African Crop Science Journal, Vol. 26, No. 1, pp. 63 - 77
Printed in Uganda.
ISSN 1021-9730/2018 $4.00

DOI: http://dx.doi.org/10.4314/acsj.v26i1.5

IDENTIFICATION OF COMMON BEAN GENOTYPES WITH DUAL LEAF AND POD RESISTANCE TO COMMON BACTERIAL BLIGHT DISEASE IN UGANDA

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(*Received 9 October, 2017; accepted 8 February, 2018*)

ABSTRACT

Common Bacterial Blight (CBB), caused by *Xanthomonas axonopodis pv. phaseoli* (Xap) and *Xanthomonas axonopodis* pv. *phaseoli var. fuscans* (Xapf), is a serious disease that affects common bean production worldwide. In Uganda, it is the most severe and widely occurring bacterial disease, causing significant yield losses in common bean. Although various sources of resistance have been developed around the world, none of the varieties grown in Uganda is known to be resistant. The objective of this study was to identify lines with combined leaf and pod resistance for introgression into locally adapted but susceptible Ugandan genotypes. A total of 132 common bean accessions was evaluated in a screenhouse and under field conditions, in an 11x12 alpha lattice design. Genotypes were inoculated with a local isolate in a screenhouse; while the plants were left to undergo natural infestation in field. Results indicated significant differences ($P<0.001$) in genotypic reactions against the CBB disease, with a range of disease scores of 2.2 - 7.8 on leaves and 2.6 - 7.1 on pods (1-9 CIAT disease scale), suggesting high genetic variability among the tested germplasm. Relatively low correlation ($r = 0.39$) was observed between leaf and pod reactions, suggesting differential expression of CBB resistance in these two plant organs. Overall, four genotypes, NE2-14-8, NE17-14-29, NE14-09-78 and VAX3, consistently showed resistance in both screenhouse and field evaluations, leaf and pod inoculations and at all sampling stages. These genotypes were, therefore, identified for transferring CBB resistance into Ugandan susceptible market class bean varieties.

Key Words: CBB, *Phaseolus vulgaris*, *Xanthomonas axonopodis*

RÉSUMÉ

Le flétrissement bactérien commun (CBB) causé par *Xanthomonas campestris pv. phaseoli* (Xcp) et *Xanthomonas* spp. var. *fuscans* (Xcpf) est une sérieuse maladie qui affecte, de façon globale, la production du haricot commun. En Ouganda, elle est, de loin, la maladie bactérienne la plus sévère et vastement répandue causant de pertes significatives au rendement du haricot commun. Malgré que de nombreuses sources de résistance aient été développées dans le monde, aucune des variétés cultivées en Ouganda n'est connue être résistante. L'objectif de cette étude était d'identifier des lignes à résistance combinée des feuilles et gousses pour son introgression dans les variétés locales adaptées mais susceptibles. Au total, 132 accessions de haricot commun étaient évaluées sous

serre et dans le champ dans un dispositif experimental alpha-lattice 11x12. Les génotypes étaient inoculés sous serre par un isolat local pendant que l'infestation était naturelle dans le champ. Les résultats montrent de différences hautement significatives dans la réaction des génotypes face à la maladie CBB avec des scores variant de 2,2 à 7,8 sur les feuilles et de 2.6 à 7.1 sur les gousses (l'échelle 1-9 de CIAT) indiquant une forte variabilté génétique au sein du germoplasm testé. Une corrélation relativement faible (r = 0.39) était observée entre la réaction des feuilles et celle des gousses suggérant une expression différentielle de la résistance à la maladie CBB dans ces deux organes de la plante. De façon générale, quatre génotypes NE2-14-8, NE17-14-29, NE14-09-78 and VAX3 ont été, de façon constante, résistants aux évaluations sous serre et dans le champ, aux inoculations des feuilles et des gousses et durant toute la période de mesure. Ces génotypes étaient donc identifiés pour le transfert de la résistance dans les variétés locales susceptibles d'Ouganda.

Mots Clés : CBB, *Phaseolus vulgaris*, *Xanthomonas axonopodis pv. phaseoli*

INTRODUCTION

Common bean (*Phaseolus vulgaris L.*; 2n = 2x = 22) is one of the most important grain legumes for human consumption worldwide (Gepts *et al*., 2008). In Africa, common bean is mainly consumed in eastern and central regions, where it provides up to 25% of total caloric intake and 45% of total dietary protein; the highest level of contribution in the world (Kilimo, 2012). Uganda ranks second in Africa, with a common bean production of 876,576 metric tonnes (FAOSTAT, 2015), but its productivity is still low (0.56 t ha^{-1}) because the crop is stressed by various abiotic and biotic factors, including common bacterial blight (CBB) disease, caused by *Xanthomonas axonopodis pv. phaseoli.*

Common bacterial blight is the most destructive bacterial disease of common bean in Uganda, and can cause up to 62% yield losses (Opio and Namayanja, 2002). Being seed-borne, it reduces seed quality through staining and browning (Yu *et al*., 2012), and constitutes a real threat to seed production. It is generally endemic in bean growing areas under high temperature, rainfall, and relative humidity (Saettler, 1991). Infected seeds constitute the major source of inoculum (He, 2010). Breeding for host plant resistance is reported as the most effective and long term measure to control the disease (Durham, 2011; Fourie *et al*., 2011) and many CBB resistant lines have been developed in this regard (Singh and Miklas, 2015).

Sources of genetic resistance to CBB have mainly been identified in common bean and its related species, tepary bean (*Phaseolus aculifolius*) and runner bean (*Phaseolus coccineus*) (Singh and Miklas, 2015). The highest level of resistance to CBB has been reported in tepary bean, followed by runner bean, and lastly common bean (Miklas *et al*., 2003). Interspecific crosses have been made between common bean and the related species, to develop most of the resistant genotypes (Osdaghi *et al*., 2009). Unlike *P. coccineus*, embryo rescue was necessary for successful crosses between *P. vulgaris* and *P. aculifolius* (Singh and Schwartz, 2010).

Common bean breeders, through these interspecific crosses, have combined resistance genes to CBB into common bean to obtain lines and cultivars with improved resistance (Miklas *et al*., 2006). ICB 3, ICB 6, ICB 8, ICB 10, XR-235-1-1 and TARS VCI-4B were the main lines derived from *P. coccineus;* while VAX 1, VAX 2, XAN 159, XAN 160, XAN 161 and OAC 88-1 were the major lines obtained from *P. acutifolius* (Singh and Miklas, 2015). Resistance to CBB has been reported as a quantitative trait and efforts have been made to develop lines with pyramided resistance genes/QTLs such as VAX 3, VAX 4, VAX 5, VAX 6, Wilk 2, XAN 309 and USPT-CBB-5 (Singh and Miklas, 2015). These resistant lines, with pyramided genes are being widely used in various breeding programmes to introgress resistance to CBB in adapted cultivars.

In East Africa, and specifically in Uganda, XAN-159 was used with other donor parents (PI-207262, lAPAR-16, BAC-6, GN Jules' GN Nebraska 1 Sel. No. 27 and XAN-112) to improve the CBB resistance of locally adapted genotypes; however, the resulting resistant genotypes were never released because they lacked consumer and market preferred attributes; and were also very susceptible to black rot disease (Opio and Namayanja, 2002). Belarmino (2015) tested and identified lines JESCA, RWV 2070, RWR 2154, MIB 456, NUA 45, MCM 2001, and ACC (3, 4, 5, 10, 16, 18, 21, and 22) as possessing resistance to CBB disease in Uganda. However, the study was limited to foliar resistance, yet it is reported that there are differential expressions of resistance to CBB in different plant organs namely leaf and pod (Arnaud-Santana *et al.*, 1994). This has been reported as a major challenge in controlling CBB disease in common bean and several past studies focused on the association between the reactions of these organs, to Xap/Xapf.

Arnaud-Santana *et al*. (1994) reported a low genetic correlation between leaf and pod reactions and leaf and seed reactions to CBB disease. Similarly, Park *et al*. (1998) found low to intermediate correlation between the leaf and pod reactions in common beans. Jung *et al*. (1997) also reported different genes controlling CBB resistance in leaf, pod and seed in common beans. All these findings have shown that some common bean genotypes possess resistance to CBB in only one organ (Singh and Miklas, 2015); hence screening of multiple organs is required to obtain genotypes with combined resistance. The aim of this study was, therefore, to identify common genotypes with dual leaf and pod CBB resistance for utilisation in the improvement of susceptible Ugandan market class and consumer preferred bean varieties.

MATERIALS AND METHODS

Study area. This study was carried out at the National Crop Resources Research Institute (NaCRRI) at Namulonge in Uganda, located at an altitude of 1150 masl on latitude 0°32'N and longitude 32°53'E. The Institute falls in a bimodal climate region with an average annual rainfall of 1200 mm and average annual temperature of 21 to 27 °C.

Genetic material. The germplasm used in this study included 30 landraces with unknown resistance status to CBB disease, 30 released varieties from NaCRRI, 21 lines from CIAT-Uganda, previously identified by Belarmino (2015) for foliar resistance to CBB; and 50 introduced lines previously selected for CBB resistance in Nebraska, USA. These introduced lines included 12 lines from the University of Nebraska Dry Bean Breeding Programme, 27 from the Andean Diversity Panel, and 11 from the Shuttle Breeding Programme between Nebraska and Puerto Rico. Two locally adapted but susceptible genotypes, Masindi Yellow and Kanyebwa, were used as susceptible checks. The groups of accessions are presented in Table 1.

Experimental design. CBB resistance was evaluated under two conditions, the first in screenhouse and the second in field during the second rainy season of 2015 (from September to December). For each experimental setup, 132 genotypes were planted in an 11x12 alpha-lattice design, with two replications. Within each replication, there were 11 lattice incomplete blocks and 12 genotypes per block. In the screenhouse, a plot consisted of a four-litre volume bucket, in which six seeds were sown and subsequently thinned to four after germination. Each bucket contained a mixture of forest black soil, lake sand and composted farm yard manure, in a ratio of 3:1:1. Three hundred grammes of NPK fertiliser was diluted in 10 l of tap water, from which 100 ml were added to the soil on a weekly basis, until the reproductive stage of pod filling (Belarmino, 2015). In the field, a single-row of 2 m length was used as a plot, with a spacing of 50 cm between rows and 10 cm between plants within row.

TABLE 1. Groups of common bean accessions tested for CBB resistance at NaCRRI in Uganda

Bean group	Number	Source	Status
Andean Diversity Pool lines	27	University of Nebraska	Resistant, Intermediate
NE Accessions	23	University of Nebraska	Resistant, Intermediate
VAX lines	06	CIAT	Resistant
ACC lines	08	CIAT	Resistant
MCM (2001, 1015, 5001)	03	CIAT	Resistant
JESCA	01	CIAT	Resistant
NUA 45	01	CIAT	Resistant
RWR 2154	01	Rwanda	Resistant
RWV 2070	01	Rwanda	Resistant
MIB 465	01	CIAT	Resistant
CAL 96	01	CIAT	Resistant
K (20, 131, 132) varieties	03	NaCRRI	Unknown
Local landraces	30	NaCRRI	Unknown
NABE varieties	24	NaCRRI	Unknown
Masind Yellow , Kanyebwa	02	NaCRRI	Susceptible
Total	132		

CIAT = International Center of Tropical Agriculture, NaCRRI = National Crop Resources Research Institute

Inoculation of plants. In the screenhouse, plants were inoculated with the isolate "Kawempe 1", a *fuscous* variant of *Xanthomonas axonopodis* pv. *phaseoli.* CIAT-Uganda had previously identified this isolate as the most prevalent and one of the most virulent pathotypes of Xapf in Uganda (Belarmino, 2015). The stored culture of "Kawempe 1" was revived, grown and multiplied on Yeast Dextrose Carbonate Agar (YDCA) medium and 48 hr after initiation of the culture, the suspension of inoculum was produced and diluted with sterilised water, up to the recommended concentration of 5 x 10^7 CFU ml^{-1} following the CIAT protocol (CIAT, 2014).

The second fully expanded trifoliate of each seedling was inoculated at 21 days after planting, using the razor blade method (Opio *et al*., 1994), by pressing the leaflet onto a sponge soaked with bacteria suspension (in a petri-dish) and making two small gentle cuts at the edge. Two pods per plant were inoculated, using multiple needle sticks at pod filling stage (Opio *et al*., 1994). Four punctures were made on both sides of each pod, which was then pressed onto the sponge soaked with inoculum sap.

In the case of the field setup, the genotypes were planted in an area of NaCRRI known to be a hotspot for common bacterial blight disease (Dr Stanley Nkalubo, Head of Legumes Programme, National Crop Resources Research Institute, 2015; personal communication), thus, genotypes were left to undergo natural infestation.

Data collection. Disease severity was measured on leaves at 14, 21 and 35 days after inoculation (DAI), and on pods at 10 days after inoculation, using the modified CIAT 1-9 rating scale of Opio *et al*. (1993). The disease severity scores of individual plants were used to calculate an average score for each genotype per plot. Average scores of 1.0 to 3.4 were considered resistant, 3.5 to 6.4 intermediate and 6.5 to 9.0 susceptible.

In the field, disease severity and incidence percentage were recorded on leaves at the reproductive stages R6 (50% of the plants developed their first open flower) and R8 (50% of the plants began to fill the seeds in their

first pods), as recommended by van Schoonhoven and Pastor-Corrales (1987). All the 20 plants in each plot were scored individually using the same modified CIAT 1-9 rating scale. Disease severity was computed as the average score per plot. Disease incidence was determined as the ratio of number of infected plants over the total number of plants, multiplied by a hundred. A late drought stress was experienced in the field during the reproductive stage; hence, did not provide favorable conditions for the disease to sufficiently express on the pods. As a result, there was no disease assessment on pods in the field.

Data analysis. The data were analysed with GenStat 12th Edition software VSN International. Restricted Maximum Likelihood (ReML) approach was used to generate the analysis of variance (ANOVA) (Smith and Cullis, 2005; Payne *et al*., 2009). Genotypes were considered as fixed factor; while replications and lattice incomplete blocks were considered as random factors. The statistical linear model used is as follows:

$$Y_{ijk} = \bar{\bar{Y}} + G_i + R_j + B/R_{jk} + e_{ijk}$$

Where:

$\bar{\bar{Y}}$= Grand mean, G_i= genotype mean effect, R_j= replication mean effect, B/R_{jk}= block within replication effect, and e_{ijk}= experimental error.

To assess the consistency in genotypes' response to CBB disease between leaf and pod reaction, Fisher's exact test of independence was computed using Fisher.test of Classical tests package in R Software Version 3.3.1. This test was used as a replacement for the Chi-square-test of independence due to low expected values (< 1). Two-sided Pearson correlation analysis was also performed to measure the strength of association between CBB disease severity scores in screenhouse (leaf and pod symptoms) and field and disease incidence. The formula used was:

$$r_{xy} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{(n-1)s_x s_y}$$

Where:

x_i and y_i were genotype means of the two variables being analysed, r_{xy} = correlation coefficient; and n = 131 observations (predicted means of the genotypes) of each variable.

RESULTS AND DISCUSSION

Response of common bean germplasm to CBB disease. In the screenhouse, genotypes had highly significant (P<0.001) mean squares for leaf symptoms at all sampling stages (Leaf_14DAI, Leaf_21DAI, Leaf_35DAI) and pod symptoms (Pod_10DAI) (Table 2). Thus, screening results from the screenhouse suggests that the accessions showed different levels of resistance to CBB disease. Similar results were obtained in the field for CBB disease incidence (P<0.01) and severity (P<0.05) at both reproductive R6 and R8 phases (Table 2), also indicating that the accessions expressed different levels of resistance to CBB disease under natural infestation.

The significant differences in reaction observed among genotypes on leaves and pods in screenhouse and on leaves in field, were indicative of high genetic variability of the tested germplasm, thus these common bean germplasm could be used to genetically improve leaf and pod resistance to CBB. Leaf and pod reaction to the CBB pathogen differed among genotypes in both screenhouse and field. In the screenhouse, mean disease severity scores ranged from 2.9 to 7.7 for leaves (35DAI), and from 2.6 to 7.1 for pods (10DAI) (Table 3). In the field, mean disease severity scores ranged from 2.0 to 6.8 for

TABLE 2. Mean squares of common bean genotypic reaction to CBB in screenhouse and field at NaCRRIin, Uganda

Source of variation	d.f.	Screenhouse				Field (Leaf)			
		Leaf_ 14DAI	Leaf_ 21DAI	Leaf_ 35DAI	Pod_ 10DAI	R6_Incid	R6_Sev	R8_Incid	R8_Sev
Rep	1	0.39 ns	2.07 ns	1.12 ns	3.15 ns	262.40 ns	0.11 ns	2360.60 **	1.44 ns
Block (Rep)	20	0.88 ns	1.21 **	0.45 ns	1.13 ns	192.00 *	0.98 **	185.20 ns	0.97 ns
Genotype	131	1.66 ***	1.88 ***	2.38 ***	2.47 ***	225.94 **	0.73 *	248.71 **	1.08 *
Residual	107	0.54	0.5	0.38	0.8	114.2	0.42	124.4	0.65
LEE	98	0.61	0.59	0.42	0.9	126.79	0.48	136.42	0.71
CV (%)		17.62	15.27	11.37	19.42	52.5	24.76	42.1	20.9
s.e.d.		0.78	0.76	0.65	0.95	11.26	0.69	11.68	0.85

ns= non-significant, *, **, *** = significance at 0.05, 0.01, 0.001 probability levels respectively, DAI= days after inoculation, d.f.= degrees of freedom, LEE= Lattice Effective Error, CV= Coefficient of variation, s.e.d. = standard error of difference, Incid = disease incidence in percentage on leaves, Sev= disease severity on leaves, R6 = reproductive stage 6, R8 = reproductive stage 8

TABLE 3. Mean percentage incidence and severity scores of the common bean genotypic reaction to CBB disease in screenhouse and field conditions at NaCRRI, in Uganda

Genotype	Screenhouse				Field			
	Leaf severity		Pod severity		Leaf incidence		Leaf severity	
	14DAI	21DAI	35DAI	10DAI	R6_Incid	R8_Incid	R6_Sev	R8_Sev
ADP-114	2.3	3.0	2.9	2.8	25.9	30.2	2.9	3.9
ADP-660	2.4	2.3	3.0	4.2	26.0	34.1	3.2	3.9
ADP-682	2.5	2.4	3.1	3.9	18.8	25.4	2.9	4.7
NE2-14-8	3.0	3.2	3.2	3.1	35.9	35.8	2.6	3.4
ADP-123	2.8	3.1	3.1	4.6	22.5	27.1	2.0	3.2
NE14-09-78	3.0	3.2	3.2	3.3	5.4	9.9	2.0	2.0
NE14-09-19	3.4	3.4	3.5	6.0	6.2	9.2	2.1	3.1
NE17-14-29	3.0	3.3	3.3	3.2	6.1	9.3	1.4	3.2
ADP-627	2.9	3.3	3.6	3.8	20.9	23.1	3.2	4.2
NE14-09-113	3.2	3.3	3.4	3.1	9.7	12.9	1.9	2.6
MIB 465	3.1	3.3	3.4	2.9	15.6	33.0	2.7	5.0
VAX3	3.0	3.3	3.4	3.2	11.0	11.4	2.5	2.7
ADP-626	3.5	4.0	3.8	6.2	11.8	25.2	2.2	4.2
NE14-09-6	3.2	3.6	3.8	4.9	6.7	10.9	2.0	2.7
ADP-643	2.8	3.2	3.9	3.3	14.2	15.8	2.6	3.5
MCM 2001	3.7	4.0	4.0	3.8	11.1	18.1	2.5	3.6
NE10-14-36	3.7	4.2	4.3	4.1	7.3	14.7	1.7	2.9
ADP-629	3.2	3.6	4.3	4.8	25.1	24.5	2.9	4.4
VAX4	3.6	4.0	4.3	2.9	6.1	8.6	1.4	2.3
NUA 45	4.0	3.9	4.3	5.0	10.7	27.1	2.5	3.5
NE14-09-10	2.7	3.0	4.3	3.4	12.2	16.1	2.3	3.6
ADP-100	3.2	3.5	4.5	6.8	18.9	18.9	2.7	4.1
NE14-09-46	4.0	4.8	4.5	4.7	17.5	20.0	2.6	3.8
ACC4	4.5	4.7	4.5	2.7	24.4	26.7	2.5	5.2
NE13-14-10	3.4	4.0	4.6	3.2	2.5	9.0	1.4	3.1
MCM 1015	3.7	4.0	4.6	5.7	18.9	27.9	2.5	4.6
ADP-97	3.8	4.5	4.7	5.5	8.5	24.0	2.6	4.4

TABLE 3. Contd.

Genotype	Screenhouse				Field			
	Leaf severity		Pod severity		Leaf incidence		Leaf severity	
	14DAI	21DAI	35DAI	10DAI	R6_Incid	R8_Incid	R6_Sev	R8_Sev
ACC5	4.1	4.4	4.7	4.3	24.2	23.2	2.9	3.9
ADP-42	3.9	4.1	4.8	5.6	19.2	22.9	2.3	3.7
VAX6	3.6	4.6	4.8	2.6	12.9	12.9	2.5	3.0
ADP-603	4.2	4.5	4.9	3.4	36.8	39.8	3.4	4.1
VAX1	3.9	4.4	4.9	4.7	1.1	4.4	1.6	2.9
ADP-71	3.3	3.3	4.9	2.9	51.4	51.8	2.9	4.0
VAX2	3.7	4.7	4.9	5.0	6.2	11.4	1.9	2.9
VAX5	4.3	4.3	5.0	3.1	7.8	9.6	1.7	3.5
ACC3	4.7	5.0	5.1	5.3	25.9	31.9	2.4	3.7
ADP-116	3.2	4.1	5.1	4.8	22.1	32.8	3.6	5.4
ADP-85	3.0	4.4	5.2	4.1	29.2	34.5	2.9	4.0
RWR 719	4.0	5.0	5.2	6.2	7.8	13.5	2.4	3.5
ADP-624	3.9	4.3	5.2	5.3	20.5	21.8	3.0	4.3
NEB1 SEL27	4.1	4.4	5.2	4.2	22.8	24.0	2.6	3.2
ADP-25	4.7	5.4	5.3	4.7	18.1	18.0	2.5	2.6
NE14-09-23	3.2	4.4	5.3	5.8	14.3	27.5	2.4	3.6
NE14-09-111	3.0	3.9	5.3	4.5	21.2	21.9	2.8	3.5
ADP-113	3.9	4.6	5.4	-	19.0	21.2	3.2	4.5
ADP-28	4.6	4.9	5.4	6.5	17.2	25.6	2.6	4.9
K132	4.2	4.8	5.5	4.4	13.2	19.0	2.7	3.9
NE13-14-11	3.7	3.9	5.5	5.1	7.1	16.3	2.2	3.7
ADP-630	3.6	4.0	5.5	5.6	26.1	28.5	3.3	3.7
NE-9-14-6	3.7	5.2	5.5	3.6	27.3	27.2	1.8	3.3
NE1-14-13	3.9	4.9	5.5	5.0	24.9	41.4	2.5	4.3
NE15-14-14	3.9	3.9	5.5	-	43.4	49.7	3.6	4.1
NE14-09-16	4.2	4.2	5.5	7.1	35.3	43.6	2.5	4.1
ADP-628	4.7	5.0	5.5	2.9	32.9	32.3	3.7	5.0

TABLE 3. Contd.

Genotype	Screenhouse				Field			
	Leaf severity		Pod severity		Leaf incidence		Leaf severity	
	14DAI	21DAI	35DAI	10DAI	R6_Incid	R8_Incid	R6_Sev	R8_Sev
ACC18	5.1	5.5	5.6	6.0	13.2	17.9	2.9	4.0
NE14-09-49	4.5	5.2	5.6	5.3	29.2	45.6	3.0	4.1
NE17-14-34	4.8	5.1	5.7	2.8	13.8	30.4	2.2	4.3
MCM 5001	4.8	5.4	5.7	4.4	40.7	48.2	3.0	4.5
NE14-09-26	4.6	4.6	5.7	3.7	26.4	38.3	3.5	4.5
White middle	5.4	5.7	5.7	4.3	45.0	56.8	3.5	6.1
ADP-112	4.6	5.2	5.8	3.3	41.1	47.7	3.0	4.4
Kanyebwa	5.3	5.3	5.8	6.0	38.1	38.9	3.2	4.1
ADP-80	2.7	4.4	5.8	4.9	19.8	24.0	2.4	3.6
K20	5.3	5.6	5.8	4.0	28.2	38.7	3.0	4.0
NABE 10C	5.5	5.3	5.9	4.9	36.4	44.3	2.6	5.0
NABE 14	4.3	5.1	5.9	4.1	27.7	28.5	4.2	4.8
NABE 5	5.1	4.9	5.9	3.8	12.9	18.9	2.5	4.4
ABCWEIHING	4.9	5.5	6.0	5.3	26.8	36.1	2.6	4.1
NE-9-14-7	5.0	5.7	6.0	5.1	36.2	38.4	2.6	4.2
NABE 3	5.5	5.1	6.0	5.5	9.2	30.8	2.4	3.7
Tazan	4.0	5.1	6.0	5.6	10.5	17.5	4.2	5.0
NABE 8C	4.7	5.3	6.0	3.8	14.1	22.0	2.9	4.7
RWV 2070	5.1	5.6	6.0	4.2	21.8	42.0	3.2	5.4
Calima	4.0	5.4	6.0	6.8	41.6	42.7	3.5	4.0
ACC10	4.1	5.1	6.0	5.5	20.4	21.0	3.0	4.3
ADP-41	4.4	4.4	6.0	5.0	23.4	25.5	2.4	3.4
RWR 2154	5.6	5.8	6.0	5.3	10.8	28.3	2.4	4.2
ADP-625	3.9	5.4	6.1	2.9	24.0	28.6	2.5	3.5
NDUME	4.5	5.5	6.1	5.7	0.5	14.6	0.9	2.6
Kigome	4.4	4.7	6.1	6.9	26.3	34.1	4.5	6.8
Very Large Purple	3.8	4.7	6.2	3.5	21.1	20.4	3.2	4.5

TABLE 3. Contd.

Genotype	Screenhouse				Field			
	Leaf severity		Pod severity		Leaf incidence		Leaf severity	
	14DAI	21DAI	35DAI	10DAI	R6_Incid	R8_Incid	R6_Sev	R8_Sev
NABE 22	3.9	5.9	6.2	5.0	28.5	27.4	2.8	4.1
ADP-664	4.4	5.3	6.3	4.4	12.8	15.7	2.5	4.1
NABE2	5.2	5.9	6.3	3.6	23.4	28.9	3.3	4.8
JESCA	5.5	5.9	6.3	6.1	25.8	33.9	2.6	3.8
Kanyebwa Long	5.1	5.8	6.4	4.8	55.5	53.4	4.2	4.5
White Small	5.1	6.1	6.4	6.4	25.2	38.2	2.1	3.7
NABE 20	5.7	6.0	6.4	6.7	46.7	53.0	4.0	4.1
Nambale_Light	5.0	5.0	6.5	4.0	20.9	27.4	3.0	4.8
Coffee Glittering	5.0	5.2	6.5	5.7	15.8	17.9	2.6	4.3
Coffee	5.0	5.7	6.5	4.3	18.2	28.0	2.6	4.0
NABE 23	5.2	6.1	6.5	5.1	25.6	26.5	3.5	3.8
NABE 12C	5.0	6.0	6.5	4.7	16.7	36.2	3.2	4.5
Masindi Yellow	4.9	5.7	6.5	7.1	19.9	19.9	3.0	4.5
ADP-663	3.7	5.5	6.5	3.2	25.2	33.1	2.4	3.5
NABE 7C	6.3	6.7	6.5	7.1	21.1	31.5	2.7	4.2
NABE 18	5.5	5.5	6.6	6.2	24.9	44.8	2.4	4.6
Kahura Round	5.4	5.7	6.6	5.1	25.7	29.8	2.7	3.2
Imotokor	5.9	6.3	6.6	5.1	28.7	53.7	3.0	4.8
NABE 29C	5.8	5.8	6.6	4.7	19.3	37.8	4.3	5.0
NABE 19	4.7	5.7	6.6	4.8	15.8	17.0	3.6	4.1
NABE 9C	5.1	6.2	6.7	4.4	38.0	37.9	3.5	4.6
NABE 16	5.7	5.8	6.7	4.3	35.9	35.2	3.3	4.0
Cream Orange Specks	5.1	5.5	6.7	6.5	23.8	24.3	3.0	3.8
NABE 13	5.8	6.0	6.7	3.3	22.2	26.2	2.7	3.6
NABE 17	5.2	5.9	6.7	5.3	19.0	25.1	2.4	3.7
K 131	5.9	6.4	6.7	5.7	29.5	30.5	3.4	4.7
NABE 6	5.6	6.0	6.7	6.4	47.6	58.3	3.2	3.5
Cream	5.0	5.8	6.7	5.1	20.8	35.2	3.3	4.7

TABLE 3. Contd.

Genotype	Screenhouse				Field			
	Leaf severity		Pod severity		Leaf incidence		Leaf severity	
	14DAI	21DAI	35DAI	10DAI	R6_Incid	R8_Incid	R6_Sev	R8_Sev
NABE 15	5.3	5.6	6.7	6.0	26.9	27.3	3.4	4.6
Ande620	4.3	5.3	6.7	6.5	29.2	29.4	2.5	3.6
Khaki Omuwanvu	5.6	6.0	6.8	5.0	27.6	27.2	3.5	4.7
Pink	4.6	6.4	6.8	5.0	22.8	22.9	3.4	4.7
Nambale	4.6	6.0	6.8	5.4	13.8	25.1	2.1	2.9
NABE1	4.7	5.5	6.8	3.7	14.6	20.7	3.6	4.5
Kanira Black specks	5.0	5.9	6.8	6.9	20.4	27.3	2.5	4.9
Kanyawawa Green	5.2	6.2	6.9	6.9	13.0	22.4	2.4	4.1
Cream Black Specks	5.3	6.3	6.9	4.9	12.2	19.8	2.9	3.1
ROBA1	5.3	6.2	7.0	6.5	11.3	30.8	3.0	3.8
NABE 21	5.2	6.5	7.0	4.9	22.7	25.6	2.9	3.5
Tinatine	5.3	5.7	7.0	5.7	22.0	32.5	3.7	4.8
NABE 4	4.8	5.5	7.1	6.4	18.2	22.1	2.6	3.4
Good Red	6.3	6.7	7.1	4.7	23.5	26.7	2.5	4.6
NABE 11	5.5	6.5	7.1	4.8	8.3	13.6	3.5	4.7
CAL 96	5.3	5.6	7.1	4.9	20.4	31.1	3.4	4.7
KATB1	6.5	6.6	7.2	5.9	15.2	25.9	2.5	3.3
RED	5.8	6.0	7.3	5.9	28.8	28.5	3.3	4.6
Ocuci	4.4	7.1	7.3	3.9	25.3	37.8	2.5	4.4
NABE 26C	5.3	6.4	7.5	5.4	15.4	27.5	3.0	4.0
CalimaTwenty	6.0	6.5	7.5	6.5	13.2	13.3	2.7	3.8
Bumwufu	6.1	7.6	7.7	6.1	25.5	34.7	3.5	5.4
Minimum	2.3	2.3	2.9	2.6	0.5	4.4	0.9	2.0
Maximum	6.5	7.6	7.7	7.1	55.5	58.3	4.5	6.8
LSD (5%)	1.5	1.5	1.3	1.9	22.3	23.2	1.4	1.7

LSD = Least Significant Difference

leaves and disease incidence ranged from 22.3 to 58.3% (Table 3). None of the genotypes had 0% incidence or a severity score of 1, implying that none of these accessions was immune to CBB disease. Based on severity scores on leaves at 35 DAI, the most resistant genotypes in the screenhouse for leaves were ADP-114, ADP-660, ADP-682, ADP-123 and NE2-14-8 (scores ranging from 2.9 to 3.2); whereas, Bumwufu and NABE 26C were the most susceptible (7.7 and, 7.5 respectively) in the screenhouse. For pods, VAX6, ACC4, ADP-114, NE17-14-34 and MIB 465 (scores ranging from 2.6 to 2.9) were the most resistant genotypes while NE14-09-16, Masindi yellow, and NABE 7C were the most susceptible (score of 7.1). Based on severity scores on leaves in the field, NE14-09-78, Vax 4, ADP-25, NE14-09-113 and VAX 3 were the most resistant genotypes (score ranging from 2 to 2.7) and landraces Kigome and Bumwufu were the most susceptible (scores of 6.8 and 5.6, respectively). These observed ranges of disease scores (2.9 to 7.7 on leaves, 2.6 to 7.1 on pods, and 2.0 to 6.8 in field) indicated that all the three categories of severity reaction (resistant, intermediate and susceptible) showed up in both screenhouse and field trials and for both leaves and pods, further confirmed, the high genetic diversity of this collection of germplasm with regard to CBB resistance.

Consistency in genotypes' response to CBB disease. Results of Fisher's exact test of independence showed a significant ($P<0.05$) dependence between genotypes' reaction to CBB on leaves in the screenhouse and in the field (Table 4). There was also a significant dependence between leaf and pod reaction to CBB disease in the screenhouse ($P<0.05$) (Table 4). Thus, these genotypes generally had similar reactions to CBB disease on leaves in both field and screenhouse and similar reactions on both plant parts under screenhouse conditions. However, although there was significant positive correlation ($P<0.001$), between leaf reaction in the screenhouse (Leaf_35DAI) and in the field (R8_severity), the strength of these correlation was relatively low ($r = 0.33^{***}$) (Table 5). Similarly, the correlation between Leaf_35DAI and Pod_10DAI in the screenhouse was significant but weak ($r = 0.39^{***}$) (Table 5). This low degree of association between leaf reaction in both environments and between leaf and pod reaction in the screenhouse suggests that a significant number of genotypes did not have a consistent response to CBB disease.

Only two categories of disease reaction (resistant and intermediate) were mainly observed in the field because 88 and 12% of the genotypes that were susceptible in the screenhouse became intermediate and resistant, respectively to CBB infestation when planted in the field (Table 4). This could have been a result of the low disease pressure that was experienced in the field. Despite this low disease pressure in the field, five genotypes (ADP-114, ADP-660, ADP-682, ADP-627 and

TABLE 4. Contingency table of categories of genotype reaction to CBB severity in field and screenhouse

Screenhouse (Leaf)	Field (Leaf)			Screenhouse (Pod)		
	R	I	S	R	I	S
R	6	6	0	5	7	0
I	12	63	1	13	55	8
S	5	38	0	2	33	8

Fisher's exact test of independence$F = 10.9^{*}$ (4 d.f.) $F = 13.4^{*}$ (4 d.f.)
R = Resistant (1-3.4), I = Intermediate (3.5-6.4), S = Susceptible (6.5-9), d.f. = degrees of freedom, * = significance at 0.05 probability level

TABLE 5. Matrix of Pearson correlation analysis of variables studied (n=131)

	Leaf_35DAI (SH)	Pod_10DAI (SH)	R8_Incidence (Field)
Pod_10DAI (SH)	0.39 ***		
R8_Incidence (Field)	0.29 ***	0.10	
R8_Severity (Field)	0.33 ***	0.11	0.49 ***

*, **, *** = significance at 0.05, 0.01, 0.001 probability levels respectively, DAI = days after inoculation, SH = Screen house, R8 = Reproductive phase 8

MIB 465) that had shown a good level of resistance to Xapf "Kawempe 1" in the screenhouse, surprisingly became intermediate in the field. A possible explanation is that genotypes, being subjected to a natural infestation in the field, were attacked by a CBB pathotype other than or in addition to "Kawempe 1" that was used in the screenhouse. This could, therefore, be evidence of pathotype specific resistance exhibited by these genotypes (Rubaihayo, 1996; Zapata *et al*., 2011).

Comparing CBB disease severity symptoms on leaf and pod, four genotypes (ADP-123, ADP-660, NE14-09-19 and ADP-627) showed resistance on leaf, but intermediate reaction on pod (Table 4). On the other hand, out of the twenty genotypes that were resistant to CBB disease on pod, two (ADP-663 and NABE13) were susceptible and the other twelve were intermediate on leaf. Although they were all inoculated by the same *Xanthomonas* isolate "Kawempe 1", these genotypes reacted differentially on pod and leaf. This was confirmed by the low correlation (0.33) observed between leaf and pod reactions to CBB disease in this study, albeit the Fisher's exact test of independence showed some association. Similar results of low correlation between leaf and pod reaction to CBB disease were reported by Fourie (2002) and Arnaud-Santana *et al*. (1994) but different from the findings by Ariyarathne *et al*. (1998). The latter reported a general trend of intermediate correlation between leaf and pod reaction to CBB disease among three RIL populations except one (PC 50' x XAN 159) that showed a low correlation when considered individually. Arnaud-Santana *et al*. (1993) also obtained two different degrees of correlation while screening 18 inbred lines for combined leaf and pod resistance to CBB in common bean. He reported that three of the 18 inbred populations showed low correlation suggesting a differential reaction of leaf and pod whereas the other fifteen had high correlation. Our findings show that the degree of association observed between leaf and pod reaction to common bacterial blight disease depends on the common bean genotypes being evaluated. Some genotypes are resistant in one organ while others combined both resistances.

In the present study, genotypes NE2-14-8, NE17-14-29, NE14-09-78 and VAX3 showed consistent resistance to CBB during both screenhouse and field evaluations, on all disease scoring dates and for both leaf and pod inoculations. Therefore, the four genotypes were identified as potential sources of combined bean leaf and pod resistance to CBB disease. Urrea (2014, Unpublished data) previously identified three of these genotypes (NE2-14-8, NE17-14-29 and NE14-09-78) as resistant against two different Nebraskan isolates of *Xanthomonas*. Likewise, Viteri *et al*. (2014) reported that VAX3 line has high level of resistance to two contrasting bacterial strains of CBB in Idaho, U.S. The findings of this study confirmed the report by Arnaud-Santana *et al*. (1993) that genotypes with leaf and pod resistance to CBB can be identified and developed by breeding. This is the case with the four genotypes identified in this study that possess combined leaf and pod resistance

to CBB disease. While using an appropriate breeding strategy, these genotypes will serve as source of genetic resistance to CBB for improving the preferred market class bean varieties in Uganda.

CONCLUSION

Four genotypes, NE2-14-8, NE17-14-29, NE14-09-78 and VAX3, are potential sources of leaf and pod resistance to CBB disease that could be utilised in the Ugandan bean breeding programme to improve preferred but susceptible local bean varieties. A differential expression of CBB resistance exists in leaf and pod with many genotypes exhibiting resistance either only in leaves or pods, and a few showing dual leaf and pod resistance. Screening procedures for resistance to CBB disease should, therefore, focus on both leaf and pod inoculation for prudence.

REFERENCES

Ariyarathne, H.M., Coyne, D.P., Vidaver, A.K. *and* Eskridge, K.M. 1998. Selecting for common bacterial blight resistance in common bean: effect of multiple leaf inoculation and detached pod inoculation test. *Journal of the American Society for Horticultural Science* 123(5):864-867.

Arnaud-Santana, E., Mmbaga, M.T., Coyne, D.P. and Steadman, J.R. 1993. Sources of resistance to common bacterial blight and rust in elite *Phaseolus vulgaris* L. germplasm. *HortScience* 28(6):644–646.

Arnaud-Santana, E., Coyne, D.P., Eskridge, K.M. and Vidaver, A.K. 1994. Inheritance/ low correlations of leaf, pod, and seed reactions to common blight disease in common beans; and implications for selection. *Journal of the American Society for Horticultural Science* 119(1):116-121.

Belarmino, D. 2015. Inheritance of resistance to common bacterial blight (*Xanthomonas campestris pv. phaseoli*) disease and yield of common bean. MSc. Thesis. Makerere University, Kampala, Uganda. 95pp.

CIAT. 2014. Phenotyping diseases of common bean (*Phaseolus vulgaris* L.) and characterisation of the disease pathogens. Training Manual. CIAT - Kawanda Agricultural Research Station, Kampala, Uganda. 33pp

Durham, K.M. 2011. Evaluation of common bacterial blight resistance in a resistant inter-cross of population of common bean. MSc. Thesis. University of Gelph, Ontario, Canada. 99pp

FAOSTAT. 2015. Agricultural production, crop primary database. Available: http:// faostat3.fao.org/browse/Q/QC/E [2016, September 23].

Fourie, D. 2002. Bacterial diseases of dry beans in South Africa with special reference to common bacterial blight and its control. PhD Thesis. University of Pretoria, Pretoria, South Africa. 222pp.

Fourie, D., Herselman, L. *and* Mienie, C. 2011. Improvement of common bacterial blight resiatnce in Southafrican dry bean cultivar Teebus. *African Crop Science Journal* 19(4):377-386.

Gepts, P., Aragão, F.J.L., Barros, E. De, Blair, M.W., Brondani, R., Broughton, W., Galasso, I. and Hernández, G. 2008. Genomics of *Phaseolus* beans, a major source of dietary protein and micronutrients in the tropics. In: *Genomics of Tropical Crop Plants*. Moore, P.H. and Ming, R. (Eds.). Springer. pp. 113-143.

He, Y. 2010. Improved seed health tests for *Xanthomonas axonopodis* pv. *phaseoli* in common bean. MSc. Thesis. Iowa State University, USA. 114pp.

Kilimo, T. 2012. Development of inclusive markets in agriculture and trade (DIMAT): The nature and markets of bean value chains in Uganda. 56pp.

Miklas, P.N., Coyne, D., Grafton, K.F., Mutlu, N., Reiser, J., Lindgren, D.T. and Singh, S.P. 2003. A major QTL for common bacterial blight resistance derives from the common bean great northern landrace cultivar Montana No. 5. *Euphytica* 131:137–146.

Miklas, P.N., Kelly, J.D., Beebe, S.E. and Blair, M.W. 2006. Common bean breeding for resistance against biotic and abiotic stresses: from classical to MAS breeding. *Euphytica* 147(1-2):105-131. DOI: 10.1007/s10681-006-4600-5.

Opio, F. and Namayanja, A. 2002. Common bacterial blight of beans research in Uganda 1986-2001. In: *Annual Report of the Bean Improvement Cooperative*. 45th ed. pp. 162-163.

Opio, A.F., Teri, J.M. and Allen, D.J. 1993. Studies on seed transmission of *Xanthomonas Campestris pv phaseoli* in common beans in Uganda. *African Crop Science Journal* 1(1):59-67.

Opio, A.F., Allen, D.J. and Teri, J.M. 1994. Evaluation of inoculation methods and inoculum concentration for *Xathomonas campestris* pv. *phaseoli.* In: *Annual report of the Bean Improvement Cooperative*. 37th ed. pp. 223-224.

Osdaghi, E., Alizadeh, A., Shams-bakhsh, M. and Lak, M.R. 2009. Evaluation of common bean lines for their reaction to the common bacterial blight pathogen. *Phtytopathology Mediterraneen* 48:461-468.

Payne R.W. 2009. The Guide to Genstat: Release 12, Part 2, Statistics. Lawes Agricultural Trust, Rothamsted, Experimental Station, Harpenden, Herts, UK.

Rubaihayo, P.R. 1996. Basic concepts of plant breeding. Nairobi: Longhorn Kenya Ltd.

Saettler, A.W. 1991. Common bacterial blight. In: *Compendium of Bean Diseases*. Hall, R. (Ed.). St Paul, MN, USA: APS. pp. 29-30.

Singh, S.P. and Miklas, P.N. 2015. Breeding common bean for resistance to common blight: A review. *Crop Science* 55(3):971-984. DOI: 10.2135/cropsci2014.07.0502.

Singh, S.P. and Schwartz, H.F. 2010. Breeding common bean for resistance to diseases: A review. *Crop Science* 50(4):2199-2223.

Smith A.B., Cullis B.R. and Thompson R. 2005. The analysis of crop cultivar breeding and evaluation trials: An overview of current mixed model approaches. *Journal of Agricultural Science* 143(6):449-462.

van Schoonhoven, A. and Pastor-Corrales, A.A. 1987. Standard system for the evaluation of bean germplasm. Cali, Colombia: Centro Internacional de Agricultura Tropical. DOI: 10.1007/s13398-014-0173-7.2.

Viteri, D.M., Cregan, P.B., Trapp, J.J., Miklas, P.N. and Singh, S.P. 2014. A new common bacterial blight resistance QTL in VAX 1 common bean and interaction of the new QTL, SAP6, and SU91 with bacterial strains. *Crop Science* 54(4):1598-1608. DOI: 10.2135/cropsci2014.01.0008.

Yu, K., Shi, C. and Zhang, B. 2012. Development and application of molecular markers to breed common bean (*Phaseolus vulgaris* L.) for resistance to common bacterial blight (CBB): Current status and future directions. In: Applied Photosynthesis. Najafpour, M. (Ed.). InTech. pp. 365-388.

Zapata, M., Beaver, J.S. and Porch, T.G. 2011. Dominant gene for common bean resistance to common bacterial blight caused by *Xanthomonas axonopodis* pv. *phaseoli*. *Euphytica* 179(1):373-382.