Journal of Agricultural Science and Food Research

Awori et al., J Agri Sci Food Res 2018, 9:2

Research Article Open Access

Resistance Sources to Bean Anthracnose Disease in Uganda and Brazil

Awori E[1,2], Kiryowa M[2*], Souza TLPO[3], Vieira AF[4], Nkalubo ST[2], Kassim S[2] and Tusiime G[1]

[1]*College of Agricultural and Environmental Sciences, Makerere University, PO Box 7062, Kampala, Uganda*

[2]*National Agricultural Research Organization, PO Box 295, Entebbe, Uganda*

[3]*Embrapa Rice and Beans, 75.375-000, Santo Antonio de Goias, GO, Brazil*

[4]*Federal University of Goiás (UFG), 74.690-900, Goiania, GO, Brazil*

[*]**Corresponding author:** Kiryowa M, National Agricultural Research Organization, PO Box 295, Entebbe, Uganda, Tel: +256783224819; E-mail: m.kiryowa@gmail.com

Rec date: April 04, 2018; **Acc date:** May 11, 2018; **Pub date:** May 27, 2018

Abstract

Bean anthracnose caused by the fungus *Colletotrichum lindemuthianum* is among the most destructive diseases of common bean in Uganda, Brazil and worldwide, especially in the high altitude and low temperature areas. This study was conducted to identify sources of effective resistance for use in bean breeding program in both Uganda and Brazil. Through mutual germplasm exchange, 11 bean cultivars were obtained from Embrapa, Brazil; and 13 cultivars were sent from Uganda to Embrapa, Brazil. The exchanged materials together with 12 differential cultivars and susceptible checks were evaluated in the field for two seasons in Uganda and Brazil. The germplasm was further evaluated in Uganda under controlled conditions using three *C. lindemuthianum* races 336, 375, and 381. The experiments were laid in a randomized complete block design with 3 replicates and disease severity data was scored using a 1-9 scale: 1=no symptoms and 9=dead plants. The results showed the cultivars G2333 (*Co-4*^{2}*, Co-5*^{2}*, Co-7=Co-3*^{5}), TU (*Co-5*), AB136 (*Co-6, Co-8*), Kaboon (*Co-1*^{2}), K10 (*Co-4*^{2}*, Co-3*^{4}*, Co-5, Co-6*), K13 (*Co-4*^{2}), SEL 1308 (*Co-4*^{2}) and BRS Cometa to be the most effective against *C. lindemuthianum* among the germplasm screened in both Uganda and Brazil. The lines BRS Ametista, BRS Horizonte as well as BRS Pontal, whose resistance genes are not yet characterized, also showed good resistance in both countries. Breeding programs in Uganda and Brazil should make use of the resistance genes *Co-4*^{2} (G2333, SEL1308), *Co-5* (G2333, Tu), *Co-3*^{4} (K10), *Co-6, Co-8* (AB136) and *Co-1* (Kaboon) through either single gene deployment or in gene pyramid combinations for effective control of diverse *C. lindemuthianum* pathotypes. The resistance in the cultivars K10, BRS Ametista, BRS Horizonte and BRS Pontal should be characterized to identify the genes responsible for the observed resistance.

Keywords: Cultivars; Anthracnose disease resistance; *Colletotrichum lindemuthianum*; *Phaseolus vulgaris*

Introduction

Common beans, *Phaseolus vulgaris* (L.), are the most important legume for human consumption in the world and are the second most important source of dietary protein and the third most important source of calories, for nearly 500 million people in Africa, Latin America and the Caribbean [1,2]. Global bean production in 2013 was approximately 23.4 million metric tons, with 23.2% and 25.8% of the world production in Latin America and Africa, respectively [3], with an annual market value of about US $10 billion [1]. Brazil is the main producer of common bean followed by India, China, United States of America and Mexico [4]; while in Africa, Tanzania, Uganda and Kenya lead in production with volumes estimated at 950,000 MT, 455,000 MT and 390,598 MT respectively [5]. Damage by insect pests and diseases, however, constrains common bean production worldwide with more than 45 diseases reported to affect the common bean [6]. Bean anthracnose disease caused by the fungus *Colletotrichum lindemuthianum* is among the most destructive of common bean diseases and with favorable conditions can cause complete yield loss on susceptible cultivars. The disease occurs worldwide wherever the common bean is grown [7,8].

Growing resistant varieties has been recommended as the most effective, easy to use, and environmentally-friendly management strategy for bean anthracnose disease [9,10]. However, due to the high degree of genetic and physiologic variability of *C. lindemuthianum*, management using especially single gene resistance is complicated due to breakdown of resistance [11]. In Uganda, Kiryowa et al. and Nkalubo et al. reported the differential cultivars G2333 (*Co-4*^{2}*, Co-5*^{2}*, Co-7=Co-3*^{5}), Cornell 49-242 (*Co-2*), Tu (*Co-5*) and AB136 (*Co-6, Co-8*) as highly effective [10,12]; while in Brazil, Souza et al. reported the differential cultivars G2333 (*Co-4*^{2}*, Co-5*^{2}) and AB136 (*Co-6, Co-8*) as highly effective in conferring broad-spectrum resistance to *C. lindemuthianum*. However, with the high pathogen diversity, and frequent emergence of new pathotypes, it is important to identify new sources of effective resistance to bean anthracnose disease. The purpose of this study, therefore, was to identify new sources of effective resistance to bean anthracnose disease in Uganda and Brazil [13,14].

Materials and Methods

In Uganda, field screening was conducted at Kachwekano Zonal Agricultural Research and Development Institute (KaZARDI), Kabale district, South western region. Kachwekano ZARDI is geographically located at 01°15'S latitude and 029°'E longitude and at an altitude of 2,200 m above sea level (a.s.l). KaZARDI experiences moderate temperature (10.9°C-24.4°C) and high moisture conditions [15], which favors development of bean anthracnose disease, making it a hot spot for bean anthracnose. Kabale district experiences bi-modally distributed rainfall with the long heavy rains from March to May and

shorter rains from October to November. Controlled screening was conducted at Abi Zonal Agricultural Research and Development Institute (Abi ZARDI), which lies within latitude of 3°4.58' N and 30°56 E and 1,206 m.a.s.l, Arua district, West Nile. In Brazil, field screening was conducted at Embrapa Arroz e Feijão, Santo Antônio de Goiás, geographically located at 16°29'S latitude and 49°18'E longitude and at an altitude of 823 m.a.s.l.

Germplasm used in the study

The germplasm used in the study (Tables 1 and 2) included 11 cultivars obtained from the Brazilian Agricultural Research Corporation (Embrapa), 12 standard bean differential cultivars used to characterize *C. lindemuthianum*, locally grown susceptible checks K132, Nabe 13, Nabe 14 and pyramided lines 136/2 (8) and 142/4 (4).

S.No	Genotype*	Resistance genes	Original source	Gene pool	Details
1	BAT93	*Co-9=Co-3*^{3}	CIAT	MA	Important resistance source worldwide
2	SEL1308	*Co-4*^{2}	CIAT	MA	Important resistance source worldwide
3	Rosinha G2	None	Brazil	MA	Susceptible check used in Brazil
4	Ouro Negro (Honduras 35)	*Co-10=Co-3*^{4}	CIAT	MA	Important resistance source in Brazil
5	K13	*Co-4*^{2}	Brazil	MA	Important resistance source in Brazil
6	K23	*Co-5*	Brazil	MA	Important resistance source in Brazil
7	K10	*Co-4*^{2}*, Co-3*^{4}*, Co-5, Co-6*	Brazil	MA	Important resistance source in Brazil
8	BRS Pontal	Unknown	Embrapa, Brazil	MA	Important resistance source in Brazil
9	BRS 9435 Cometa	Unknown	Embrapa, Brazil	MA	Important resistance source in Brazil
10	BRS Horizonte	Unknown	Embrapa, Brazil	MA	Important resistance source in Brazil
11	BRS Ametista	Unknown	Embrapa, Brazil	MA	Important resistance source in Brazil
12	K132	None	Uganda	A	Released variety in Uganda
13	Nabe13	None	NARO, Uganda	A	Released variety in Uganda
14	Nabe14	None	NARO, Uganda	A	Released variety in Uganda
15	136/2(8)	*Co-4*^{3}	NARO, Uganda	MA	Line developed in Uganda
16	142/4(4)	*Co-5*	NARO, Uganda	MA	Line developed in Uganda

Table 1: Germplasm and source of origin. *A=Andean; MA=Mesoamerica.

Place number	Differential Cultivar	*Notation (n)	*Binary Code (2^n)	Resistance Gene	Gene Pool
1	Michelite	0	1	*Co-11*	MA
2	MDRK	1	2	*Co-1*	A
3	Perry Marrow	2	4	*Co-1*^{3}	A
4	Cornell 49-242	3	8	*Co-2*	MA
5	Widusa	4	16	*Co-1*^{5}	A
6	Kaboon	5	32	*Co-1*^{2}	A
7	Mexico 222	6	64	*Co-3*	MA
8	PI 207262	7	128	*Co-4*^{3}*, Co-9=Co-3*^{3}	MA
9	TO	8	256	*Co-4*	MA
10	TU	9	512	*Co-5*	MA
11	AB 136	10	1024	*Co-6*	MA

12	G2333	11	2048	*Co-4*^{2}, *Co-5*^{2}, *Co-7=Co-3*^{5}	MA

Table 2: The 12 standard differential cultivars. *The Notation and designated binary codes are used in *C. lindemuthianum* race assignment. A=Andean; MA=Mesoamerica.

Field screening of germplasm and data collection

In Uganda, the entire set of germplasm was evaluated for two seasons using randomized complete block design (RCBD) with three (3) replicates in plots measuring 1.5 m × 1.5 m at spacing of 50 cm × 20 cm. In Brazil, the field screening was conducted using a randomized complete block design (RCBD) with three replicates in single row plots of 1 m and spacing of 50 cm × 20 cm.

In both Uganda and Brazil, field screening for disease severity was performed at plant growth stages V5 and R9, using a 1-9 disease severity scale [16]; where 1=plots with no disease symptoms and 9=plots with 80 to 100% of infected plants. In this scale, 1 to 3.0 mean 1%-10% pods with lesion (resistant), 3.1 to 4.0 means 11%-25% pods with lesion (moderately resistant), 4.1 to 5 mean 26%-50% pods with lesions (susceptible), 5.1 to 7 means over 50% pods with lesions (susceptible) while 7.1 to 9 means defoliation and plant death (susceptible).

Controlled screening of germplasm

Inoculum preparation: Cultures were prepared on petri-dishes using modified Mathur's Agar media (500 g) made up of 4 g of Dextrose, 1.25 g of Magnesium Sulphate, 1.35 g of Potassium Phosphate, 1.2 g of Neopeptone, 1 g of Yeast extract and 8 g of Agar, to get pure isolates and increase sporulation [7]. Cultures were incubated at 22-24°C for 7 to 10 days to allow formation of conidial spores. For inoculation purposes, conidial spores were scrapped off the growth medium into a small amount of water to make a suspension. Using a haemocytometer the concentration was adjusted to 1.2×10^6 conidia ml^{-1} [17] and 0.1% Tween 20 was added as a surfactant.

Characterization of *C. lindemuthianum* races: In Uganda, five *C. lindemuthianum* isolates were obtained from CIAT-Uganda and characterized using the binary nomenclature system [18] that uses 12 standard differential cultivars (Table 2). According to this system, each cultivar has a notation (n) and a designated binary code (2^n). The sum of the numbers assigned to each infected cultivar of the differential set determined the number or race designation of the isolate used. Three races 336, 375, and 381 were characterized and used in Uganda.

Inoculation, data collection and analysis: In Brazil, screening was done by spraying inoculum on seedlings in an anthracnose-controlled screen-house. In Uganda, pre-germinated seeds of the germplasm were inoculated by soaking for 30 minutes in inoculum of each of the *C. lindemuthianum* races and the seedlings transplanted in plastic trays containing a mixture of sterile loam soil and sand at a ratio of 2:1. Experiments in both Uganda and Brazil were laid out using RCBD with three replicates. The trays were placed in a humidity chamber maintained at 95% and above humidity; receiving 12 hours of day light supplementation using fluorescent tubes and 12 hours of darkness; and with temperatures controlled within a range of 20°C and 25°C using a portable air conditioner. Data collection was done after two (2) weeks. Disease severity was scored using a scale of 1-9 [16], where; severities 1.0-3.9=Resistant; 4.0-9.0=Susceptible. Disease incidence (I) data were collected as percentage number of plants infected by the disease (Eqn 1)

$$I = \text{Number of plants infected} / \text{Number of plants planted} \times 100 \quad (1)$$

Severity and incidence data were subjected to analysis of variance (ANOVA) using GenStat Discovery 14th edition.

Results

Field screening in Uganda

The analysis of variance of mean disease severity and incidence under field conditions revealed highly significant differences ($P \leq 0.001$) among cultivars. Among the 12 standard differentials, incidence was highest in MDKR (76%) followed by PI 207262 (75.3%) and Mexico 222 (66%) and lowest in G2333 (3.3%), while among the introduced Brazilian lines, incidence was highest in Rosinha G2 (77.8%) followed by SEL1308 (41%) and lowest in BRS Pontal (7.2%) (Table 3). Among the 11 introduced Brazilian lines, K13 (1.0), BRS Pontal (1.8), BRS Ametista (2.0), BRS Horizonte (2.3), SEL 1308 (2.5) and K10 (2.5) had the lowest severity scores. Their scores were not significantly ($P \leq 0.001$) different from that of differentials cultivars G2333 (1.2), Perry Marrow (1.5), AB136 (1.9), TU (2.0) and Cornel 49-242 (2.5) and 142/4(4) (2.6) in both seasons. The lines Rosinha G2 (5.2) and K23 (4.0) had the highest mean severity scores in the field and were not significantly different ($P \leq 0.001$) from the susceptible check K132 (6.2).

S.No	Cultivars	Genes available	Mean severity 2015B**	Mean severity 2016B	Mean severity	% Incidence 2015B	% Incidence 2016B	Mean Incidence
1	Michelite	*Co-11*	4.7	3	3.9	37.9	17.5	27.7
2	MDRK	*Co-1*	3.7	7	5.4	67.1	84.8	76
3	Perry Marrow	*Co-1*^{3}	1.7	1.3	1.5	13.6	3.1	8.4
4	Cornel 49-242	*Co-2*	2.3	2.7	2.5	21.5	15.9	18.7
5	Widusa	*Co-1*^{5}	2.3	3.7	3	29.5	55.2	42.4

6	Kaboon	*Co-1*^{2}	1.3	4.3	2.8	5.5	70	37.8
7	Mexico 222	*Co-3*	4.3	4.3	4.3	83.3	48.7	66
8	PI 207262	*Co-4*^{3}, *Co-9=Co-3*^{3}	6.3	5	5.7	87.1	63.5	75.3
9	TO	*Co-4*	4	3.7	3.9	41.4	17.7	29.6
10	TU	*Co-5*	1.3	2.7	2	9.5	43.6	26.6
11	AB 136	*Co-6, Co-8*	2.7	1	1.9	12.2	4.8	8.5
12	G2333	*Co-4*^{2}, *Co-5*^{2}, *Co-7=Co-3*^{5}	1.3	1	1.2	6.6	0	3.3
13	BAT 93	*Co-9=Co-3*^{3}	-	2	2	-	39.4	39.4
14	SEL 1308	*Co-4*^{2}	3.3	1.7	2.5	65	18	41.5
15	Rosinha G2	None	5.7	4.7	5.2	63.8	91.7	77.8
16	Ouro Negro	*Co-10=Co-3*^{4}	-	3.3	3.3	-	13.5	13.5
17	K13	*Co-4*^{2}	-	1	1	-	3.8	3.8
18	K23	*Co-5*	-	4	4	-	31.3	31.3
19	K10	*Co-4*^{2}, *Co-3*^{4}, *Co-5, Co-6*	2	3	2.5	13.9	19.8	16.9
20	BRS Pontal	Unknown	2.3	1.3	1.8	11.3	3	7.2
21	BRS Cometa	Unknown	-	2.7	2.7	-	14.8	14.8
22	BRS Horizonte	Unknown	2.3	2.3	2.3	15.1	52.3	33.7
23	BRS Ametista	Unknown	2.3	1.7	2	20	31.8	25.9
24	136/2 (8)a	*Co-4*^{3}	3.4	-	3.4	28.1	-	28.1
25	142/4 (4)a	*Co-5*	2.6	-	2.6	20	-	20
26	K132	Unknown	6.3	6	6.2	100	86.3	93.2
27	NABE 13	Unknown	5	-	5	55	-	55
28	NABE 14	Unknown	4	-	4	77	-	77
Mean			3.2	3.1	3.1	37.1	34.6	34.1
Standard Deviation			1.6	1.6	1.4	30.9	28.7	25.9

Table 3: Disease severity and incidence of common bean anthracnose on germplasm comprising of 12 common differential cultivars, 11 lines from Embrapa-Brazil and local checks screened under field conditions in Uganda. *1 to 12 are standard bean differentials; 13 to 23 were introduced from Embrapa, Brazil. ** 1.0-3.9 are considered resistant while 4.0-9.0 are considered susceptible. A Pedigree 12 × 8 × RWR719 × NABE13.

Screening under controlled conditions in Uganda

Analysis of variance for disease severity among the 25 cultivars revealed highly significant differences ($P \leq 0.001$) among cultivars and pathogen races. Variation due to cultivar × race interaction was highly significant ($P \leq 0.001$), with races contributing highest to total variation (45%) followed by cultivars (43.6%) and interaction (8%). Among the differentials, cultivars PI 207262 (1.75), G2333 (1.83), TU (1.83), AB 136 (1.92) and Cornell 49-242 (3.75) had mean severity scores less than 4.0; while cultivars SEL 1308 (1.0), K23 (1.25), BRS 9435 Cometa (1.33), BRS Ametista (2.08), BRS Horizonte (2.16), Ouro Negro (2.75) and K10 (3.10) also had mean severity scores less than 4.0 (Table 4). This implies that the resistant genes carried by these cultivars are effective in Ugandan and are potential sources of resistance to bean anthracnose.

*Cultivar I. D	Cultivar	Genes available	375	336	381	**Mean severity
1	Michelite	*Co-11*	6.50 b	2.25 cd	6.50 ab	5.08 bc
2	MDKR	*Co-1*	7.75 ab	2.50 cd	3.25 cd	4.50 bc
3	Perry Marrow	*Co-1*^{3}	4.75 bc	3.25 cd	4.50 bc	4.17 c
4	Cornel 49-242	*Co-2*	3.75 cd	2.25 cd	5.25 bc	3.67 cd
5	Widusa	*Co-1*^{5}	5.75 bc	4.75 bc	5.00 bc	5.17 bc
6	Kaboon	*Co-1*^{2}	5.50 bc	3.00 cd	4.00 c	4.17 c
7	Mexico 222	*Co-3*	5.00 bc	6.25 b	8.75 a	6.67 ab
8	PI 207262	*Co-4*^{3}, *Co-9=Co-3*^{3}	2.00 cd	1.50 d	1.75 d	1.75 de
9	TO	*Co-4*	5.25 bc	8.00 ab	6.50 ab	6.58 ab
10	TU	*Co-5*	1.50 d	2.00 cd	2.00 cd	1.83 de
11	AB 136	*Co-6, Co-8*	1.75 d	1.50 d	2.50 cd	1.92 de
12	G2333	*Co-4*^{2}, *Co-5*^{2}, *Co-7=Co-3*^{5}	3.50 cd	1.00 d	1.00 d	1.83 de
13	BAT 93	*Co-9=Co-3*^{3}	4.25 c	5.00 bc	4.50 bc	4.58 bc
14	SEL 1308	*Co-4*^{2}	1.00 d	1.00 d	1.00 d	1.00 e
15	Rosinha G2	None	4.50 bc	4.75 bc	7.25 ab	5.50 b
16	Ouro Negro	*Co-10=Co-3*^{4}	2.00 cd	1.75 d	4.50 bc	2.75 d
17	K13	*Co-4*^{2}	9.00 a	1.50 d	7.25 ab	5.92 ab
18	K23	*Co-5*	1.00 d	1.50 d	1.25 d	1.25 e
19	K10	Un-known	2.25 cd	1.00 d	6.00 bc	3.08 cd
20	BRS Pontal	Un-known	5.00 bc	4.00 c	6.00 bc	5.00 bc
21	BRS 9435 Cometa	Un-known	2.00 cd	1.00 d	1.00 d	1.33 e
22	BRS Horizonte	Un-known	2.75 cd	1.00 d	2.75 cd	2.17 de
23	BRS Ametista	Un-known	3.00 cd	1.25 d	2.00 cd	2.08 de
24	K132	None	6.50 b	9.00 c	6.00 bc	7.17 a
25	Farmers' variety	None	7.00 ab	5.00 bc	6.25 b	6.08 ab

Table 4: Mean severity of the 11 introduced lines, 12 standard bean differentials and 2 susceptible checks for three races of *C. lindemuthianum* in Uganda. *Cultivars 1 to 12=standard differential; 13 to 23=lines introduced from Embrapa, Brazil; 24 and 25=susceptible checks. **1.0-3.9=resistant cultivars/ lines; 4.0-9.0=susceptible. abc are significantly ($P \leq 0.001$) different means; means followed by the same letters are not significantly different.

Results of field screening in Brazil

Similar cultivars were evaluated under field conditions in Brazil and results showed that the cultivars Ouro Negro (1.7), SEL 1308 (1.8), K13 (1.8), K10 (1.8) and 136/2(8) (1.8) had the lowest mean severity scores and were not significantly different ($P \leq 0.001$) from K132 (2.3) used as a susceptible check in Uganda (Table 4). Among the differentials Kaboon (1.8), G2333 (2.0), AB136 (2.0), Tu (2.0), PI 207262 (2.0), TO (2.3) and Widusa (2.3) had the lowest severity scores. This implies the effectiveness of resistance genes in these cultivars against *C. lindemuthianum* in Brazil. The cultivars Rosinha G2 (8.0), BAT93 (7.2), BRS Ametista (6.2), BRS Pontal (5.0) and BRS Horizonte (4.5) had the highest severity scores among the Brazilian lines; while the differential cultivars Cornell-49-242 (7.0) and Michelite (6.7) also had high severity scores.

S. No	Genotype	Genes	Severity
1	Michelite	*Co-11*	6.7 c
2	MDRK	*Co-1*	2.5 a
3	Perry marrow	*Co-1*^{3}	2.0 a
4	Cornell 49-242	*Co-2*	7.0 c

5	Widusa	*Co-1*^{5}	2.3 a
6	Kaboon	*Co-1*^{2}	1.8 a
7	Mexico 222	*Co-3*	3.0 a
8	PI 207262	*Co-4*^{3}, *Co-9*=*Co-3*^{3}	2.0 a
9	TO	*Co-4*	2.3 a
10	TU	*Co-5*	2.0 a
11	AB 136	*Co-6*, *Co-8*	2.0 a
12	G 2333	*Co-4*^{2}, *Co-5*^{2}, *Co-7*=*Co-3*^{5}	2.0 a
13	BAT 93	*Co-9*=*Co-3*^{3}	7.2 c
14	SEL 1308	*Co-42*	1.8 a
15	Rosinha G2	None	8.0 c
16	Ouro Negro	*Co-10*=*Co-3*^{4}	1.7 a
17	K13	*Co-4*^{2}	1.8 a
18	K23	*Co-5*	3.3 a
19	K10	*Co-4*^{2}, *Co-3*^{4}, *Co-5*, *Co-6*	1.8 a
20	BRS Pontal	Un-known	5.2 b
21	BRS Cometa	Un-known	3.2 a
22	BRS Horizonte	Un-known	4.5 b
23	BRS Ametista	Un-known	6.2 c
24	136/2 (8) a	*Co-4*^{3}	1.8 a
25	142/4 (4) a	*Co-5*	2.3 a
26	RWR719	Unknown	6.8 c
27	Nabe 13	Unknown	2.2 a
28	Nabe 14	Unknown	1.7 a
29	K 132	Unknown	2.3 a

Table 5: Mean severity of bean anthracnose for 12 standard differential cultivars, 11 Brazilian cultivars and K132 under field condition in Brazil. *1 to 12=standard bean differentials cultivars; 13 to 23=Brazilian lines. **1.0-4.9 are considered resistant while 5-9 are considered susceptible. [a] Pedigree 12 × 8 × RWR719 × NABE13.

Discussion

Analysis of variance revealed that cultivars and *C. lindemuthianum* races significantly affected disease severity and are therefore important in the development and progress of the anthracnose disease. The significance of 'cultivar × race' interaction indicates that the effect of *C. lindemuthianum* races on disease severity highly depended on cultivar genotype.

Field and controlled screening in both Uganda and Brazil revealed that the differential cultivars G2333 (*Co-4*^{2}, *Co-5*^{2}, *Co-7*), TU (*Co-5*), AB136 (*Co-6*, *Co-8*), Kaboon (*Co-1*^{2}) and the Brazilian lines K10 (*Co-4*^{2}, *Co-3*^{4}, *Co-5*, *Co-6*), K13 (*Co-4*^{2}), SEL 1308 (*Co-4*^{2}) and BRS Cometa were the most resistant among the germplasm screened. This implies that the genes possessed by these cultivars have the capacity to control a wide range of pathogens across different environments. Specifically, in Uganda, the cultivars G2333, Perry marrow (*Co-1*^{3}), AB136, TU, Cornell 49-242 (*Co-2*) and lines K13, BRS Pontal, BRS Ametista, BAT93 (*Co-9*), BRS Horizonte and SEL1308 (*Co-4*^{2}) had the highest resistance implying the importance of their resistance genes against Ugandan *C. lindemuthianum* races. In Brazil, the cultivars G2333, TU, AB136, TO (*Co-4*), Widusa (*Co-1*^{5}), MDRK (*Co-1*), PI 207262, Mexico 222 (*Co-3*), Kaboon (*Co-1*^{2}) and lines SEL 1308, Ouro Negro (*Co-10*), K10, K13, K23 and BRS Cometa had the highest resistance implying the importance of their resistant genes against Brazilian *C. lindemuthianum* races.

The cultivars BRS Ametista, BRS Cometa and BRS Horizontal though not effective in Brazil, exhibited high resistance under controlled and field screening in Uganda. However, the genes responsible for the observed resistance are unknown. Similarly, the cultivars K132, Nabe 13 and Nabe 14 used in Uganda as susceptible checks were found to be among the resistant cultivars in Brazil. This observation could be explained by presence of resistance genes in these cultivars that act specifically against Mesoamerican races in Uganda and Andean races in Brazil. There is need for characterizing these cultivars to discover the genes responsible for the observed resistance in both countries.

The study found that the cultivar Cornell 49-242 was highly effective in Uganda but not in Brazil. The extensive deployment of the *Co-2* gene in North America [19,20], South America [21] and Europe [22] could have resulted in its declining effectiveness. However, in the case of Uganda where, the *Co-2* gene was not deployed before, it is still effective against *C. lindemuthianum* races. Kiryowa et al. [12] demonstrated that the gene was still highly beneficial having emerged among the most effective cultivars against diverse *C. lindemuthianum* races. Davide and Souza found cultivars G2333, Cornell 49-242, TU and AB 136 among the differentials to be highly resistant to race 65 in Brazil. They further revealed that Rosinha G2 was the most highly susceptible commercial cultivar as was observed in this study [23].

Field data also showed that the cultivar PI207262 (*Co-4*^{3}, *Co-9*) was highly effective in Brazil in agreement with Davide and Souza but was among the least effective in Uganda. Similarly, the line 136/2 (8) carrying the *Co-4*^{3} gene, was more effective in Brazil (1.8) than in Uganda (3.4). Kiryowa et al. found PI207262 to be the least effective among the differentials cultivars [12]. Data under controlled conditions contrarily revealed the cultivar PI207262 to be highly resistant. This may be due to the highly specific nature of the resistance genes in the cultivar especially against Andean *C. lindemuthianum* races as observed in the filed data from Brazil [24]. The cultivar PI207262 is reported to show high level of resistance under controlled screening but highly susceptible in the field [25].

Conclusion

The differential cultivars G2333, TU, Kaboon, K10, K13, SEL 1308 and BRS Cometa were the most effective against *C. lindemuthianum* in among the germplasm screened in Uganda and Brazil. The lines BRS Ametista, BRS Horizonte as well as BRS Pontal, whose resistance genes are not characterized also showed high levels of resistance in both Uganda and Brazil. Therefore, the above cultivars are potential sources of effective resistance for Uganda, Brazil and other geographical locations with diverse *C. lindemuthianum* populations.

Recommendations

The resistance in the cultivars K10, BRS Ametista, BRS Horizonte and BRS Pontal should be characterized to identify the genes responsible for the observed resistance. A clear understanding of the nature of inheritance of resistance in these cultivars will allow for their proper selection and transfer to susceptible commercial cultivars, as well as enable the development of molecular markers for marker assisted selection breeding. Breeding programs in Uganda and Brazil should make use of the resistance genes *Co-4*^{2} (G2333, SEL 1308), *Co-5* (G2333, Tu), *Co-6*, *Co-8* (AB136) and *Co-1* (Kaboon) through either single gene deployment or in gene pyramid combinations for effective control of diverse *C. lindemuthianum* pathotypes. The varieties K132, NABE 13 and NABE 13 should be used cautiously as susceptible checks in Uganda since they showed resistance in Brazil. These varieties need further characterization to identify their source of resistance as observed in Brazil. The cultivar Rosinha G2 should therefore be adopted in Uganda as a susceptible check. The varieties K10, K13, SEL 1308, BRS Ametista, BRS Horizonte as well as BRS Pontal could be considered for variety release in Uganda.

Acknowledgement

This research study was conducted at NARO, Uganda, and Embrapa, Brazil, with support from Africa-Brazil Agricultural Innovation Marketplace. Grant number 396.

References

1. FAOSTAT (2012) Available from: http://www.fao.org/faostat/en/#data/BC.
2. Ramirez-Villegas J, Madrinan S, Cortés AJ, Monserrate FA, Blair MW (2013) Drought Tolerance in Wild Plant Populations: The Case of Common Beans.
3. Murrell D (2016) Global research and funding survey on pulse productivity and sustainability. Global Pulse Confederation, Dubai.
4. FAOSTAT (2008) Available from http://faostat.fao.org/site/339/default.aspx.
5. Trust K (2012) Development of inclusive markets in agriculture and trade (DIMAT): The nature and markets of bean value chains in Uganda.
6. Vieira C (1983) Diseases and pests of common bean. Federal University of Vicosa Press, Vicosa, MG, Brazil.
7. Champion R, Brunet D, Maudult ML, Llami R (1973) Method of controlling the resistance of bean varieties to anthracnose (*Colletotrichum lindemuthianum*) (Sau. and Magn.) Briosi and Cav. CR Seances Acad Agric Fr.
8. Benard-Capelle J, Soubeyrand S, Neema C (2006) Reproductive consequences of *Colletotrichum lindemuthianum* (Ascomycota) infection on wild bean plants (*Phaseolus vulgaris*). Botany 84: 1542-1547.
9. Vidigal Filho PS, Gonçalves-Vidigal MC, Kelly JD, Kirk WW (2007) Sources of resistance to anthracnose in traditional common bean cultivars from Paraná, Brazil. Journal of Phytopathology 155: 108-113.
10. Nkalubo ST, Melis R, Derera J, Laing MD, Opio F (2009) Genetic analysis of anthracnose resistance in common bean breeding source germplasm. Euphytica 167: 303-312.
11. Melotto M, Kelly JD (2000) An allelic series at the Co-1 locus conditioning resistance to anthracnose in common bean of Andean origin. Euphytica 116: 143-149.
12. Kiryowa JM, Ebinu A, Kyaligonza V, Nkalubo ST, Paparu P, et al. (2017) Pathogenic variation of *Colletotrichum lindemuthianum* causing anthracnose of beans (phaseolus vulgaris) in Uganda. International Journal of Phytopathology 5: 89-98.
13. Souza TL, Wendland A, Rodrigues MS, Almeida LC, Correia FR, et al. (2014) Anthracnose resistance sources to be explored by the common bean breeding programs in Brazil. Embrapa Rice and Beans -Article in Indexed Journal (ALICE).
14. Mahuku GS, Riascos JJ (2004) Virulence and molecular diversity within *Colletotrichum lindemuthianum* isolates from Andean and Mesoamerican bean varieties and regions. European Journal of Plant Pathology 110: 253-263.
15. Lindblade KA, Carswell G, Tumuhairwe JK (1998) Mitigating the relationship between population growth and land degradation: land-use change and farm management in southwestern Uganda. Ambio 27: 565-571.
16. Balardin RS, Jarosz AM, Kelly JD (1997) Virulence and molecular diversity in *Colletotrichum lindemuthianum* from South, Central, and North America. Phytopathology 87: 1184-1191.
17. Inglis DA, Hagedorn DJ, Rand RE (1988) Use of dry inoculum to evaluate beans for resistance to anthracnose and angular leaf spot. Plant Disease 72: 771-774.
18. Pastor-Corrales MA (1991) Standardization of differential varieties and breed designations of *Colletotrichum lindemuthianum*. Phytopathology 81: 694.
19. Kelly JD, Afanador L, Cameron LS (1994) New races of *Colletotrichum lindemuthianum* in Michigan and implications in dry bean resistance breeding. Plant Disease 78: 892-894.
20. Tu JC (1983) Epidemiology of anthracnose caused by *Colletotrichum lindemuthianum* on white bean (Phaseolus vulgaris) in southern Ontario: survival of the pathogen. Plant Disease 67: 402-404.
21. Pastor-Corrales MA, Erazo OA, Estrada EI, Singh SP (1994) Inheritance of anthracnose resistance in common bean accession G 2333. Plant Disease 78: 959-961.
22. Fouilloux G (1978) New races of bean anthracnose and consequences on our breeding programs. In: Maraite H, Meyer JA (eds). Diseases of tropical food crops: Proceedings of an international symposium, UCL, Louvain-la-Neuve, Belgium.
23. Davide LM, de Souza EA (2009) Pathogenic variability within race 65 of *Colletotrichum lindemuthianum* and its implications for common bean breeding. Crop Breeding and Applied Biotechnology, p: 9.
24. Kelly JD, Vallejo VA (2004) A comprehensive review of the major genes conditioning resistance to anthracnose in common bean. Hort Science 39: 1196-1207.
25. Mwesigwa JB (2008) Diversity of *Colletotrichum lindemuthianum* and reaction of common bean germplasm to anthracnose disease. M Sc Thesis, University of Makerere, Uganda.