INCIDENCE AND SEVERITY OF ANTHRACNOSE (*Colletotrichum lindemuthianum*) ON SELECTED COMMON BEAN (*Phaseolus vulgaris* L.) GENOTYPES

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ABSTRACT

Common bean (*Phaseolus vulgaris* L.), is among the most important legume crop for protein source in peoples' diet globally and including Kenya. Anthracnose (*Colletotrichum lindemuthianum*) is a common disease of legumes that causes yield loss of upto 90-100%. Potential production of common beans in Kenya is expected to be above 2000 kg ha^{-1} but due to challenges of pests and diseases among them anthracnose, it remains below potential yields. The aim of the recent study was to investigate selected common bean genotypes for anthracnose resistance in Kenya. The study was done in three varied agro-ecological zones; Busia, Bungoma and University of Eldoret. Fifteen genotypes were evaluated on field experiment to ascertain anthracnose incidence and severity. Four bean genotypes were used as experimental controls; two resistant and two susceptible controls. Data was collected on incidences and severity and subjected to Analysis of variance in SAS version 9.1. Mean values were separated using Tukeys' Studentized Range Test. The results revealed tolerant and resistant genotypes with lower incidences and severity than those of resistant controls while susceptible genotypes recorded higher incidences and severity than those of the susceptible controls. Tolerant genotypes were; Ciankui, Tasha, and KK8 while the resistant genotypes were; Miezi mbili, KK15 and Chelalang. Site variation was significant at (P≤0.05) with Busia 82%, Bungoma 76% and University of 53%. KK15, Tasha and Chelalang were tolerant in all sites, and this could be attributed to their genetic resistance. The six genotypes identified to be potentially tolerant and resistant to anthracnose and high yielding could be further studied and used in breeding programs for development of resistant lines globally and in Kenya.

Keywords: Common bean, anthracnose, resistance, tolerant and susceptible.

INTRODUCTION

Background information

Common bean (*Phaseolus vulgaris* L.) is one of the most important leguminous vegetable and grain crops grown due to its nutrient and protein content rich pods and grains (Kiptoo *et al.* 2016.; Wagara & Kimani. 2007) and it is a major food security crop in Kenya (Mogita *et al.* 2017). Anthracnose caused by *Colletotrichum lindemuthianum* (Sacc. and Magn.) is a seed-borne fungal disease of the common bean that develops well in relatively cool and humid conditions (Leitich *et al.* 2016). This pathogen is distributed worldwide and affects all vegetative anatomy as well as seeds (Campa *et al.* 2017). It was first discovered in Germany, in 1875.

Food security remains a major challenge in Africa including Kenya. This is due to biotic and abiotic stresses (Mangeni *et al.* 2014). Anthracnose is among the destructive disease of common beans globally and in Kenya (Valentini *et al.* 2017). The fungus *C. lindemuthianum* is primarily a seed-borne pathogen, which can attack all aerial plant parts and may cause yield losses as high as 100% (Mohammed 2014). Infected seed is the main means for spreading from year to year and from location to location for the pathogen. The fungus is highly viable with more than 100 pathogenic variants and races reported in the scientific literature (Katungi *et al.* 2009). Most subsistence farmers in cool areas in Kenya grow common beans, which ultimately are destroyed by diseases, including anthracnose.

A number of common bean breeding lines, landraces and varieties found in Kenyan are also susceptible to anthracnose or their reaction to the fungus is unknown, thereby limiting their improvement for anthracnose resistance (Leitich *et al.* 2016). Despite extensive pathological and molecular studies, the nature and extent of pathogen variability and its reaction to common beans have not been clearly established. *C. lindemuthianum* pathogen is of particular concern because, unlike other fungus, a strategy for the management of bean anthracnose disease is inadequate, especially given the limited chemical options available (Julius *et al.* 2017). Therefore the incidence and severity cases of anthracnose disease in Kenya has posed a serious threat for bean growing areas (Choudhary *et al.* 2018)

Use of anthracnose resistant seeds, which reduces production cost and environmental contamination, is the most efficient strategy for the control of anthracnose. Other cultural methods used to manage the disease include incorporation of the plant debris in the soil which hastens the breakdown of the debris which reduces fungal inoculum and hence reduces the amount of initial inoculum source and crop rotation that include crops other than legumes especially in the areas where anthracnose is known to be present. However, the major limitation for the development of durable resistance in common bean genotypes is the high pathogenic and genetic variability of *C. lindemuthianum*. Because of this high variability, constant monitoring of the common bean genotype seeds to be planted in the field is essential to support breeders in the development of resistant genotypes (Pinto *et al.* 2012). There is therefore need to characterize common bean genotypes grown in Kenya for their tolerance in Kenya basing on their morphological and molecular nature and their reaction to bean anthracnose infection.

MATERIALS AND METHODS

Description of experiment and experimental sites

The field study was carried out at; Busia Agricultural Training Centre (ATC), Bungoma Agricultural Training Centre (ATC) and University of Eldoret (Chepkoilel) Biotechnology field (**Figure 1**). The field experiment was conducted during the long rainy season of 2017 which involved the growing of selected common bean genotypes on the three sites (**Figure 1**) and left for natural infestation of *C. lindemuthianum*.

The field experimental design was a randomized complete block design (RCBD) with three replications. There were 15 blocks and each block had one bean genotype replicated three times, therefore the total blocks in the field experiment were 45. The spacing of bean genotypes was 45 cm between the rows and 15 cm within the rows.

a) Busia Agricultural Training Centre experimental field

Busia lies on $00^0 27'$ 48.0''N, $34^0 06'$ 19.0'' E (Latitude 0.463333; Longitude 34.105278). It is at an average elevation of 1,227 meters above sea level. Busia has an average annual rainfall of 1691 mm. The average temperature is 22℃. Busia climate is classified as tropical (Jaetzold et al., 2009).

The climatic conditions of Busia are favourable for beans. The site is neighbouring Uganda which is a large producer of common beans. The site was therefore chosen for the study to promote growing of common bean genotypes which can be grown in other regions in the country (**Fig. 1**).
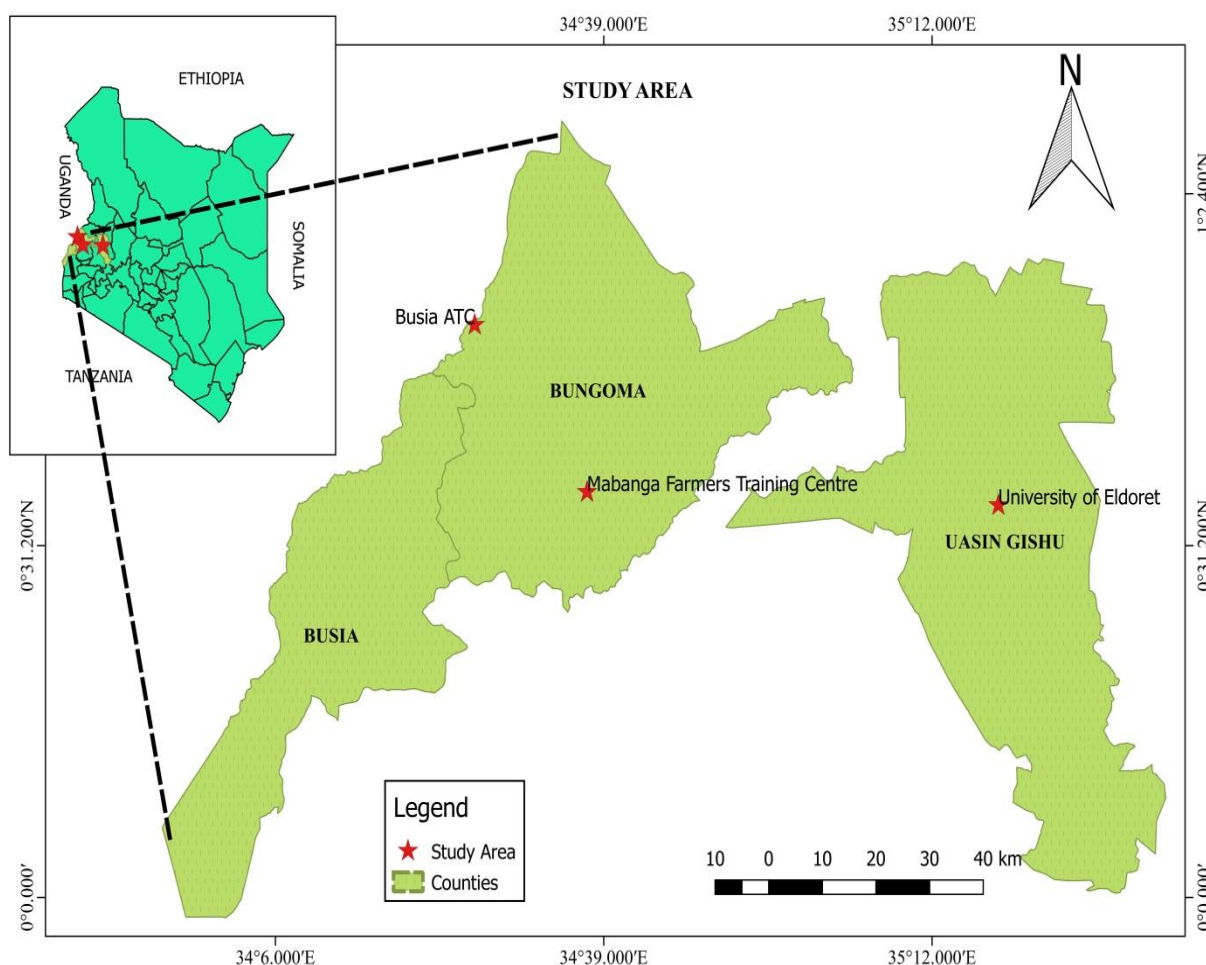
Fig. 1: **Map showing field experimental sites (**Source**; www.mapsofworld.com)**

b) Bungoma Agricultural Training Centre experimental field

Bungoma lies at latitude of 0.569525N and longitude of 34.558376E. It is located at 0.56^0 N 34.56^0 E and has an altitude ranging between 1400-1600 meters above sea level. The mean maximum temperature is 25℃ and relative humidity ranges between 70% and 80% (Jaetzold *et al.* 2009). The site is neighbouring Kakamega region which is a hot spot for bean growing, therefore the study was done in

Bungoma to promote diverse common bean genotypes in the region (**Fig. 1 above**).

c) University of Eldoret (Chepkoilel), Biotechnology field

University of Eldoret lies at latitude 00^0 30' N, longitude 35^0 15'E and an altitude of 2180 meters above sea level. The area is within Uasin-Gishu plateau, which is the lower highlands (LH3) agro—ecological zone. The site

has a maximum temperature of 23℃ and relative humidity ranging between 45% and 55% (Okalebo *et al* 2002). The site is among major maize growing regions in Kenya. Common bean is among the short season crop which can be cultivated for two seasons in a year. The site was therefore selected to promote common bean growing in the region along with maize and to improve the acidic soils of Uasin-Gishu (**Fig. 1 above**).

Table 1: Selected common bean genotypes with description of production altitude, maturity period and grain yields

Genotype	Optional production altitude (mm)	Maturity period (months)	Grain yields (t/ha)	Remarks
KK8	1500-1800	2.5-3.0	1.8-2.0	Tolerant to root rot
KK15	1500-1800	2.5-3.0	1.8-2.0	Tolerant to root rot
Tasha	1000-2000	2.5-3.0	1.5-2.0	Disease and insect pest tolerant
Chelalang	1000-2000	2.5-3.0	1.5-2.0	Disease and insect pest tolerant
Miezi mbili	1000-2000	2.5-3.0	1.2-2.3	Moderately resistant to ALS, Anthracnose, CBB, CBMV
Ciankui	1500-1800	2.5-3.0	1.5-2.0	Disease and insect pest tolerant
Redbean	1500-1800	2.5-3.0	1.8-2.0	
GLP92-Resistant control	1000-1500	3.0-3.5	1.2-1.7	Wide adaptability, resistant to Anthracnose, HB and Bean Common Mosaic Virus (BCMV)
GLP1127-Resistant control	1000-1500	2.5-3.0	1.0-1.5	Wide adaptability, resistant to CBMV, tolerant to rust
GLP2	1000-2000	2.5-3.0	1.0-1.2	Tolerant to Common Mosaic Virus and Anthracnose
B1-Susceptible control	1000-1500	2.5-3.0	1.0-1.2	Moderately susceptible to anthracnose
B2-Susceptible control	1000-2000	2.5-3.0	1.0-1.5	Moderately susceptible to anthracnose
CAL194	1000-2000	2.5-3.0	1.5-1.8	Moderately susceptible to anthracnose
CAL33	1000-2000	2.5-3.0	1.5-1.8	Moderately susceptible to anthracnose
RED13	1000-2000	2.5-3.0	1.5-1.8	Moderately susceptible to anthracnose

Field experiment data collection

Incidences and severities of anthracnose on selected common bean genotypes across the three agro-ecological zones (Busia, Bungoma and University of Eldoret).

Ten plants were selected and pre-tagged from each plot using W-shaped sampling after the plants emerged. Disease epidemic data were collected from pre-tagged plants starting from the onset of the first anthracnose symptoms at

vegetative and reproductive stages. At vegetative stage, the data was taken as from 14 days after bean plant emergence when the cotyledon had started appearing at soil level and begin to separate and develop primary leaves which continue to develop into first, second and third trifoliate leaves which open and the buds on the lower nodes produce branches. At reproductive stage the data was taken from bean plants at flowering when the first flower opens, pod formation when the first pod appeared being

more than 2.5 cm long and at pod filling when the first pod begun to fill (seed growth).

Plants that showed symptoms of anthracnose were counted and the percentage of disease incidence was calculated according to the formula by Wheeler 1969.Disease incidence (I) data were collected as percentage number of plants infected by the disease. Equation (1);
Incidence= Number of plants infected/Number of plants planted x 100%. (1)

The severity of anthracnose on the leaves of pre-tagged common beans plants were graded using standard disease scales of 1-9, where 1- 2= no visible disease symptoms; 3-4= Presence of very small lesions, mostly on the primary vein of the lower leaf's lower side or on the pod, that covers approximately 1% of surface area; 5-6= presents of several small lesions on the petiole or on the primary and secondary veins of the leaf's lower side or small round lesions on the pods with or without reduced sporulation, that covers approximately 5% of the pods surface area; 7-9= presence of enlarged lesions on the lower side of the leaf (Wheeler 2012). Necrotic lesions were also observed on the upper leaf surface and on the petioles.

Table 2: General scale to evaluate the reaction of the selected common bean genotypes to anthracnose (*C. lindemuthianum*)

Rating	Category	Description	Comments
1-2	Resistant	No visible symptoms	Germplasm is useful
3-4	Intermediate	Very light visible symptoms	Germplasm can be used as commercial varieties or as source of resistance to anthracnose
5-6	Susceptible	Symptoms resulting in limited economic damage	Germplasm can be used as commercial varieties
7-9	Susceptible	Severe to very severe symptoms causing considerable yield losses or plant death	Germplasm not useful as resistant parents for anthracnose

Source(van Schoonhoven 1987)

Statistical Data Analysis

Colletotrichum lindemuthianum severity and incidence data were subjected to analysis of variance (ANOVA) using SAS program version 9.1. The general linear model was;

$$X_{ijk} = \mu + R_i + E_j + V_k + EV_{jk} + \varepsilon_{ijk}$$ where;

X_{ijk} – was the overall plot observation

μ- was the grant mean effects for the whole experiment

R_i – was the replication effect of the blocks

E_j – was the environment effects

V_k – was the genotype effects

G*E$_{jk}$ – was the Genotype * Environment interaction effects

ε_{ijk} – was the error term effects

Data was rearranged for ANOVA per site before a combined Analysis of Variance across sites was performed.

Disease Incidence (I) data were collected as percentage (%) number of plants infected/Number of plants planted x 100%.Severity and Incidence of the selected common bean genotype data were subjected to analysis of variance (ANOVA) using SAS program version 9.1. Mean separation was done using tukeys test. Analysis of variance and Pearson Product Moment Correlations was performed for all quantitative traits. Minimum significance difference by tukeys was used to compare the means.

RESULTS AND DISCUSSIONS

Field experiment

Incidence and severity of anthracnose on selected common bean genotypes across the three agro-ecological zones (Busia, Bungoma and University of Eldoret).

Incidence and severity of anthracnose (*Colletotrichum lindemuthianum*) were evident on leaves and pods of the infected common bean genotypes. Resistant common bean genotypes had healthy leaves (**Plate 1**) and pods (**Plate 3**). The susceptible common bean genotypes had symptoms and signs of anthracnose (*C. lindemuthianium*) on leaves (**Plate 2**) and pods (**Plate 4**).

Plate 1: Healthy bean Plant

Plate 2: Bean plant infected with anthracnose

Plate 3: Healthy bean pods

Plate 4: Bean pods infected with anthracnose

In Busia, some genotypes recorded low incidence and severity and these were; Chelalang, GLP2, GLP1127, Miezi mbili and KK15. The genotypes which had moderate incidence and severity were; KK8, Tasha and Ciankui. The high incidence and severity were realized in; RED13, Redbean16, CAL33, CAL194, GLP92, B2 and B1 genotypes (**Table 3**).

The mean incidence and severity in Bungoma also varied among the genotypes (**Table 4**). The low incidence and severity were realized in; Chelalang, GLP2, GLP1127, Miezi mbili and KK8. Moderate incidence and severity was recorded in; KK15 and Tasha and high incidence and severity was evident in; RED13, Redbean16, CAL33, CAL194, GLP92, B2, B1 and Ciankui.

Mean values of incidence and severities among the fifteen genotypes in University of Eldoret site varied significantly *P*≤.05 (**Table 5**). The genotypes which recorded high anthracnose incidence and severities were; RED13, Redbean16, CAL33, CAL194, GLP92, and Ciankui while the genotypes which recorded low incidence and severities were; Tasha, KK15, KK8, Miezi mbili and Chelalang (**Table 5**).

The genotypes which recorded high anthracnose incidence and severities were; RED13, Redbean16, CAL33, CAL194, GLP92 and Ciankui while the genotypes which recorded low incidence and severity were; Tasha, KK15, KK8, Miezi mbili, GLP1127, GLP2 and Chelalang (**Table 6**).

Site variation of incidence on genotypes were highly significant $P \leq 0.05$ at14 days after emergence (DAEI14), days after flowering (DAFI) and days after podding (DAPI) while 28 days after emergence was not significant. Site variation of severity on genotypes was significant $P \leq 0.05$ at 14 days after emergence (DAES14) while 28 days after emergence (DAES28), days after flowering (DAFS) and days after podding were not significant.

Genotype by environment (**Table 6**) was of significance on this study. DAEI14, DAES14, DAES28, DAFS and DAPS were significant at $P \leq 0.05$ and DAEI28, DAFI and DAPI were not significant (ns).

Table 3: Incidence and Severity of anthracnose (*C. lindemuthianum*) in Busia.

Genotype	DAEI14	DAEI28	DAFI	DAPI	DAES14	DAES28	DAFS	DAPS
RED13- **S**	70.00[a]	80.00[a]	75.00[a]	83.33[ab]	7.33[ab]	8.33[a]	8.33[a]	9.00[a]
Redbean16- **S**	70.00[a]	80.00[a]	73.33[ab]	88.33[a]	7.33[ab]	8.00[a]	8.33[a]	9.00[a]
CAL33- **S**	73.33[a]	83.33[a]	76.66[a]	88.33[a]	7.66[a]	8.66[a]	8.66[a]	9.00[a]
CAL194-**S**	50.00[b]	60.00[ab]	53.33[bc]	65.00[bc]	5.00[bcd]	6.00[abc]	6.00[abc]	7.00[ab]
GLP92-**S**	50.00[b]	60.00[ab]	53.33[bc]	65.00[bc]	4.33[cd]	5.00[bcd]	5.00[bcd]	5.66[bc]
B2- **SC**	40.00[bc]	50.00[b]	43.33[cd]	56.66[c]	5.33[abc]	6.33[ab]	6.33[ab]	7.00[ab]
B1- **SC**	40.00[bc]	50.00[b]	43.33[cd]	53.33[c]	4.00[cde]	5.00[bcd]	5.00[bcd]	6.00[abc]
Ciankui- **T**	33.33[bc]	43.33[bc]	36.66[cde]	50.00[cd]	3.33[cdef]	4.33[bcde]	4.33[bcde]	4.66[bcd]
Tasha- **T**	26.66[cd]	36.66[bc]	31.66[def]	45.00[cde]	3.66[cde]	4.00[bcde]	4.00[bcde]	4.33[bcd]
KK15- **R**	10.00[ed]	23.33[cd]	16.66[ef]	28.33[def]	3.00[cdef]	3.00[de]	3.00[de]	3.00[cd]
KK8- **T**	10.00[ed]	23.33[cd]	16.66[ef]	26.66[ef]	2.66[def]	3.33[cde]	3.33[cde]	3.33[cd]
Miezi mbili- **R**	10.00[ed]	20.00[cd]	15.00[f]	23.33[ef]	3.00[cdef]	3.00[de]	3.00[de]	3.00[cd]
GLP1127- **RC**	4.00[e]	11.33[d]	13.33[f]	21.66[f]	1.66[ef]	2.33[de]	2.33[de]	2.33[d]
GLP2- **RC**	1.00[e]	2.00[d]	11.66[f]	21.66[f]	1.00[f]	2.00[e]	2.00[e]	2.00[d]
Chelalang	1.00[e]	2.00[d]	13.33[f]	20.00[f]	1.00[f]	2.00[e]	2.00[e]	2.00[d]
CV%	19.81	18.63	17.58	15.38	21.88	20.19	20.30	20.41
Grand mean	32.62	41.68	38.22	49.11	4.02	4.75	4.77	5.15
Genotype	***	***	***	***	***	***	***	***
MSD	19.56	23.51	20.34	22.87	2.66	2.90	2.93	3.18

Means with the same letter are not significantly different. (*, **, ***) and ns=significant at ((P≤0.05, P≤0.01, P≤0.001) and not significant at (P≤0.05) respectively. S- Susceptible, R- Resistant, T- Tolerance, SC- Susceptible control and RC- Resistant control **DAEI14**=Incidence at 14 days after emergence, **DAEI28**=Incidence at 28 days after emergence, **DAFI**=Incidence at days after flowering, **DAPI**=Incidence at days after podding, **DAES14**=Severity at 14 days after emergence, **DAES28**=Severity at 28 days after emergence, **DAFS**=Severity at days after flowering, **DAPS**=Severity at days after podding.

Table 4: Incidence and Severity of anthracnose (*C. lindemuthianum*) in Bungoma.

Genotype	DAEI14	DAEI28	DAFI	DAPI	DAES14	DAES28	DAFS	DAPS
RED13- **S**	66.66ª	76.66ª	71.66ª	81.66ª	6.66ª	8.33ª	8.33ª	9.00ª
Redbean16- **S**	60.00ᵃᵇ	70.00ᵃᵇ	65.00ᵃᵇ	75.00ᵃᵇ	6.00ᵃᵇ	7.66ᵃᵇ	7.66ᵃᵇ	8.66ᵃᵇ
CAL33- **S**	56.66ᵃᵇᶜ	66.66ᵃᵇᶜ	61.66ᵃᵇᶜ	71.66ᵃᵇᶜ	5.66ᵃᵇᶜ	7.00ᵃᵇᶜ	7.33ᵃᵇ	8.00ᵃᵇ
CAL194- **S**	50.00ᵃᵇᶜᵈ	60.00ᵃᵇᶜ	53.33ᵇᶜᵈ	65.00ᵃᵇᶜ	5.00ᵃᵇᶜᵈ	6.00ᵇᶜ	6.33ᵃᵇ	7.33ᵃᵇ
GLP92- **S**	40.00ᶜᵈᵉ	56.66ᵃᵇᶜ	45.00ᶜᵈᵉ	60.00ᵃᵇᶜ	4.00ᵇᶜᵈᵉ	5.66ᵇᶜᵈ	6.33ᵃᵇ	7.33ᵃᵇ
B2- **SC**	40.00ᶜᵈᵉ	50.00ᵇᶜᵈ	45.00ᶜᵈᵉ	55.00ᵇᶜᵈ	4.00ᵇᶜᵈᵉ	5.00ᶜᵈᵉ	5.33ᵇᶜᵈ	6.00ᵇᶜᵈ
B1- **SC**	46.66ᵇᶜᵈ	60.00ᵃᵇᶜ	51.66ᵇᶜᵈ	65.00ᵃᵇᶜ	5.00ᵃᵇᶜᵈ	6.66ᵃᵇᶜ	7.33ᵃᵇ	8.33ᵃᵇ
Ciankui- **T**	33.33ᵈᵉᶠ	46.66ᶜᵈ	36.66ᵈᵉᶠ	50.00ᶜᵈᵉ	3.66ᶜᵈᵉᶠ	5.00ᶜᵈᵉ	5.66ᵇᶜ	6.33ᵃᵇᶜ
Tasha-**T**	23.33ᵉᶠᵍ	30.00ᵈᵉ	28.33ᵉᶠᵍ	35.00ᵈᵉᶠ	2.00ᵉᶠᵍ	3.66ᵈᵉᶠ	3.66ᶜᵈᵉ	3.66ᶜᵈᵉ
KK15-**T**	20.00ᶠᵍʰ	30.00ᵈᵉ	21.66ᶠᵍʰ	33.33ᵈᵉᶠ	2.33ᵉᶠᵍ	3.33ᵉᶠ	3.33ᶜᵈᵉ	3.33ᵈᵉ
KK8-**T**	13.33ᵍʰⁱ	23.33ᵉᶠ	18.33ᵍʰ	28.33ᵉᶠ	3.00ᵈᵉᶠᵍ	3.00ᵉᶠ	3.00ᵈᵉ	3.00ᵉ
Miezi mbili- **R**	10.00ᵍʰⁱ	23.33ᵉᶠ	15.00ᵍʰ	26.66ᶠ	3.00ᵈᵉᶠᵍ	3.00ᵉᶠ	3.00ᵈᵉ	3.00ᵉ
GLP1127- **RC**	8.33ᵍʰⁱ	16.66ᵉᶠ	13.33ᵍʰ	18.33ᶠ	1.66ᶠᵍ	2.33ᶠ	2.33ᵉ	2.33ᵉ
GLP2- **RC**	4.00ʰⁱ	8.00ᶠ	13.33ᵍʰ	20.00ᶠ	1.00ᵍ	2.00ᶠ	2.00ᵉ	2.00ᵉ
Chelalang- **R**	1.00ⁱ	2.00ᶠ	10.00ʰ	20.00ᶠ	1.00ᵍ	2.33ᶠ	2.33ᵉ	2.33ᵉ
CV%	18.56	17.29	16.48	15.34	18.48	15.35	16.43	16.91
Grand mean	31.55	41.33	36.66	47	3.6	4.73	4.93	5.37
Genotype	***	***	***	***	***	***	***	***
MSD	17.72	21.63	18.29	21.82	2.01	2.20	2.45	2.75

Means with the same letter are not significantly different. (*, **, ***) and ns=significant at ((P≤0.05, P≤0.01, P≤0.001) and not significant at (P≤0.05) respectively. S- Susceptible, R- Resistant, T- Tolerance, SC- Susceptible control and RC- Resistant control. **DAEI14**=Incidence at 14 days after emergence, **DAEI28**=Incidence at 28 days after emergence, **DAFI**=Incidence at days after flowering, **DAPI**=Incidence at days after podding, **DAES14**=Severity at 14 days after emergence, **DAES28**=Severity at 28 days after emergence, **DAFS**=Severity at days after flowering, **DAPS**=Severity at days after podding

Table 5: Incidence and Severity of anthracnose (*C. lindemuthianum*) in University of Eldoret.

Genotype	DAEI14	DAEI28	DAFI	DAPI	DAES14	DAES28	DAFS	DAPS
RED13- **S**	56.66^a	66.66^{ab}	61.66^a	71.66^a	5.66^a	7.66^a	7.66^a	8.66^a
Redbean16- **S**	56.66^a	70.00^a	61.66^a	75.00^a	5.66^a	7.66^a	7.66^a	8.33^a
CAL33- **S**	53.33^{ab}	70.00^a	55.00^{ab}	73.33^a	5.66^a	7.66^a	7.66^a	8.33^a
CAL194- **S**	50.00^{ab}	63.33^{ab}	51.66^{abc}	63.33^{abc}	5.33^{ab}	7.00^{ab}	7.33^{ab}	8.33^a
GLP92- **S**	50.00^{ab}	60.00^{abc}	55.00^{ab}	65.00^{ab}	5.00^{abc}	7.00^{ab}	7.33^{ab}	8.33^a
B2- **SC**	36.66^{bc}	46.66^{bcd}	38.33^{bcd}	48.33^{bcd}	3.66^{abcd}	4.66^{bc}	5.33^{abc}	6.00^{ab}
B1- **SC**	30.00^c	40.00^{cde}	35.00^{cd}	43.33^{cde}	3.00^{cde}	3.66^{cd}	4.00^{cd}	4.33^{bcd}
Ciankui- **T**	30.00^c	46.66^{bcd}	31.66^{de}	48.33^{bcd}	3.33^{bcd}	4.66^{bc}	5.00^{bc}	5.33^{bc}
Tasha- **T**	20.00^{cd}	30.00^{de}	25.00def	31.66^{def}	2.66^{de}	3.00^{cd}	3.00^{cd}	3.00^{cd}
KK15- **R**	10.00^{de}	23.33^{ef}	15.00^{ef}	25.00^{ef}	3.00^{cde}	3.00^{cd}	3.00^{cd}	3.00^{cd}
KK8- **T**	10.00^{de}	23.33^{ef}	13.33^f	25.00^{ef}	3.00^{cde}	3.00^{cd}	3.00^{cd}	3.00^{cd}
Miezi mbili- **R**	10.00^{de}	23.33^{ef}	13.33^f	25.00^{ef}	3.00^{cde}	3.00^{cd}	3.00^{cd}	3.00^{cd}
GLP1127- **RC**	4.00^{de}	8.00^{fg}	11.66^f	18.33^f	1.66^{de}	2.33^{cd}	2.33^d	2.33^d
GLP2- **RC**	1.00^e	2.00^g	10.00^f	15.00^f	1.00^e	2.00^d	2.00^d	2.00^d
Chelalang-**R**	1.00^e	2.00^g	8.66^f	13.33^f	1.00^e	1.66^d	1.66^d	2.00^d
CV%	20.90	17.38	18.23	16.54	19.42	17.08	18.29	19.16
Grand mean	27.95	38.35	32.46	42.77	3.51	4.53	4.66	5.06
Genotype	***	***	***	***	***	***	***	***
MSD	17.69	20.18	17.91	21.41	2.06	2.34	2.58	2.93

Means with the same letter are not significantly different. (*, **, ***) and ns=significant at ((P≤0.05, P≤0.01, P≤0.001) and not significant at (P≤0.05) respectively. S- Susceptible, R- Resistant, T- Tolerant, SC- Susceptible control and RC- Resistant control. **DAEI14**=Incidence at 14 days after emergence, **DAEI28**=Incidence at 28 days after emergence, **DAFI**=Incidence at days after flowering, **DAPI**=Incidence at days after podding, **DAES14**=Severity at 14 days after emergence, **DAES28**=Severity at 28 days after emergence, **DAFS**=Severity at days after flowering, **DAPS**=Severity at days after podding.

Table 6: Incidence and severity cases across the three agro-ecological zones

Genotype	DAEI14	DAEI28	DAFI	DAPI	DAES14	DAES28	DAFS	DAPS
RED13	64.44[a]	74.44[a]	69.44[a]	78.88[a]	6.55[a]	8.11[a]	8.11[a]	8.88[a]
Redbean16	62.22[a]	73.33[a]	66.66[a]	79.44[a]	6.33[ab]	7.77[a]	7.88[ab]	8.66[ab]
CAL33	61.11[a]	73.33[a]	64.44[a]	77.77[a]	6.33[ab]	7.77[a]	7.88[ab]	8.44[ab]
CAL194	50.00[b]	61.11[b]	52.77[b]	64.44[b]	5.11[bc]	6.33[b]	6.55[bc]	7.55[abc]
GLP92	46.66[bc]	58.88[bc]	51.11[bc]	63.33[b]	4.44[cd]	5.88[bc]	6.22[cd]	7.11[bc]
B2	38.88[cd]	48.88[cd]	42.22[cd]	53.33[bc]	4.33[cd]	5.33[bc]	5.66[cd]	6.33[cd]
B1	38.88[cd]	50.00[bcd]	43.33[bcd]	53.88[bc]	4.00[cd]	5.11[bc]	5.44[cd]	6.22[cd]
Ciankui	32.22[ed]	45.55[d]	35.00[de]	49.44[c]	3.44[de]	4.66[cd]	5.00[d]	5.44[d]
Tasha	23.33[ef]	32.22[e]	28.33[e]	37.22[d]	2.77[ef]	3.55[de]	3.55[e]	3.66[e]
KK15	13.33[fg]	25.55[e]	17.77[f]	28.88[de]	2.77[ef]	3.11[ef]	3.11[ef]	3.11[ef]
KK8	11.11[gh]	23.33[ef]	16.11[f]	26.66[de]	2.88[ef]	3.11[ef]	3.11[ef]	3.11[ef]
Miezi mbili	10.00[gh]	22.22[ef]	14.44[f]	25.00[e]	3.00[e]	3.00[ef]	3.00[ef]	3.00[ef]
GLP1127	5.44[gh]	12.00[fg]	12.77[f]	19.44[e]	1.66[fg]	2.33[ef]	2.33[ef]	2.33[ef]
GLP2	2.00[h]	4.00[g]	11.66[f]	18.88[e]	1.00[g]	2.00[f]	2.00[f]	2.00[f]
Chelalang	1.00[h]	2.00[g]	10.66[f]	17.77[e]	1.00[g]	2.00[f]	2.00[f]	2.11[ef]
CV%	20.21	17.88	17.65	15.72	20.20	17.45	18.31	18.60
Grand mean	30.71	40.45	35.78	46.29	3.71	4.67	4.79	5.2
Environment	**	ns	**	**	**	ns	ns	ns
Genotype	***	***	***	***	***	***	***	***
Genotype*Environment	*	ns	ns	ns	*	*	*	*
MSD	10.21	11.90	10.39	11.97	1.23	1.34	1.44	1.59

Means with the same letter are not significantly different. (*, **, ***) and ns=significant at ((P≤0.05, P≤0.01, P≤0.001) and not significant at (P≤0.05) respectively. **DAEI14**=Incidence at 14 days after emergence, **DAEI28**=Incidence at 28 days after emergence, **DAFI**=Incidence at days after flowering, **DAPI**=Incidence at days after podding, **DAES14**=Severity at 14 days after emergence, **DAES28**=Severity at 28 days after emergence, **DAFS**=Severity at days after flowering, **DAPS**=Severity at days after podding.

Results from this study showed that incidence and severity of anthracnose (*C. lindemuthianum*) in the three agro-ecological zones varied significantly (*P*≤0.05). Analysis of variance revealed that selected common bean genotypes were significantly affected by *C. lindemuthianum* pathogen which contributed to high, moderate and low disease incidence and severity depending on the genotype. This is in agreement with studies made by Awori et al., (2018) which reports on pathogen invasion which varies significantly in different genotypes. The analysis of variance of mean disease severity and incidence under field conditions revealed highly significant differences (*P*≤0.001) among the genotypes. The three regions of study showed site variations on incidence and severity among the genotypes and from these results therefore, it is evident that disease incidence and severity differs in different locations and this is in agreement with studies made by Moral *et al.* 2017. From the results, Busia had high incidence and severity of anthracnose on the selected common bean genotypes, followed by Bungoma and University of Eldoret.

The disease incidence and severity variation in the three regions of study could be attributed by the fact that the regions had different agro-climatic conditions, agronomic practices and agro-ecological conditions which could bring about different influences in disease development as in agreement by studies made by Mogita *et al.* 2017. In this study it was observed that the selected common bean genotypes were different in their morphological variations which could be a contributing factor towards *Colletotrichum lindemuthianum* reaction hence variance in anthracnose incidence and severities among the genotypes.

From this study, genotype by environment interaction (G*E) has significant effect on common bean resistance to anthracnose disease, these results are similar those made by Bursin et al., (2007) who reported significant effect of G*E on pests and diseases. Occurrence of significant G*E interaction indicates inconsistent performance of selected common bean genotypes across locations which may be due to selection made in one environment performing better in another environment and this is attributed to distinct agro-ecologies with different longitude, latitude and elevation and this is similar to findings made by Pagi *et al.* 2017

Conclusions and Recommendations

Anthracnose incidence and severity on the susceptible common bean genotypes in the three agro-ecological zones were detected as early as when the plants were at vegetative stage (trifoliate leaves) and progressed to reproductive stage (podding stage), however resistant genotypes did not show any signs of the disease infection. Anthracnose (*Colletotrichum lindemuthianum*) causes great destruction on both leaves and pods and hence may cause major bean yields. Moreover, resistance to bean anthracnose genotypes has historically been overcomed by new pathotypes of *C. lindemuthianum*; hence the genotypes intended for release to farmers should be selected based on genotype disease resistance.

Management of anthracnose by use of resistant common bean genotypes is essential to provide increased bean yields globally and in Kenya. Integrated disease management (IDM), which combines biological, cultural, physical and chemical control strategies may not be enough but rather requires plant genetic resistant which could prove to be more effective and sustainable solution. Growing resistant genotypes is recommended as it is the most effective, easy to use and environmentally friendly management strategy for bean anthracnose disease.

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