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Morphological traits associated with anthracnose (*Colletotrichum lindemuthianum*) resistance in selected common bean (*Phaseolus vulgaris* L.) genotypes

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Common bean is among the most important legume crop for protein source in people's diet globally and including Kenya. Anthracnose is a common disease of legumes that causes yield loss of up to 90-100%. The aim of the study is to investigate the morphological traits associated with anthracnose resistance in selected common bean genotypes in Kenya. The study was done in three varied agro-ecological zones; University of Eldoret, Bungoma and Busia. Fifteen genotypes were evaluated on field experiment to ascertain morphological traits associated with anthracnose resistance. Field experiment was done in a random complete block design. Data were collected on morphological traits and subjected to analysis of variance in SAS version 9.1. The genotypes, Ciankui, Tasha, KK15, KK8, Miezi mbili and Chelalang showed morphological traits that were significantly ($P \leq 0.05$) associated with anthracnose resistance, and also with high grain yields of 1.5 to 2.0 t/ha. Morphological traits associated with common bean anthracnose resistance included Leaf width, leaf length, length of fifth internode of the stems, bracteolate size classification and flower colour. It is recommended that management of anthracnose by use of resistant common bean genotype seeds is essential to provide increased bean yields globally and in Kenya.

Key words: Common bean, anthracnose, morphological traits, resistance.

INTRODUCTION

Background information

Common bean (*Phaseolus vulgaris* L.) is one of the most important grain crops grown globally and in Kenya (Wagara and Kimani, 2007). it is considered a major food security crop in Kenya (Mogita et al*.,* 2017). Beans are rich in vitamins (Ekesa et al*.,* 2019) which constitute lysine, tryptophan, methionine, vitamin B, nicotine acid, calcium and iron (Wagara and Kimani, 2007). Beans in Kenya are also valued for their nitrogen-fixing quality in

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Table 1. Selected common bean genotypes.

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
Red bean 16	1500-1800	2.5-3.0	1.8-2.0	Moderately susceptible to anthracnose
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	Susceptible to anthracnose
B2-Susceptible control	1000-2000	2.5-3.0	1.0-1.5	Susceptible to anthracnose
CAL194	1000-2000	2.5-3.0	1.5-1.8	Susceptible to anthracnose
CAL33	1000-2000	2.5-3.0	1.5-1.8	Susceptible to anthracnose
RED13	1000-2000	2.5-3.0	1.5-1.8	Susceptible to anthracnose

symbiotic relationship with the rhizobium bacteria (Zinga et al*.,* 2017) in the soils.

Anthracnose disease caused by *Colletotrichum lindemuthianum* (Sacc. and Magn.) is a seed-borne fungal disease of the common bean (Leitich et al*.,* 2016). This pathogen is distributed worldwide and also it is found in Kenya. Disease symptoms on bean leaves are evident as dark, linear, and black to brick-red lesions found on the lower surface of the leaf and are mainly seen at primary and trifoliate leaf stage along the veins (Lemessa and Tesfaye, 2005; Manjunath et al., 2012). Field losses may be up to 100% under climatic and soil conditions favourable to the disease (Bassanezi et al., 2001; Lopes and Berger, 2001; Paulert et al., 2009; Tullu et al., 2003). The production and the use of anthracnose resistant seeds is one control and management measure that is effective, safe and cheap in dealing with the disease (Chen et al*.,* 2017).

Food security remains a major challenge in Africa including Kenya. This may be due to biotic and abiotic stresses (Mangeni et al., 2014). Anthracnose is among the destructive disease of common beans globally and including Kenya (Valentini et al., 2017). Most subsistence farmers in cool areas in Kenya grow common beans, which ultimately are destroyed by diseases, including anthracnose (Mangeni et al., 2014).

Quite a number of common bean breeding lines, landraces and varieties used by Kenyan farmers are susceptible to anthracnose or their reaction to the fungus is unknown, thereby limiting common bean genotypes on their improvement for anthracnose resistance (Leitich et al*.,* 2016). Therefore, constant monitoring of the common bean genotypes to be planted in the field is essential to support breeders in the development of resistant genotypes (Pinto et al., 2012). There is, therefore, a need to characterize common bean genotypes grown in Kenya for their tolerance and resistance basing on their morphological trait associated with bean anthracnose infection.

MATERIALS AND METHODS

Description of study areas

Selected common bean genotypes (Table 1) were grown in the fields in different agro-ecological zones; Busia, Bungoma and University of Eldoret.

Busia Agricultural Training Centre experimental field

Busia lies on 00°27’ 48.0’’N, 34°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°C. 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.

Bungoma Agricultural Training Centre experimental field

Bungoma lies at latitude of 0.569525 N and longitude of 34.558376 E. It is located at 0.56° N 34.56° E and has an altitude ranging between 1400-1600 meters above sea level. The mean maximum

temperature is 25°C 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 and therefore the study was done in Bungoma to promote diverse common bean genotypes in the region.

University of Eldoret, Biotechnology field

University of Eldoret lies at latitude 00° 30' N, longitude 35° 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°C and relative humidity ranging between 45 and 55% (Okalebo et al., 2007). 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.

Experimental design and procedures

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.

The selected common beans were left for natural infestation of anthracnose disease. The morphological traits were measured at the vegetative (opening of primary leaves and the development of first, second and third trifoliate leaves) and reproductive stage (flowering, pod formation and pod filling) of development (van Schoonhoven, 1987). Characteristics were measured on ten common bean plants chosen at random from the experimental plot. A total of nine morphological traits were evaluated.

Morphological traits

Leaf width

Ten randomly selected common bean plants were sampled in each plot and three center trifoliate leaves were measured across the leaf veins and the midrib to determine the leaf width using 30 cm ruler. The measurements were recorded in centimeters and later converted to means by SAS program. Leaf width was considered a very important trait in morphological characterization of beans (Nassar et al., 2010) as this could associate with genotype resistance to anthracnose disease.

Leaf length

Ten randomly selected plants were sampled in each plot and three center trifoliate leaves were measured at the leaf base to the apex (along the midrib) using 30cm ruler. The measurements were recorded in centimeters and later converted to means by SAS program. Common bean anthracnose leaf symptoms occur as dark, linear, and black to brick-red lesions on the lower surface of the leaf and along the veins at the trifoliate and primary leaf stage (Lemessa and Tesfaye, 2005; Manjunath et al., 2012); therefore the leaf length could determine association of the genotype resistance to anthracnose.

C. lindemuthianum

Length of the fifth internode

Length of the fifth internode on the main stem was measured in centimeters on ten randomly selected plants using a 30cm ruler and the measurements were recorded. Anthracnose (*C. lindemuthianum*) affects the common bean stems; also brown dark eyespot develops on the young seedlings and stems. Anthracnose infections may cause the common bean leaves, pods and stems to rot and die (Masangwa et al., 2013) length of the fifth internode could therefore be an important trait to determine association with anthracnose resistance in common beans.

Bracteole leaf shape

Three leaves from each bean plant were plucked and evaluated on the bracteole leaf shape by visual determination according to earlier reports, and classification was made as; cordate, ovate, lanceolate or triangular following classification developed by Singh et al. (1991). Anthracnose (*C. lindemuthianum*) symptoms may be evident by the presence of enlarged lesions on the lower side of the leaf (Wheeler, 2012). Necrotic lesions may also be observed on the upper leaf surface and on the petioles of the bean plant. Bracteole leaf shape is therefore an important trait that could determine association of bracteole leaf shape trait with anthracnose resistance in the common beans.

Bracteolate size

The three leaves plucked from each bean plant were then measured using a 30-cm ruler to determine bracteolate of the leaves and classified as small, medium and large. Early anthracnose (*C. lindemuthianum*) symptoms are found on leaves, pods and stems of the cotyledon; the growth and development of the bean plant is stunted due to infection and anthracnose diseased areas may girdle the affected areas like leaves, pods and stems and eventually kill the seedlings (Abraham, 2015). Therefore the size of the bracteolate size was considered an important trait in determining the effects of the disease on different genotypes.

Classification of the corolla

The outer base of the corolla was classified using standard classification; striped or smooth. Different common bean genotypes were classified according to their morphology whether striped or smooth (Vazin, 2015).

Pod beak position classification

Pod beak position was classified as either placental or central. By visual look of the shape of the bean pods, their shapes at the bottom of the pod could give true picture of the pod which gave its classification (Duran et al., 2005) and the pod beak position of all the selected genotypes were evaluated on their association with the anthracnose disease. The most common signs of presence of anthracnose (*C. lindemuthianum*) are on the common bean leaves, pods and stems. Small brown-reddish to black blemishes and distinct circulated dish black to brown border with a black-grayish interior (Vazin, 2015).

Table 2. Growth habit classification and description of *Phaseolus vulgaris.*

Growth habit	Description
Type I	Determinate habit; reproductive terminals on main stem and no further node production on main stem after flowering
Type II	Indeterminate habit (vegetative terminal on main stem); further node production on main stem after flowering; erect branches borne on lower nodes; erect plant with extremely variable guide development.
Type IIIa	Indeterminate habit; moderate note production on main stem after flowering ; prostrate canopy with variable number of branches borne on lower nodes; main stem guide development extremely variable but generally showing poor climbing ability.
Type IIIb	Indeterminate habit; considerable node production on main stem after flowering; heavily branched with variable number of facultative climbing branches borne on lower nodes; guide development variable; plants generally show moderate climbing tendency on supports with resulting cone-shaped canopy
Type Iva	Indeterminate habit; heavy node production on main stem after flowering; branches not well developed compared to main stem development; moderate climbing ability on supports, with fruits load carried relatively uniformly along length of the plant.

Source: van Schoonhoven, 1987.

Growth habit

Growth habit was classified using the CIAT 1-to-4 scale where 1= determinate, 2= erect indeterminate, stems and branches prostrate with little or no climbing ability (Table 2). The common bean genotypes were characterized for growth habit because according to earlier reports, there was an indication of plant growth habit and disease development (van Schoonhoven, 1987)

Flower colour

At reproductive stage when the beans started flowering, (the first flower opened until it was fully opened), visual observation was made to identify the flower colour of each common bean genotype (De Ron et al., 2016).

Data collection

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 were taken as from 14 days after bean plant emergence when the cotyledon had started appearing at soil level and begun to separate and develop primary leaves which continued to develop into first, second and third trifoliate leaves which opened and the buds on the lower nodes produced branches. At reproductive stage the data were taken from bean plants at flowering when the first flower opened, 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).

Data analysis

Data were collected on morphological traits and subjected to ANOVA in SAS version 9.1. Means were separated using Tukeys' and Pearson correlation analysis was done to estimate interrelationships between the morphological traits association with anthracnose resistance on the genotypes. Variability among the qualitative traits was evaluated on varied percentage rates on the traits. Also, morphological clustering was constructed using UPGMA-based dendrogram depicting Euclidean dissimilarity estimates for morphological traits.

RESULTS AND DISCUSSION

Results from the study showed that incidence and severity of anthracnose (*C. lindemuthianum*) in the three agro-ecological zones varied significantly ($p \leq 0.05$). 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 resulted to resistant (R), tolerant (T) and susceptible (S) genotypes. This is in agreement with studies made by Awori et al. (2018) who report pathogen invasion varies significantly in different genotypes. The analysis of variance of mean disease severity and incidence under field conditions revealed highly significant differences ($p \leq 0.001$) among the genotypes. 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).

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 same letters are not significantly different. (*, **, ***) and ns is significant at ((P≤0.05, P≤0.01, P≤0.001) and none 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. S, Susceptible; R, Resistant; T, Tolerance; SC, Susceptible control; RC, Resistant control.

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

Morphological data were collected on quantitative and qualitative traits. Quantitative traits included; leaf width (LW), leaf length (LL) and length of the fifth internode (Table 6), while qualitative traits included; growth habit (GH) which was realized to be determinate in all the genotypes; bracteole shape (BSH) which was found to be ovate in all genotypes; bracteole size (BSI) which was found to be large and medium; standard corolla (STC) in which all genotypes had smooth and pod beak position (PBP) in which all genotypes were placental (Table 6).

Variability among the qualitative traits

Variability among the qualitative traits was evaluated and results showed varied percentage rates on the traits (Table 7). Flower colour (FC) had three types of colour (variables); white (73%), light purple (20%) and dark purple (7%). Growth habit (GH) had only one type of growth habit (variable); determinate (100%). Bracteolate shape (BSH) had only one type of shape (variable); ovate (100%). Bracteolate size (BSI) had two types (variables); medium (27%) and large (73%). The outer base of the standard of the corolla (STC) had one variable; smooth (100%) and pod beak position (PBP) had one variable (100%).

Morphological clustering

UPGMA-based dendrogram depicting Euclidean dissimilarity estimates for morphological traits was constructed (Figure 1). Both quantitative and qualitative traits were grouped by ascending hierarchical clustering into four groups at 0.88 Euclidian distances. The genotypes which were morphologically related based on their morphological characterization were numbered numerically (1-5). Number 1- indicated that; Ciankui, Tasha, KK8, Miezi mbili, Chelalang, GLP1127 and GLP2 were closely related. Number 2- indicated that; KK15 was more close to number 1. Number 3- indicated that; Redbean16 and RED13 were more close to each other. Number 4 (0.86)- showed that; CAL33 and B1 were closely related to each other. Number 5 (0.84), showed

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

Genotype	DAEI14	DAEI28	DAFI	DAPI	DAES14	DAES28	DAFS	DAPS
RED13- S	66.66^{a}	76.66^{a}	71.66^{a}	81.66^{a}	6.66^{a}	8.33^{a}	8.33^{a}	9.00^{a}
Redbean16- S	60.00^{ab}	70.00^{ab}	65.00^{ab}	75.00^{ab}	6.00^{ab}	7.66^{ab}	7.66^{ab}	8.66^{ab}
CAL33- S	56.66^{abc}	66.66^{abc}	61.66^{abc}	71.66^{abc}	5.66^{abc}	7.00^{abc}	7.33^{ab}	8.00^{ab}
CAL194- S	50.00^{abcd}	60.00^{abc}	53.33^{bcd}	65.00^{abc}	5.00^{abcd}	6.00^{bc}	6.33^{ab}	7.33^{ab}
GLP92- S	40.00^{cde}	56.66^{abc}	45.00^{cde}	60.00^{abc}	4.00^{bcde}	5.66^{bcd}	6.33^{ab}	7.33^{ab}
B2- SC	40.00^{cde}	50.00^{bcd}	45.00^{cde}	55.00^{bcd}	4.00^{bcde}	5.00^{cde}	5.33^{bcd}	6.00^{bcd}
B1- SC	46.66^{bcd}	60.00^{abc}	51.66^{bcd}	65.00^{abc}	5.00^{abcd}	6.66^{abc}	7.33^{ab}	8.33^{ab}
Ciankui- T	33.33^{def}	46.66^{cd}	36.66^{def}	50.00^{cde}	3.66^{cdef}	5.00^{cde}	5.66^{bc}	6.33^{abc}
Tasha-T	23.33^{efg}	30.00^{de}	28.33^{efg}	35.00^{def}	2.00^{efg}	3.66^{def}	3.66^{cde}	3.66^{cde}
KK15-T	20.00^{fgh}	30.00^{de}	21.66^{fgh}	33.33^{def}	2.33^{efg}	3.33^{ef}	3.33^{cde}	3.33^{de}
KK8-T	13.33^{ghi}	23.33^{ef}	18.33^{gh}	28.33^{ef}	3.00^{defg}	3.00^{ef}	3.00^{de}	3.00^{e}
Miezi mbili- R	10.00^{ghi}	23.33^{ef}	15.00^{gh}	26.66^{f}	3.00^{defg}	3.00^{ef}	3.00^{de}	3.00^{e}
GLP1127- RC	8.33^{ghi}	16.66^{ef}	13.33^{gh}	18.33^{f}	1.66^{fg}	2.33^{f}	2.33^{e}	2.33^{e}
GLP2- RC	4.00^{hi}	8.00^{f}	13.33^{gh}	20.00^{f}	1.00^{g}	2.00^{f}	2.00^{e}	2.00^{e}
Chelalang- R	1.00^{i}	2.00^{f}	10.00^{h}	20.00^{f}	1.00^{g}	2.33^{f}	2.33^{e}	2.33^{e}
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 same letters are not significantly different. (*, **, ***) and ns is significant at ((P≤0.05, P≤0.01, P≤0.001) and none 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. S, Susceptible; R, Resistant; T, Tolerance; SC, Susceptible control; RC, Resistant control.

that; B2 and GLP92 were more closely related to each other than CAL194 which is distantly related.

Some of the common bean genotypes that were grown in different sites of the study had different flower colours. Majority of the genotypes (CAL33, CAL194, GLP92, B2, Ciankui, Tasha, Miezi mbili, KK8, GLP1127, GLP2 and Chelalang) had white flower colour while few of them (RED13, Redbean16, B1 and KK15) had purple flower colour (Figures 2 and 3).

Leaf width

The results of the common bean leaf width in centimeters of the three center trifoliate leaves in the fifteen common bean genotypes revealed significant different measurements. Twelve genotypes; CAL33, RED13, Redbean16, B1, Ciankui, Tasha, Miezi mbili, KK8, KK15, GLP1127, GLP2 and Chelalang had long leaf width above 10 cm while three genotypes; CAL194, GLP92 and B2 had leaf length of below 10 cm. The bean genotypes which had long leaf width of above 10 cm were realized to be resistant and tolerant to anthracnose (*C. lindemuthianum*) while the genotypes which had short leaf width of average 7 to 10 cm showed anthracnose susceptibility on the genotypes. Similarly, Nassar et al. (2010) reported that leaf width may influence disease damage on the leaf. Wide leaf width has large surface area hence the time taken by disease invasion could be long and finally the bean plant may survive through escape mechanism in host plant resistance. Leaf width in the recent research therefore had significant influence on the anthracnose resistance on common bean genotypes.

Leaf length

The results of leaf length proved that, Leaf length was a trait that seems to have contributed to anthracnose resistance and tolerance in most of the common bean genotypes. Among the fifteen genotypes, which were under study, only three (CAL194, GLP92 and B2 were found to have leaf length measuring less than 10 cm and these genotypes recorded high incidence and severities of anthracnose and were considered to be susceptible. The remaining twelve genotypes; CAL33, RED13, Redbean16, B1 Ciankui, Tasha, Miezi mbili, KK8, KK15, GLP1127, GLP2 and Chelalang had leaf length measuring more than 10 cm and these genotypes proved to be anthracnose tolerant. Therefore from the results, leaf length is associated with anthracnose resistance; the longer the leaf the better it could be able to overcome the

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 same letters are not significantly different. (*, **, ***) and ns is significant at ((P≤0.05, P≤0.01, P≤0.001) and none 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. S, Susceptible; R, Resistant; T, Tolerance; SC, Susceptible control; RC, Resistant control.

diseases invasion like anthracnose (*C. lindemuthianum*). Leaf length was not dependent on environment and hence the environment was not significant. Environment and genotype interaction was not significant on leaf length trait but genotypes were highly significant on leaf length trait. This is explained by research of Siahpoosh et al. (2015) which reported leaf length trait as a factor that influenced disease resistance in common bean genotypes. Leaf length therefore in this study had significance in anthracnose resistance.

Length of the fifth internode

The length of the common bean stem fifth internode on the main stem measured in the fifteen genotypes showed some discrimination between the resistant, tolerant and susceptible genotypes. The measurements varied among all the genotypes and these results are in agreement with the studies made by Maras et al. (2016) who reported the stem length of fifth internode on the main stem of common bean genotypes to be associated with disease incidence and severity cases. Environment x genotype interaction was not significant but the genotypes were highly significant at $p \leq 0.001$. Length of the fifth internode on the common bean genotypes was significant to anthracnose resistance.

Bracteolate shape classification

The fifteen genotypes were characterized as having ovate bracteole shape leaves. Visual observation made on the fifteen genotypes revealed broadly ovate leaflets with acuminate apices, the petial of the terminal leaflets were longer than those below. Past research made by Buah et al. (2017) and Maras et al. (2016) classified bracteole shape of plant leaves into; cordate, ovate, lanceolate and triangle. Therefore the recent research characterized the fifteen bean genotypes under field study as having one variable (100%), which was ovate leave shape and therefore there was no significance of leaf shapes in anthracnose resistance.

Bracteolate size classification

Bracteole size revealed to be broadly ovate, thin, glabrous to pubescent which measured 4-16 cm long and 2.5-11 cm broad. Bracteolate size varied significantly among the genotypes at $p \leq 0.001$ and this is in accordance with earlier studies made by Buah et al.

Table 6. Morphological traits associated with *C. lindemuthianum* resistance in the selected common beans.

Genotype	LW	LL	LC	FC	GH	BSH	BSI	STC	PBP
CAL33-S	11.00^{a}	11.00^{a}	11.44^{ab}	White	Determinate	Ovate	Medium	Smooth	Placental
RED13-S	10.77^{a}	7.38^{a}	10.11^{d}	Pink	Determinate	Ovate	Large	Smooth	Placental
Redbean16-S	10.94^{a}	10.94^{a}	10.11^{d}	Pink	Determinate	Ovate	Large	Smooth	Placental
CAL194-S	7.38^{b}	6.11^{b}	8.00^{g}	White	Determinate	Ovate	Large	Smooth	Placental
GLP92-S	7.50^{b}	6.00^{b}	8.44^{fg}	White	Determinate	Ovate	Medium	Smooth	Placental
B2-SC	7.44^{b}	6.00^{b}	9.00^{e}	White	Determinate	Ovate	Medium	Smooth	Placental
B1-SC	10.88^{a}	10.88^{a}	11.77^{a}	Pink	Determinate	Ovate	Medium	Smooth	Placental
Ciankui-T	11.05^{a}	11.05^{a}	10.88^{c}	White	Determinate	Ovate	Large	Smooth	Placental
Tasha-T	10.88^{a}	10.88^{a}	11.38^{abc}	White	Determinate	Ovate	Large	Smooth	Placental
Miezi mbili-R	10.66^{a}	7.33^{a}	8.77^{ef}	White	Determinate	Ovate	Large	Smooth	Placental
KK8-T	11.11^{a}	11.11^{a}	10.00^{d}	White	Determinate	Ovate	Large	Smooth	Placental
KK15-R	11.11^{a}	11.11^{a}	11.00^{bc}	Purple	Determinate	Ovate	Large	Smooth	Placental
GLP1127-RC	11.00^{a}	11.00^{a}	11.50^{ab}	White	Determinate	Ovate	Large	Smooth	Placental
GLP2-RC	10.66^{a}	7.33^{a}	11.88^{a}	White	Determinate	Ovate	Large	Smooth	Placental
Chelalang-R	10.77^{a}	10.77^{a}	11.44^{ab}	White	Determinate	Ovate	Large	Smooth	Placental
CV%	4.39	3.09	2.98						
Grand mean	10.21	7.12	10.38						
Environment	ns	ns	ns						
Genotype	**	**	**						
Genotype*Environment	ns	ns	ns						
MSD	0.73	0.36	0.51						

Means with same letters within column are not significantly different. (*, **, ***) and ns is 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. LW=Leaf width; LL=Leaf length; LC=Length of fifth internode; GH=Growth habit; BSH=Bracteole shape; BSI=Bracteole size; STC=Standard corolla; PBP=Pod beak position.

Table 7. Percentages of genotypes showing different qualitative traits.

Variability	Variable	Rate (%)
Flower colour	White	73
	pink	20
	purple	7
Growth habit	Determinate	100
Bracteolate Shape	Ovate	100
Bracteolate Size	Medium	27
	Large	73
Standard Corolla	Smooth	100
Pod Beak Position	Placental	100

FC=Flower colour; GH=Growth habit; BSH=Bracteole shape; BSI=Bracteole size; STC=Standard corolla; PBP=Pod beak position.

(2017) in which the bracteole size of plants was classified to small, medium and large. The fifteen genotypes were therefore characterized into two types; medium and large. Genotypes with large bracteolate size had variability of 73% while genotypes with small bracteolate size had 27%. Therefore larger population of genotypes had large bracteolate size and most of the genotypes having large bracteolate size were those which exhibited anthracnose

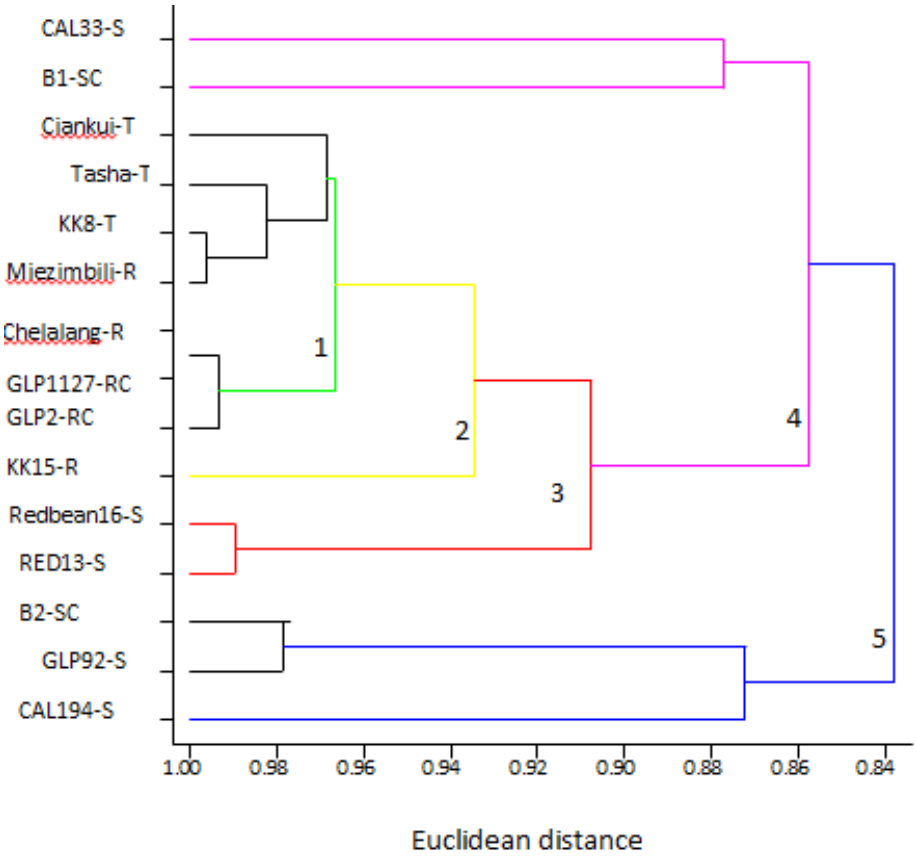

Figure 1. Morphological clustering. S, Susceptible; R, Resistant; T, Tolerant; SC, Susceptible control; RC, Resistant control.

Figure 2. Purple flower colour.

Figure 3**.** White flower colour.

resistance and tolerance. The bracteolate size classification in the study therefore had significance in association with anthracnose resistance.

The outer base of the standard of the corolla of common bean genotypes

The outer base of the standard of the corolla in common beans was all classified as smooth and therefore had one variable (100%), the smooth base. There was no significant difference among the selected common bean genotypes regarding the morphological characteristic of the outer base of the corolla. Therefore the outer base of the corolla did not have any significance in the anthracnose resistance.

The pod beak position of common bean classified as either placental or central

Pod beak positions of the fifteen genotypes studied under field experiment were characterized as having placental pod position only and this was considered as one variable (100%). Similarly, Neupane et al. (2008) reported that most of the common bean genotypes are classified as having either placental or central pod beak position and in relation to anthracnose resistance. The pod beak position is one of the major characters of beans used to identify a particular genotype in association with disease resistance as reported by Neupane et al. (2008). The pod beak position in this study did not show any significance on anthracnose resistance.

Growth habit classification

Growth habit for the genotypes was characterized as determinate type (Type I) where the common bean plant reproductive terminals were on main stem and no further node production on main stem after flowering. Earlier report made by Singh et al. (1996) is able to determine growth habit of common beans into two types; determinate and indeterminate growth habit. The selected common bean genotypes under the recent study demonstrated determinate growth habit only which was considered to be one variable (100%). The determinate growth habit has been exploited for crop breeding to decrease plant biomass and to optimize allocation between vegetative and reproductive growth and this may reduce disease and pests incidence and severities as reported by Sonah et al. (2015). Therefore the growth habit of the genotypes in the study did not demonstrate any significance of anthracnose resistance.

Flower colour

The fifteen genotypes grouped themselves into three groups according to flower colour: those with white and purple, pink and purple flower colour. The flower colour therefore had three variables; white (73%), pink (20%)

and purple (7%). The white flower colour was seen in; CAL33, CAL194, GLP92, B2, Ciankui, Tasha, Miezi mbili, KK8, GLP1127, GLP2 and Chelalang. The genotypes with pink flower colour were; Red13, Red bean16 and B1. The genotype with purple flower colour was KK15 and which was realized to be resistant to anthracnose. The genotypes that had purple flower colour were associated with anthracnose resistance. This is in accordance with research made by Rodiño et al. (2003), where flower colour was associated with disease resistance. Therefore, from the results purple colour was associated with disease resistance because the genotype KK15 which had purple colour were resistant to anthracnose unlike the genotypes which had white flower colour and most of them (CAL33, CAL 194, and B2) were susceptible to the anthracnose disease. Therefore, flower colour trait was significant in this research in associating with anthracnose resistance.

Conclusions and recommendations

Five morphological traits of the selected common bean genotypes which showed significant ($p \leq 0.05$) association with anthracnose resistance in the genotypes were; leaf width, leaf length, length of fifth internode of the stems, bracteole and flower colour. Therefore, morphological traits association with anthracnose resistance was a good indicator for determining potential best genotypes which were resistant and tolerant to anthracnose (*C lindemuthianum*) and of potential use to farmers and plant breeders. The germplasm used represented a valuable source of morphological diversity which could be exploited by plant breeders towards the improvement of the common bean resistance against pest and diseases. Thus, selection of common bean genotypes which are resistant based on morphological traits could certainly lead to genetic improvement in common bean production, hence boost the country's economy through providing income and improved food security.

It is therefore recommended that the five morphological traits which were found to associate with anthracnose resistance (leaf width, leaf length, length of fifth internode of the stems, bracteole and flower colour) can be considered for use by farmers when selecting anthracnose resistant genotypes to plant in their fields.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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