGIC284
NAROCOWPEA 4	2.0	R	MAGIC243	3.5	S	MAGIC116	3.0	MR	MAGIC283	3.9	S	MAGIC296	3.3	S	MAGIC296
MAGIC196	2.0	R	MAGIC104	3.6	S	MAGIC066	3.0	MR	MAGIC248	3.9	S	MAGIC335	3.3	S	MAGIC335
MAGIC205	3.9	S	MAGIC169	5.0	S	MAGIC273	4.5	S	MAGIC256	5.0	S	MAGIC286	4.1	S	MAGIC286
MAGIC147	4.0	S	MAGIC011	5.0	S	MAGIC162	4.5	S	MAGIC130	5.0	S	MAGIC075	4.3	S	MAGIC075
MAGIC034	4.0	S	MAGIC183	5.0	S	MAGIC044	4.5	S	MAGIC222	5.0	S	MAGIC113	4.3	S	MAGIC113
MAGIC250	4.1	S	MAGIC336	5.0	S	MAGIC209	4.5	S	MAGIC042	5.0	S	MAGIC130	4.3	S	MAGIC130
MAGIC144	4.4	S	MAGIC087	5.0	S	MAGIC223	4.5	S	MAGIC129	5.0	S	MAGIC144	4.3	S	MAGIC144
MAGIC044	4.4	S	MAGIC311	5.0	S	MAGIC234	4.5	S	MAGIC141	5.0	S	MAGIC281	4.3	S	MAGIC281
MAGIC097	4.4	S	MAGIC325	5.0	S	MAGIC097	4.5	S	WC 10	5.0	S	MAGIC190	4.3	S	MAGIC190
MAGIC292	4.4	S	MAGIC100	5.0	S	MAGIC114	4.5	S	MAGIC078	5.0	S	MAGIC202	4.3	S	MAGIC202
MAGIC207	4.5	S	MAGIC134	5.0	S	MAGIC178	4.6	S	MAGIC219	5.0	S	MAGIC097	4.4	S	MAGIC097
MAGIC117	4.5	S	MAGIC204	5.0	S	MAGIC205	4.6	S	MAGIC276	5.0	S	MAGIC162	4.4	S	MAGIC162
MAGIC311	4.5	S	MAGIC024	5.1	S	IT82E-18	4.6	S	MAGIC336	5.0	S	MAGIC205	4.4	S	MAGIC205
MAGIC331	4.6	S	MAGIC042	5.1	S	MAGIC260	4.6	S	MAGIC149	5.0	S	MAGIC207	4.4	S	MAGIC207
MAGIC042	4.6	S	MAGIC089	5.1	S	MAGIC180	4.6	S	MAGIC211	5.0	S	MAGIC233	4.4	S	MAGIC233
MAGIC273	4.7	S	MAGIC222	5.1	S	MAGIC233	4.6	S	MAGIC162	5.0	S	MAGIC311	4.4	S	MAGIC311
IT00K-1263	5.0	S	MAGIC305	5.1	S	MAGIC212	4.6	S	MAGIC043	5.1	S	MAGIC042	4.5	S	MAGIC042
MAGIC336	5.0	S	MAGIC154	5.1	S	MAGIC281	4.6	S	MAGIC091	5.1	S	MAGIC089	4.5	S	MAGIC089
MAGIC075	5.0	S	MAGIC166	5.1	S	MAGIC337	5.0	S	MAGIC017	5.1	S	MAGIC331	4.6	S	MAGIC331
MAGIC089	5.1	S	MAGIC270	5.1	S	MAGIC113	5.0	S	MAGIC337	5.1	S	IT00K-1263	4.6	S	IT00K-1263
MAGIC180	5.1	S	MAGIC068	5.2	S	MAGIC331	5.1	S	MAGIC125	5.1	S	MAGIC180	4.6	S	MAGIC180
MAGIC202	5.1	S	MAGIC120	5.2	S	MAGIC313	5.1	S	MAGIC139	5.1	S	MAGIC336	4.8	S	MAGIC336

ARAP = Arapai, KAB = Kabanyolo, 23A = Season 2023A, 23B = Season 2023B, WAP = Weeks after planting, R.S = Resistance Status



Box-plots showing the distribution of cowpea genotype response to scab disease in week 10 after planting and the AUDPC, at Kabanyolo and Arapai during seasons 2023A and 2023B. Inside the boxplot, the bold line represents the median, box edges, represent upper and lower quartiles, and whiskers show the maximum and minimum values. ARAP = Arapai, KAB = Kabanyolo, 23A = Season 2023A, 23B = Season 2023B, WAP = Weeks after planting, AUDPC = Area under disease progress curve.

Figure 1. Distribution of cowpea genotypes to scab disease.

yield, number of pods per plant (POD/PLT), number of peduncles per plant (PDC/PLT) (Table 5). For number of pods per peduncle (POD/PDC) and seeds per pod (SEED/POD), genotypes showed significant differences ($P < 0.05$) for genotype by environment interaction effects and environment effects, respectively. In Kabanyolo 2023A and Arapai 2023A, there were significant differences ($P < 0.001$) among the genotypes for only number of seeds per pods and grain yield traits. Kabanyolo 2023B, showed significant differences among genotypes for the number of pods per plant (POD/PLT), number of peduncles per plant (PDC/PLT), pods per peduncle (POD/PDC), grain yield but not for the number of seeds per pod (SD/POD). Overall, Kabanyolo 2023A recorded the highest proportion of the different yield parameters, yet Kabanyolo 2023B recorded the least proportions in the yield parameters (Table 5).

Grain yield. Across the three environments, average grain yield ranged from 138.72 to 1607.77 kg ha⁻¹ with a mean of 830 kg ha⁻¹ (Table 6). Cowpea genotype, MAGIC184 was ranked the best performing genotype with highest mean grain yield of 1607.77 kg ha⁻¹;

though had ranked susceptible for resistance to scab (Table 8). This was followed by MAGIC125 (mean = 1537.33 kg ha⁻¹) and NAROCOWPEA 3 (mean = 1515.89 kg ha⁻¹), which ranked susceptible and resistant, respectively for resistance to scab disease. MAGIC153, on the other hand, ranked the lowest with average grain yield of 138.72 kg ha⁻¹ with a ranking of moderate resistance to scab disease. Overall, NAROCOWPEA 3 (mean = 1515.89 kg ha⁻¹) recorded the highest grain yield values and the least scab disease severity scores across the three environments (Kabanyolo 2023A, Kabanyolo 2023B and Arapai 2023A (Fig. 2).

Based on environment performance, cowpea grain yield in Kabanyolo 2023A, ranged from 56.66 to 3445.6 kg ha⁻¹, with a mean value of 1563.68. NAROCOWPEA 3 had the highest average grain yield of 3445.6 kg ha⁻¹, and ranked moderately resistant to Scab, followed by MAGIC184 with 3375.9 kg ha⁻¹, which was moderately resistant to Scab, and MAGIC327 (mean = 107.3 kg ha⁻¹) had the least amount of grain yield and ranked resistant to Scab.

Cowpea grain yield of Kabanyolo 2023B ranged from 100 to 1406 kg ha⁻¹ with a mean

TABLE 5. Analysis of variance for agronomic traits of cowpea genotypes evaluated in Kabanyolo 2023A, Kabanyolo 2023B and Arapai 2023A

Combined analysis	SOV	Df	POD/PLT	PDC/PLT	POD/PDC	SD/POD	Grain yield (kg ha ⁻¹)
Combined datasets	Genotype	207	86.72***	53.73***	0.13	2.26	430539***
	Env	2	249.4	13.13	0.18	27.12*	11519572**
	Geno*Env	412	72.44***	51.60***	0.13*	2.45	408728***
	Residual	592	50.64	35.33	0.11	31.88	135900
	Mean		19.00	19.52	1.83	10.66	834.48
	CV%		58.98	51.35	34.42	22.13	96.46
	H ²		11.15	8.07	0.00	1.50	4.00
Individual environment							
KAB 23A	Genotype	207	98.06	58.18	0.13	2.49***	1153530***
	Residual	183	84.77	55.26	0.11	1.62	306300
	Mean		28.57	26.04	2.43	12.36	1556
	LSD		18.21	14.68	0.66	2.51	1107
	CV%		32.30	28.57	13.85	10.31	36.06
	H ²		22.00	9.13	26.00	51.78	74.00
KAB 23B	Genotype	207	41.04***	32.74***	0.10***	3.26	128041***
	Residual	183	18.31	12.74	0.05	2.78	45826
	Mean		12.59	11.23	1.27	9.83	590.60
	LSD		8.44	7.04	0.45	3.30	422.40
	CV%		34.00	31.79	17.83	16.96	36.25
	H ²		71.28	75.84	66.66	25.66	78.20
ARAP 23A	Genotype	205	55.46	53.03*	0.13	4.58	48775
	Residual	151	55.14	40.84	0.16	4.83	39669
	Mean		15.48	21.44	1.78	9.723	314.40
	LSD		15.53	13.37	0.84	4.597	416.60
	CV%		47.97	29.80	22.65	22.60	63.36
	H ²		28.78	37.38	0.00	3.35	40.45

*** = Significant at 0.001; ** = Significant at 0.01; * = Significant at 0.05, POD/PLT = Number of pods per plant, PDC/PLT = Number of peduncles per plant, POD/PDC = Number of pods per peduncle, SD/POD = Number of seeds per pod

of 590.62 kg ha⁻¹, and was lower than that of Kabanyolo 2023A. MAGIC083 had the highest average grain yield of 1406 kg ha⁻¹, though it had a disease resistance rating of moderate resistance. This was followed by MAGIC086 (mean = 1405 kg ha⁻¹), also with a disease resistance rating of moderate resistance. MAGIC153 (mean = 100 kg ha⁻¹) and MAGIC091 (mean = 112 kg ha⁻¹), on the other

hand, had the least grain yield, with moderate Scab resistance and susceptible disease ratings, respectively.

In Arapai 2023A, the average grain yield ranged from 8.93 to 985.15 kg ha⁻¹ with a mean of 314.21 kg ha⁻¹. MAGIC200 (mean = 8.93 kg ha⁻¹), ranking susceptible to Scab and MAGIC166 (mean = 17.16 kg ha⁻¹), which ranked moderately resistant to Scab had the

TABLE 6. Mean performance of high yielding and low yielding genotypes in Kabanyolo 2023A, 2023B and Arapai 2023A

Genotypes	D50FLO	D50MAT	PD/PLT	PDC/PLT	PD/PDC	SD/PD	Grain yield (kg ha ⁻¹)
10 top yielding genotypes							
MAGIC184	55.83	80.67	20.43	19.91	1.94	12.13	1607.77
MAGIC125	56.2	83	20	23.4	1.88	12.44	1537.33
NAROCOWPEA 3	53.67	79.17	20.33	18.33	2.07	11.5	1515.89
MAGIC278	54.17	79.33	19.17	18.13	1.67	10.47	1438.3
MAGIC106	51.17	80.17	15.17	18.75	1.8	10.63	1398.89
MAGIC051	54.5	81.67	19.39	22.33	1.65	10.94	1397.38
NAROCOWPEA 4	54.5	78.33	18.8	16.57	1.9	11.27	1378.73
MAGIC209	53.83	79	18.3	22.23	2	10.8	1365.92
MAGIC324	52.4	81	18.2	14.24	1.8	11.4	1350.42
MAGIC190	53.8	81.6	14.2	11.76	1.63	8.8	1343.27
5 low yielding genotypes							
MAGIC120	57.2	87.8	12.34	15.88	1.68	10.02	316.89
MAGIC296	59.83	83.67	15.87	20.2	1.62	9.23	312.78
MAGIC037	62.4	88.4	17.9	24.24	1.89	11.38	255.07
MAGIC166	57.6	83.6	19.41	17.39	1.93	10.54	190.67
MAGIC153	57.4	85	30.68	36	2.43	10.93	138.72
Checks							
NAROCOWPEA 4	54.5	78.33	18.8	16.57	1.9	11.27	1378.73
NAROCOWPEA 2	54.83	83.5	14.7	13.6	1.75	11.67	812.86
NAROCOWPEA 3	53.67	79.17	20.33	18.33	2.07	11.5	1515.89
Mean	55.14	81.25	19.00	19.52	1.83	10.66	830.00
LSD	0.51	0.56	1.44	1.19	0.06	0.34	72.45
CV%	11.91	10.65	58.98	51.35	34.42	22.13	96.46

POD/PLT = Number of pods per plant, PDC/PLT = Number of peduncles per plant, POD/PDC = Number of pods per peduncle, SD/POD = Number of seeds per pod, D50_FLO = Flowering date of 50% of the plot, D50_MAT = Maturity date of 50% of the plot

least grain yield; whereas MAGIC125 (mean = 985.15 kg ha⁻¹), MAGIC313 (mean = 908.72 kg ha⁻¹), and NAROCOWPEA 4 (mean = 840.85 kg ha⁻¹) had the highest grain yield; rated moderately resistant, susceptible and moderately resistant, respectively, for resistance to the disease.

Heritability. To assess the proportion of phenotypic variance attributable to genetic

factors, entry mean basis broad-sense heritability (H^2) was calculated based on single location and combined data across the environments, respectively (Tables 4 and 5); for scab and yield components. Heritability was classified as low (<30%), medium (30-60%) and high (>60%). In the present study, high entry mean basis broad-sense heritability was recorded for scab severity at 10 WAP, ranging

TABLE 7. Phenotypic correlation among 8 quantitative traits of 208 MAGIC population cowpea genotypes evaluated at Kabanyolo 2023A, 2023B and Arapai 2023A

	10 WAP	AUDPC	D50_ FLO	D50_ MAT	POD/ PLT	PDC/ PLT	POD/ PDC	SD/ POD
10 WAP								
AUDPC	0.88***							
D50_FLO	-0.01	0.08						
D50_MAT	-0.14*	-0.08	0.48***					
POD/PLT	-0.05	-0.03	0.11	0.01				
PEDUNCLE/PLT	-0.03	0.04	0.12	-0.04	0.68***			
POD/PDC	-0.01	0.03	0.03	-0.08	0.47***	0.41***		
SEED_POD	-0.05	0.01	0.07	-0.05	0.37***	0.33***	0.29***	
Grain yield_kgha	0.18**	0.11	-0.24***	-0.44***	0.04	0.05	0.13	0.28***

Pearson's correlation coefficients were plotted using means of Scab disease severity scores in week 10 (10_WAP); the AUDPC (Area under disease progress curve) scores calculated from week 8, 9 and 10, excluding week 6 and 7 in which the cowpea plants are still developing the yield components and the Number of pods per plant (POD/PLT), Number of peduncles per plant (PDC/PLT), Number of pods per peduncle (POD/PDC), Number of seeds per pod (SD/POD) and Grain yield (kg ha^{-1})

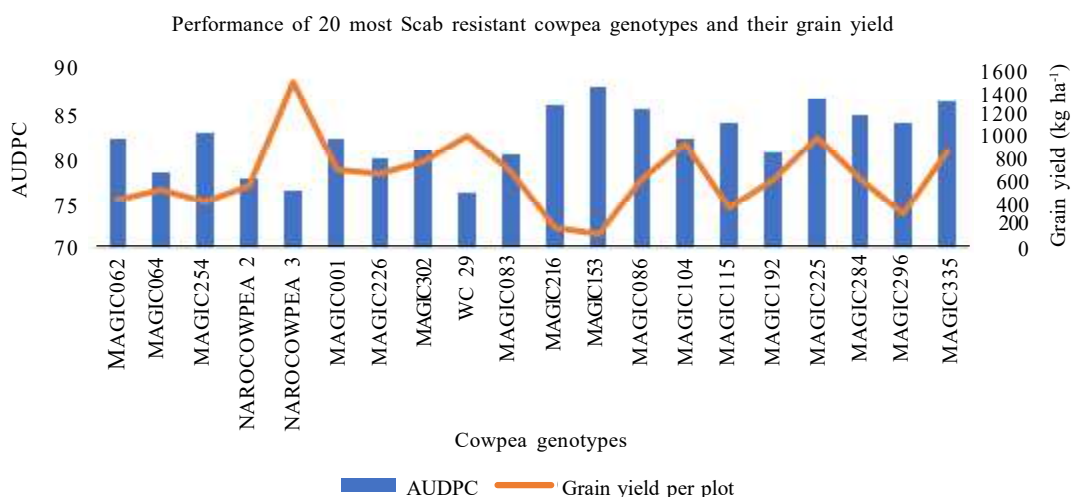


Figure 2. Scab disease severity among 20 most resistant MAGIC lines and their associated grain yield.

from 58 to 75% in Kabanyolo 2023A, Kabanyolo 2023B and Arapai 2023B.

Similarly, medium but stable heritability of 34.13% across environments was recorded at 10 WAP, Grain yield recorded medium to high entry mean basis heritability (74%) for

Kabanyolo 2023A, 78.2% for Kabanyolo 2023B and 40.45% for Arapai 2023A.

Parameter relationships. Scab severity at 10 WAP was negatively correlated with all the yield components studied, that is, number of days

to 50% flowering ($r = -0.01$), the number of peduncles per plant ($r = -0.03$), number of pods per peduncle ($r = -0.01$) and the number of seeds per pod ($r = -0.05$), and high significance with the number of days to 50% maturity ($r = -0.14$, $P < 0.05$). Number of seeds per pod, which was significantly positively correlated ($r = 0.28$; $P < 0.001$) with grain yield, showed a negative correlation with scab severity at 10 WAP. Correlation analysis generally showed that as scab severity increases with the age of the plant, the damage on yield components also increases (Table 7).

DISCUSSION

Disease severity. The highly significant genotypic effects ($P < 0.001$) for the disease traits (10 WAP and AUDPC) across environments and individual environments (Kabanyolo 2023A, 2023B and Arapai 2023B) (Table 3), indicated the presence of substantial phenotypic variation among the cowpea genotypes. This response signifies the presence of different gene combinations within the population, thus, termed as a wide genetic variability, that leads to observable phenotypic differences; which are essential for effective identification and selection of superior and resilient genotypes for trait improvement (Swarup *et al.*, 2021). This wide variability in genotype response justifies the use of the MAGIC population for discovery of additional sources of stable candidate genes associated and genotypes with scab resistance in cowpea (Alvarez *et al.*, 2007).

Results showed a strong influence of environmental factors on the expression of scab disease resistance, by the highly significant environment and genotype-by-environment interaction effects to scab disease (Table 3). Scab resistant genotypes in one environment were found to be moderately resistant or susceptible in the other environments (Table 4). This inconsistent response of genotypes confirms that environmental conditions play a pivotal role in

governing phenotypic outcome of scab resistance and can obscure the true genetic potential of a trait, which complicates selection in breeding programmes (Nakawuka and Adipala, 1997; Afutu *et al.*, 2016). This observation is in agreement with that of Afutu *et al.* (2016), who attributed such inconsistencies to the existence of multiple *Sphaceloma* pathotypes, each potentially adapted to specific environmental conditions. This suggests that cowpea in different growing regions in Uganda may be exposed to pathotypes with varying levels of virulence; leading to location specific difference in disease severity. Thus, careful consideration of target environments is essential when selecting and breeding for stable scab resistance in cowpea breeding.

In the present study, genotypes NAROCOWPEA 2, MAGIC 086 and MAGIC 153, demonstrated that they were specifically adapted to Kabanyolo through their consistent low mean scab severity scores; whereas MAGIC 120, MAGIC 254, MAGIC 083 and MAGIC 064, showed specific adaptation to Arapai environment. Overall, across environments, lines MAGIC 064, MAGIC 254, NAROCOWPEA 2, NAROCOWPEA 3, and MAGIC 062 consistently exhibited lowest scab severity (resistance score 2.1 - 3) (Table 4). These can, therefore, be used as promising parents for breeding of scab resistant cowpea varieties.

The highly diverse MAGIC population as described by (Huynh *et al.*, 2019b), is characterised by different genome blocks inherited from multiple founder parents for resistance or tolerance to biotic and abiotic stresses. The results of this study suggest that this MAGIC population possesses novel and unique combination of alleles, which could confer scab resistance to cowpea scab and also be introgressed into the susceptible cowpea cultivars in Uganda to provide opportunities for improvement of scab resistance in cowpea. In comparison with the checks, the resistant check NE 15 (AUDPC =

70.00, Table 4), expressed lower disease progress compared to the above recommended genotypes. This genotype was identified by Afutu *et al.* (2016; 2017) as a high yielding and resistant cowpea line, against scab in Kabanyolo and Serere locations, and further recommended its use in breeding for scab resistance.

In addition to the effect of genetic factors, the contribution of genotype-by-environment interaction (GEI) and environment factors was also observed to influence the grain yield and other yield traits by highly significant differences ($P < 0.001$) among genotypes (Table 5). The presence of GEI has been reported to reduce selection efficiency in breeding, thus complicating the process of recommending the best performing varieties (Kwabena *et al.*, 2019; Osei *et al.*, 2019). This result justifies the need to explore for stability of genotypes for the grain yield trait in various environments, in order to support cowpea grain yield improvement; especially in low yield areas. Three cowpea genotypes, MAGIC184, MAGIC 125 and NAROCOWPEA 3, recorded the highest grain yield compared to the high yielding checks (NAROCOWPEA 2 (grain yield = 812.86 kg ha⁻¹) and NAROCOWPEA 4 (grain yield = 1378.73) across the three environments, and these will be useful to breeders for improvement of the low yielding types (Table 6).

Disease severity in Kabanyolo environments. Based on individual environments, Kabanyolo 2023B, demonstrated the highest disease pressure (AUDPC = 105.2), possibly due to the high precipitation (680.2 mm day⁻¹) and moderate temperatures (22.3 °C) in that season, which favoured fungal infection and sporulation, thus leading to an increase in *Sphaceloma* spp. inoculum in this location. Scab disease development has been reported to be influenced by lower temperatures and high precipitation, which extends leaf surface wetness and modify the crop microclimate (Agrios, 2005). These conditions enhance pathogen infection, conidial

germination, development; and further dispersal and infection through rain splash and wind drive moisture (Yáñez-López, 2012). Afutu *et al.* (2017), also reported that areas above 1200 m.a.s.l, with moderate temperatures of 23-28 °C, recorded highest scab incidence and severity. This high disease pressure in Kabanyolo 2023B could have led to observation of high phenotypic variation among genotypes, and is suitable for easy identification and selection of scab resistant genotypes. This environment is commendable for selective breeding for the improvement of cowpea yield components. This conforms to the findings of Kityo *et al.* (2021) in a study of aphid resistance in MAGIC population, in which they reported higher aphid pressure in NaSARRI, compared to other locations, and therefore recommended the latter environment as the best for evaluating promising genotypes for resistance of aphids.

Disease severity in Arapai environments.

Generally, in the Arapai location, most of the genotypes were susceptible to scab, indicating that this location had higher *Sphaceloma* sp inoculum, which was represented by the initial average disease pressure (AUDPC = 97.4), compared to that of Kabanyolo (AUDPC = 91.3) in the combined data for both seasons 2023A and 2023B. This high disease pressure could have been triggered by the constant environmental conditions of lower precipitation and moderately high temperatures in both seasons in Arapai (Table 2). This general comparison between the two locations under study, agrees with that of Afutu *et al.* (2017) conducted in Eastern Uganda, close to Arapai, which had a final disease incidence of 100%; yet that in Kabanyolo was between 0 and 43%. They attributed the observation to the more favourable environmental conditions in Serere for scab disease development, thus higher disease pressure. Although in the Afutu *et al.* (2017) study, scab fungus was more virulent under low moisture conditions (136.3 mm in Serere) than of higher rainfall (162.8 mm in Kabanyolo), in the present study, mean annual

precipitation in Arapai was also lower (221.6 mm), than in Kabanyolo (580.6 mm). It is possible that the high disease pressure was triggered by the constant environmental conditions of lower precipitation and moderately high temperatures in Arapai. Talley *et al.* (2020) also demonstrated that scab was more prevalent in low moisture seasons. Therefore, the combination of high inoculum, low moisture conditions and higher temperatures (25.4 °C) than those in Kabanyolo (22.3 °C) could have weakened the defense system of the plants, thus leading to higher scab infections in Arapai.

This finding agrees with conclusions that development of scab disease is favoured by prevailing conditions (Nakawuka and Adipala, 1997; Afutu *et al.*, 2017) relating to the host plant, the pathogen, and the environment; and how they interact (Agrios, 2005; Fitt *et al.*, 2006). For other yield component traits (number of pods per plant, peduncles per plant, pods per peduncle, seeds per pods traits), genotypes responded with non-significant differences across environments and in individual environments, Kabanyolo 2023A and Arapai 2023A, thus showing consistent response, despite the variations in the environmental conditions in the four environments. This further suggests that these yield components can be bred for in any of the above environments, since the genotypes will maintain relatively similar yield levels, regardless of the environmental conditions; thus reducing the negative effects of genotype-by-environment interaction that interfere with selection of superior lines. These results relate to those reported by Konate *et al.* (2016), whereby the evaluation of genetic variability of agro-morphological traits of rice revealed that, except for leaf area and 1000 grain weight, all other characters exhibited stability across the seasons due to insignificant differences among the genotypes.

Heritability. The phenotypic variation observed among genotypes, signifies a high genetic contribution of both scab resistance

and grain yield traits as shown by the high heritability values of Kabanyolo 2023A (66 - 78%), Kabanyolo 2023B (63 -79%) and Arapai 2023B (73 -75%). Similarly, Nakawuka and Adipala (1997) reported that resistance to cowpea scab was controlled by genetic factors, particularly, additive gene action, which is a component of genetic variation (Tables 4 and 5). This finding suggests that traditional selection (such as mass selection, pure-line selection and recurrent selection) based on phenotypic mean scores on genotypes' scab disease severity can be effective and reliable, and result in good response to selection, but also genetic advance (Singh 2001; Tesfaye, 2021).

Moderate heritability estimates ($H^2 = 34.13 - 40.4$) across environments demonstrated the contribution of both genetic and environmental factors; whereas the low heritability values observed across environments and individual environments (Kabanyolo 2023A, Arapai 2023A) for the grain yield trait, showed high contribution of environmental effects to the phenotypic variations by genotypes in these traits. Studies have shown that yield is a complex trait that is influenced by yield components, which are affected by environmental conditions (Tefaye, 2021). Such effects caused by the environmental factors lead to low response to selection and genetic gain, as found in a study by Adewale *et al.* (2010), whereby loss of potential genetic gain was 24% for seeds/ pod and 26% for pod yield.

Correlation of disease and yield traits. The interrelationships between scab disease with all the yield parameters studied (Table 7) signified that the disease is capable of negatively affecting all above ground parts of the plant, with deleterious effects on yield components. By 10 WAP, scab disease was highly severe on the cowpea plants parts, and could lead to 100% yield loss at this high severity, as was also reported earlier by Emechebe (1980); Tumwegamire *et al.* (1998). This finding was supported by

Nakawuka and Adipala (1997), who reported that at 10 WAP of the genotypes, cowpea scab was fully developed, thus highly severe and negatively affecting the yield parameters in susceptible lines.

The negative correlation between number of days to 50% maturity and scab severity at 10 WAP and AUDPC could indicate that the progression of scab severity with age could have led to a reduction in the number of days taken for pods to mature, thus interfering with grain filling processes in the pods, and causing a major reduction in harvest index and grain yield.

Baye *et al.* (2020) reported that grain yield had a significant positive correlation with days to maturity and grain filling period, whereas Dabi *et al.*, 2016 showed that grain yield positively correlated with harvest index. Relating to our study, therefore, scab severity at 10 WAP and AUDPC could have negatively affected the grain filling period, thus reducing the grain yield of cowpea. Furthermore, grain yield, though with low significance, correlated positively (0.28; $P < 0.001$) with number of seeds per pod, signifying that any factor affecting the latter, will reduce grain yield, as demonstrated in these results (Mbong *et al.*, 2012; Afutu *et al.*, 2016). Therefore, since number of seeds per pod is directly related to grain yield, it can be used in selection in order to improve on grain yield trait (Tumwegamire *et al.*, 1998).

CONCLUSION

The variability in MAGIC population observed in the present study can be harnessed to breed for scab disease resistance. The study identified new scab resistant and stable cowpea genotypes across environments; these included MAGIC 064, MAGIC 254, NAROCOWPEA 2, NAROCOWPEA 3, MAGIC 062 from the MAGIC panel. These can be used as parents for breeding varieties that exhibit resistant reaction to the disease in across environments. At Kabanyolo site, lines MAGIC153, MAGIC086 and NAROCOWPEA 2 maintained

resistance; while at Arapai, lines MAGIC254, MAGIC064, MAGIC083 and MAGIC120 exhibited a resistant reaction to scab disease. These lines identified could further be screened for scab disease resistance under artificial inoculation. NAROCOWPEA 3, that was both resistant to scab and high yielding across the three environments is recommended for use in the cowpea improvement program to breed for scab resistance and grain yield traits. Significant genotypic variation observed within and across environments indicated potential for identifying key resistance genes involved in the control of scab expression.

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