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Evaluation of Rice Germplasm Reveals Sources of Bacterial Leaf Streak Disease Resistance in Uganda

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Abstract In 2014, researchers in Uganda spotted signs typical bacterial leaf streak disease (*Xanthomonas oryzae pv. oryzicola*) in rice fields in Eastern Uganda. The disease was later confirmed to be bacterial leaf streak. In order to effectively plan for measures to manage this potentially devastating disease, it was imperative to score rice germplasm in Uganda for reaction to *Xoc*. Eighty four genotypes from the National Rice Improvement program were evaluated for their reaction to BLS using two *Xoc* isolates collected from Namulonge and Iganga. These were inoculated by the infiltration method using a needless syringe 30 days after planting. Data were collected on the streak length induced by BLS on the leaves 15 days after inoculation. The mean streak length per genotype was interpreted as; Resistant (R), 0<SL≤1mm, Moderately Resistant (MR), 1<SL≤10mm, Moderately Susceptible (MS), 10<SL≤30 mm, Susceptible (S) SL>30mm. Genotypes showed signficant variability ($P < 0.001$) in their reaction to BLS. The *Xoc* isolates reacted signficantly differently ($P=0.011$) on the rice genotypes. For the Iganga isolate, 6 genotypes were resistant while 17 were moderately resistant. For the Namulonge isolate, 3 genotypes were resistant while 7 were moderately resistant. Three genotypes were resistant to both isolates. The observations ranged from highly resistant in Nerica1 to highly susceptible in Du 363. The resistant genotypes identified could be used as sources of genes for introgression into susceptible but agronomically desirable genotypes.

Keywords: *genotype, infiltration, Oryza sativa, xanthomonas oryzae pv. oryzicola*

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1. Introduction

Rice is both a food and cash crop in Uganda [1]. The crop is mostly grown by small scale farmers who cultivate both upland and lowland varieties with an estimated annual production of 191,000 metric tonnes [2]. This production is still low and like in many African countries it cannot meet the increasing local demand for rice. The average rice yield in Uganda is 2.5t/ha [2] which compares poorly with China at 14t/ha [3]. The low production of rice is due to many constraints which include diseases, pests like birds, changing weather patterns and soil fertility challenges [4].

In 2014, signs typical of bacterial leaf streak disease (*Xanthomonas oryzae pv. oryzicola*) were observed in rice fields in Uganda's Eastern districts of Butaleja, Iganga and Namutumba with an incidence of 80, 40 and 30% respectively [5]. The researchers went ahead to confirm the disease as bacterial leaf streak. In Asia, bacterial leaf streak is a serious constraint to rice production, causing yield losses of 10-20%, reaching 40 to 60% in severe cases [6]. Bacterial leaf streak is considered so important in some parts of the world to the extent that in China and the United states, the disease is of quarantine importance [7,8]. Bacterial leaf streak disease has a great potential to destroy rice and jeopardise food and income security in Uganda. Host resistance has been suggested as the most effective means of controlling the disease [7,9]. In Uganda, no information was available on the reaction of the various rice varieties and lines to this disease, yet this is a prerequisite to the design of management measures. A study was therefore conducted to access Ugandan rice germplasm for reaction to bacterial leaf streak disease.

2. Methodology

2.1. The Study Site

The study was conducted in a screen house at the National Crops Resources Research Institute (NaCRRI) located in Namulonge; Kyadondo County, Wakiso district 30 Km North East of Kampala; at an elevation of 1,160 meters and coordinates 00°31′30″N32°36′54″E. NaCRRI climate is characterized by a bi-modal rainfall pattern averaging 1270 mm annually with a mean annual temperature

of 22.2°C. The soils are sandy clay loams, with a pH of 4.9 to 5.0.

2.2. Materials and Methods

Eighty-four rice genotypes were evaluated for their reaction to two *Xanthomonas oryzae pv. oryzicola* (*Xoc*) isolates in a screen house at the National Crops Resources Research Institute (NaCRRI) in Namulonge, Wakiso district. These comprised of released commercial varieties, land races, crosses and advanced breeding lines in NARO's rice breeding program. The *Xo*c isolates were collected from Namulonge (*Nam Xoc*) in Central Uganda and Iganga in Eastern Uganda (*Iga Xoc*) respectively. The rice genotypes were sown in a completely randomized design with a split plot treatment structure in two replicates. Six seeds were sown genotype at a spacing 10 cm within the rows and 10 cm between adjacent rows. The *Xoc* isolates were the main plot factors while the rice genotypes were the sub-plot factors. The study was repeated once.

Table 1. Description of rice genotypes used in the study

Genotype	Pedigree	Origin	Remarks
1189	-	Africa Rice	Aromatic, not released, low land
1190	-	Africa Rice	Aromatic, not released, low land
1191	-	Africa Rice	Aromatic, not released, low land
326104	-	Africa Rice	Not released
AGORO	IR 09A136	IRRI	GSR variety, high yield, low land
AROMA (2015) PLOT 1	-	-	Not released, aromatic
AROMA (2015) PLOT 4	-	-	Not released, aromatic
AROMA (2015) PLOT 5	-	-	Not released, aromatic
AROMA 4 X NERICA 4	-	-	Not released, aromatic
DU 363	-	-	Not released, high yield, low land
E 20	-	-	High yield, low land
E 22	-	-	High yield, low land
GSR 24 A	-	-	Not released
GSR IRLL 2015	-	IRRI	Not released
IIRON (2015) ENT 1	-	IRRI	Not released
IIRON (2015) ENT 23	-	IRRI	Not released
IIRON (2015) ENT 26	-	IRRI	Not released
IIRON (2015) ENT 27	-	-	Not released
IIRON (2015) ENT 3	-	IRRI	Not released
IIRON (2015) ENT 48	-	IRRI	Not released
IIRON (2015) PLOT 219	-	IRRI	Not released
IIRON 1 (2015) PLOT 106	-	IRRI	Not released
IIRON 1 (2015) PLOT 128	-	IRRI	Not released
IIRON 1 (2015) PLOT 142	-	IRRI	Not released
IIRON 1 (2015) PLOT 153	-	IRRI	Not released
IIRON 2 (2015) ENT 30	-	IRRI	Not released
IIRON 2 (2015) PLOT 216	-	IRRI	Not released
IIRON 2 (2015) PLOT 224	-	IRRI	Not released
IIRON 2 (2015) PLOT 227	-	IRRI	Not released
IIRON 50 ENT	-	IRRI	Not released
IIRON-2 225 PLOT	-	IRRI	Not released
IR SUPA 1	IR 97011-6-2-4-1	IRRI	Aromatic, not released
IR SUPA 2	IR 97011-7-5-2-B	IRRI	Aromatic, not released
IR SUPA 3	IR 97011-7-3-1-B	IRRI	Aromatic, not released
IR SUPA 4	IR 97011-7-7-3-1-B	IRRI	Aromatic, not released
IR SUPA 5	-	IRRI	Aromatic, not released
IR SUPA 6	IR 9712-4-1-2-1-1	IRRI	Aromatic, not released
IRBN (2014) ENT 15	-	IRRI	Not released
IRLON (2014) ENT 33	-	IRRI	Not released
IRLON (2014) ENT 38	-	IRRI	Not released
IURON (2014) ENT 24	IR 60080-464	IRRI	Not released
IURON (2015) PLOT 110	-	IRRI	Not released
IURON (2015) PLOT 4	-	IRRI	Not released
IURON (2015) PLOT 7	-	IRRI	Not released
JARIBU (TXD 220)	-	IRRI	High yield, not released
K85	-	LANDRACE	
KAFACI CROSS 1	WAC 18-WAT 15-3-1	NaCRRI	F3 Cross
KAFACI CROSS 10	SR33859-HB3324-93 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 11	WAB 1573-22-B-B-FKR 4-2 WAC1 TGR 3-WAT9-1	NaCRRI	F3 Cross
KAFACI CROSS 13	SR33701-HB3330-78 X SR33859-HB3324-93	NaCRRI	F3 Cross

Genotype	Pedigree	Origin	Remarks
KAFACI CROSS 14	WAB2135-WAC B-2-TGR 2-WAT1-1 X SR33859-HB3324-93	NaCRRI	F3 Cross
KAFACI CROSS 15	WAB 1573-22-B-B-FKR 4-2-WAC 1-TGR 3-WAT9-1	NaCRRI	F3 Cross
KAFACI CROSS 16	WAC 18-WAT 15-3-1 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 2	WAB2135-WAC B-2-TGR 2-WAT1-1	NaCRRI	F3 Cross
KAFACI CROSS 24	WAB 1573-22-B-B-FKR 4-2-WAC 1-TGR 3-WAT9-1 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 26	WAB2135-WAC B-2-TGR 2-WAT1-1 X SR33701-HB3330-78	NaCRRI	F3 Cross
KAFACI CROSS 33	WAB 1573-22-B-B-FKR 4-2-WAC 1-TGR 3-WAT9-1 X WAB2135-WAC B-2-TGR 2-WAT1-1	NaCRRI	F3 Cross
KAFACI CROSS 34	SR33859-HB3324-93 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 36	SR33701-HB3330-78 X SR33859-HB3324-93	NaCRRI	F3 Cross
KAFACI CROSS 37	FAROX 521-357-H1 X SR33859-HB3324-93	NaCRRI	F3 Cross
KAFACI CROSS 39	FAROX 521-357-H1 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 40	SR33859-HB3324-93	NaCRRI	F3 Cross
KAFACI CROSS 44	WAB 1573-22-B-B-FKR 4-2-WAC 1-TGR 3-WAT9-1 X SR33701-HB3330-78	NaCRRI	F3 Cross
KAFACI CROSS 45	WAB 1573-22-B-B-FKR 4-2-WAC 1-TGR 3-WAT9-1 X WAC 18-WAT 15-3-1	NaCRRI	F3 Cross
KAFACI CROSS 48	SR33701-HB3330-78 X SR33859-HB3324-133	NaCRRI	F3 Cross
KAFACI CROSS 49	WAB2135-WAC B-2-TGR 2-WAT1-1 X FAROX 521-357-H1	NaCRRI	F3 Cross
KAFACI CROSS 5	SR33701-HB3330-78 X SR33859-HB3324-133	NaCRRI	F3 Cross
KOMBOKA	IR 05N 221	IRRI	Released, early maturing, aromatic
MOREBEREKAN	-	CÔTE D'IVOIRE	-
NAMCHE 1	-	NaCRRI	Released, high yield, upland
NAMCHE 2	-	NaCRRI	Released, high yield, upland
NAMCHE 3	-	NaCRRI	Released, high yield, upland
NAMCHE 4	-	NaCRRI	Released, high yield, upland
NAMCHE 5 X SUPA 1052	-	NaCRRI	Not released
NERICA 1	WAB 450-1-B-P-38-HB	WARDA/Africa Rice	Released, early maturity, upland
NERICA 10	WAB 450-11-1-1-P41-HB	WARDA/Africa Rice	Released, upland, early maturity
NERICA 4	WAB 450-1-B-P-91-HB	WARDA/Africa Rice	Released, early maturity, upland
NERICA 4 X GIGANTE	-	NaCRRI	Not released
NERICA 4 X WAC 116	-	NaCRRI	Not released
NERICA 6	WAB 450-I-B-P-160-HB	WARDA/Africa Rice	Released , upland
RUMBUKA	-	LANDRACE	-
SUPA 1024	-	AFRICARICE	Aromatic
SUPA 1052	-	AFRICARICE	Aromatic
SUPA LOCAL	-	LANDRACE	Aromatic, preferred by farmers, low yielding

ENT-Entry

2.3. Inoculum Preparation and Inoculation

Inoculum for the two isolates was prepared by growing bacterial cells on modified Wakimoto media (sucrose 20g/l, peptone 5 g/l, calcium nitrate 0.5 g, sodium phosphate 0.82 g/l and bactor agar 17 g/l) for 72 hours at 28°C. The bacterial cultures were then re-suspended in sterile distilled water and diluted to approx. 1 x 10^8 c.f.u ml^{-1} at an optical density of 0.35 and a wavelength of 600 nm [9,10] using a spectrophotometer. This was then used to inoculate all the functioning leaves of each plant. Inoculation was done 30 days after planting using the infiltration method with a needless 10 ml syringe [9,10,11,12]. Six plants were inoculated per genotype. Control, plants were similarly inoculated with sterile distilled water. Humid conditions were maintained around inoculated plants by constructing a chamber around the experiment using a translucent polythene sheet. This procedure was followed for *Xoc* BLS isolates. The experiment was repeated once.

2.4. Data Collection and Analysis

Data were collected on the length of streaks (SL) induced by bacteria on the rice genotypes 15 days after inoculation. Measurements were taken on six randomly selected leaves per genotype using a 300 mm calibrated ruler. The reaction of plants was characterized using mean streak length per genotype in accordance to the scale used by [9] as; Resistant (R), 0<SL≤1mm, Moderately Resistant (MR), 1 < SL≤10mm, Moderately Susceptible (MS), 10< SL≤30 mm and Susceptible (S) SL>30mm. Mean streak length data were subjected to analysis of variance (ANOVA) using Genstat statistical software to further test for the signficance of observed differences in mean streak length between the genotypes and between the two isolates.

3. Results

Analysis of variance for mean streak length due to *Xoc* on the eighty four rice genotypes is given in Table 2. The mean streak length due to *Xoc* varied signficantly with both rice genotype (P<0.001) and *Xoc* isolate (P=0.011). The interaction effect of genotypes and Xoc isolates was also signficant (P<0.001).

Table 2. Analysis of variance for mean streak length on eighty-four rice genotypes separately inoculated with two BLS isolates 15 days after inoculation (DAI) in a screen house at NaCRRI

Variate: Average streak length						
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Cv %
REP	1	10.030	10.030	17.85	1.0 0	
ISOLATE	1	1943.780	1943.780	3458.7	0.011	0.30
Residual	1	0.562	0.562	0.39		
GENOTYPE	83	61865.250	745.364	511.20	<.001	4.70
ISOLATE.GENOTYPE	83	17144.611	206.562	141.67	<.001	8.50
Residual	166	242.038	1.458	0.62		
	336	789.972	2.351			
Total	671	81996.244				14.50

On the rest of the genotypes, the first symptoms of BLS were observed 5 days after inoculation, manifesting as small water soaked streaks, progressing into translucent streaks expanding vertically along the leaf veins. At 7 days after inoculation, the Namulonge isolate formed yellow droplets of bacterial ooze along the streaks on varieties Du 363, Agoro, Jaribu, GSR IRLL 2015, IRBN (2014) Entry 15, IRLON (2014) Entry 38, IR Supa 1, IR Supa 6, Kafaci cross 1, Kafaci cross 14, IIRON 2 (2015) Plot 216, IURON (2015) Plot 4 and Aroma (2015) Plot 5. For the Iganga isolate, these signs were observed on the genotypes Du 363, Agoro, Jaribu, GSR IRLL 2015, IIRON (2015) Entry 26, Komboka, Aroma (2015) Plot 5, Namche 2, Moreberekan, IIRON 2 (2015) Plot 216, IIRON 2 (2015) Plot 224, IR Supa 6, IRBN (2014) Entry 15, IRLON (2014) Entry 38, Kafaci cross 14 and Kafaci cross 34 (Figure 1) 9 days after inoculation.

3.2. Streak Length Induced by Xoc on Rice Genotypes

The mean streak length induced on the rice genotypes due to the two *Xoc* isolates is presented in Table 2. The mean streak length ranged from 0.5-43mm for the Iganga isolate and 0.4-76.3mm for the Iganga isolate. For both isolates, the least streak length were observed on Nerica 6 , IURON (2015) Plot 7, and Nerica 1 respectively. For both isolates, the longest streak was observed on DU 363. On the basis of streak length induced by the Iganga isolate, 16 genotypes were found to be susceptible (S), 6 resistant (R), 17 moderately resistant (MR) while 45 were moderately susceptible (MS). For the Namulonge isolate, 11 genotypes were found to be susceptible, 3 resistant, 7 moderately resistant while 63 were moderately susceptible.

Generally, mean streak length due to the Namulonge isolate was 19.8 mm which was signficantly (P = 0.011) higher than the Iganga isolate at 16.0 mm. The genotypes Agoro, Du 363, Jaribu, GSR IRLL 2015, IR Supa 6, Kafaci cross 14, IRBN (2014) Entry 15, Aroma Plot 5, IIRON 2 (2015) Plot 216 and IRLON (2014) entry 38 were found to be susceptible to both BLS isolates while Nerica 1, Nerica 6 and IURON (2015) Plot 7 were highly resistant to both isolates, producing a hypersensitive response 3 days after inoculation. The genotype IURON (2015) Plot 227, Kafaci cross 37, Namche 1 and Nerica 4 X WAC 116 were found to be moderately resistant to both BLS isolates while 42 genotypes were moderate susceptible to both (Table 3).

Twenty six genotypes produced varying reaction when separately inoculated with both isolates of the pathogen (Table 3). With the exception of Agoro, Du 363, Jaribu, GSR IRLL 2015, IR Supa 6, Kafaci cross 14, IRBN (2014) Entry 15, Aroma Plot 5, IIRON 2 (2015) Plot 216 and IRLON (2014) entry 38 which are susceptible to both isolates, all other genotypes susceptible (S) to the Iganga BLS isolate were found to be only moderately susceptible (MS) to the Namulonge isolate. The genotype IR Supa 1 which was only moderate susceptible to the Iganga isolate was found to be susceptible to the Namulonge isolate. The rest of the genotypes that exhibited moderate resistance (MR) to the Iganga isolate were moderately susceptible (MS) to the Namulonge isolate (Table 3).

Figure 1. Reaction of the rice genotypes to the BLS 15 days after inoculation. S-Susceptible, MS-Moderately Susceptible, MR-Moderately Resistant, R-Resistant

Table 3. Reaction of rice genotypes to the Iganga and Namulonge BLS isolates fifteen days after inoculation

	Reaction to BLS			
	Iganga isolate		Namulonge isolate	
Rice genotype	MSL (mm)	Rating	MSL (mm)	Rating
1189	20.9	MS	21.7	MS
1190	21.7	MS	19.6	MS
1191	22.1	MS	17.8	MS
326104	21.8	MS	13.9	MS
AGORO	32.0	S	36	S
AROMA (2015) PLOT 1	12.1	MS	21.3	MS
AROMA (2015) PLOT 4	6.5	MR	12.3	MS
AROMA (2015) PLOT 5	31.8	S	36.8	S
AROMA 4 X NERICA 4	15.8	MS	15.3	MS
DU 363	43.0	S	76.3	S
E 20	14.1	MS	19.1	MS
E 22	0.9	R	9.0	MR
GSR 24 A	24.5	MS	24.8	MS
GSR IRLL 2015	32.3	S	31.3	S
IIRON (2015) ENT 1	15.0	MS	18.7	MS
IIRON (2015) ENT 23	21.2	MS	23.0	MS
IIRON (2015) ENT 26	36.2	S	13.6	MS
IIRON (2015) ENT 27	13.4	MS	18.6	MS
IIRON (2015) ENT 3	13.6	MS	15.5	MS
IIRON (2015) ENT 48	14.8	MS	22.1	MS
IIRON (2015) PLOT 219	14.8	MS	17.3	MS
IIRON 1 (2015) PLOT 106	14.7	MS	23.0	MS
IIRON 1 (2015) PLOT 128	13.8	MS	13.1	MS
IIRON 1 (2015) PLOT 142	14.5	MS	26.7	MS
IIRON 1 (2015) PLOT 153	16.8	MS	15.3	MS
IIRON 2 (2015) ENT 30	5.3	MR	17.0	MS
IIRON 2 (2015) PLOT 216	34.4	S	34.5	S
IIRON 2 (2015) PLOT 224	41.0	S	9.1	MR
IIRON 2 (2015) PLOT 227	2.6	MR	5.7	MR
IIRON 50 ENT	12.0	MS	20.1	MS
IIRON-2 225 PLOT	15.5	MS	23.6	MS
IR SUPA 1	23.4	MS	31.7	S
IR SUPA 2	16.3	MS	16.3	MS
IR SUPA 3	12.8	MS	16.9	MS
IR SUPA 4	16.0	MS	22.4	MS
IR SUPA 5	3.3	R	17.6	MS
IR SUPA 6	31.0	S	32.2	S
IRBN (2014) ENT 15	40.2	S	39.0	S
IRLON (2014) ENT 33	20.6	MS	32.3	S
IRLON (2014) ENT 38	32.3	S	37.5	S
IURON (2014) ENT 24	11.5	MS	15.1	MS
IURON (2015) PLOT 110	0.5	R	8.5	MR
IURON (2015) PLOT 4	3.3	MR	42.3	S
IURON (2015) PLOT 7	0.8	R	0.5	R
JARIBU	34.0	S	37.6	S
K85	18.6	MS	26.6	MS
KAFACI CROSS 1	16.4	MS	40.1	S
KAFACI CROSS 10	16.7	MS	14.7	MS
KAFACI CROSS 11	15.3	MS	18.1	MS
KAFACI CROSS 13	5.5	MR	21.7	MS
KAFACI CROSS 14	35.6	S	33.3	S
KAFACI CROSS 15	25.2	MS	12.3	MS
KAFACI CROSS 16	11.5	MS	18.5	MS
KAFACI CROSS 2	12.7	MS	22.7	MS
KAFACI CROSS 24	12.9	MS	19.4	MS
KAFACI CROSS 26	13.0	MS	13.3	MS
KAFACI CROSS 33	16.9	MS	17.6	MS
KAFACI CROSS 34	32.4	S	16.3	MS
KAFACI CROSS 36	13.5	MS	18.2	MS

	Reaction to BLS			
	Iganga isolate		Namulonge isolate	
Rice genotype	MSL (mm)	Rating	MSL (mm)	Rating
KAFACI CROSS 37	6.6	MR	9.1	MR
KAFACI CROSS 39	1.3	R	7.3	MR
KAFACI CROSS 40	16.2	MS	17.0	MS
KAFACI CROSS 44	13.4	MS	15.0	MS
KAFACI CROSS 45	14.3	MS	19.7	MS
KAFACI CROSS 48	8.8	MR	11.6	MS
KAFACI CROSS 49	6.5	MR	21.8	MS
KAFACI CROSS 5	4.7	MR	12.0	MS
KOMBOKA	32.8	S	14.7	MS
MOREBEREKAN	31.7	S	13.7	MS
NAMCHE 1	8.0	MR	7.3	MR
NAMCHE 2	33.2	S	12.7	MS
NAMCHE 3	17.7	MS	19.8	MS
NAMCHE 4	8.4	MR	20.0	MS
NAMCHE 5 X SUPA 1052	3.6	MR	17.7	MS
NERICA 1	0.6	R	0.8	R
NERICA 10	7.1	MR	17.3	MS
NERICA 4	12.4	MS	13.1	MS
NERICA 4 X GIGANTE	12.3	MS	16.1	MS
NERICA 4 X WAC 116	6.8	MR	8.9	MR
NERICA 6	0.5	R	0.4	R
RUMBUKA	0.7	R	8.0	MR
SUPA 1024	21.3	MS	21.4	MS
SUPA 1052	6.9	MR	16.4	MS
SUPA LOCAL	7.1	MR	23.9	MS

MSL-Mean Streak Length mm-millimeters R-Resistant MR-Moderate resistant S-Susceptible MS-Moderate susceptible. LSD (Genotype = 1.2; Isolate = 0.7, Isolate. Genotype = 1.8).

4. Discussion

The analysis of variance for the reaction of rice genotypes to BLS revealed signficant (P<0.001) genotype and isolate (P=0.011) effects. The mean streak length induced by the Iganga BLS isolate on the rice leaves was 16.0 mm. This was signficantly (P=0.011) lower that the mean streak length induced by the Namulonge isolate (19.8 mm). ANOVA further revealed significant (P<0.001) interactions between rice genotypes and *Xoc* isolates. The reaction of rice genotypes to the two *Xoc* isolates was found to be normally distributed, ranging from highly resistant to highly susceptible with majority of the genotypes being moderately susceptible. Indeed, several authors have documented this general trend in the reaction of rice genotypes to BLS [7,9,13,14,15]. This reaction of genotypes to BLS suggests that resistance to the pathogen is quantitative in nature. Indeed, [7] and [14] suggested that resistance to BLS is polygenic. However, [16] identified a recessive BLS resistance gene *bls1* in wild rice (O*ryza rufipogon).*

The hypersensitive reaction on the the resistant genotypes Nerica 1 and Nerica 6 is not unique. [17] while working with trangenic rice lines cloned with Rx01 observed a rapid hypersensitive reaction to *Xoc*. [9] while screenig rice genotypes for resistance to several *Xoc* isolates observed that the genotype FKR 14 consitently produced a hypersensitive reaction with all isolates. [15] found the rice varieties FKR19, FKR28, FKR43, NERICA 9, NERICA 12, NERICA 13 and NERICA-L-19 to be resistant to the African *Xoc* strains BAI6 and BAI1, producing a hypersensitive reaction (HR) within four days of inoculation. The hypersensitive reaction is associated with non-host resistance in which a plant species exhbits resistances to all genotypes in the pathogen species, often resulting into localised cell death at the site of infection [18]. In this study, genotypes Nerica 1 and Nerica 6 exhbited non host resistance to the Namulonge *Xoc* isolate while IURON (2015) Plot 7, IURON (2015) Plot 110, E22, Rumbuka and Kafaci cross 3 exhibited non host resistance to the Iganga *Xoc* isolate. These genotypes can be said to be non hosts. Indeed [19,20,21] provided evidence that the hypersensitive reaction is part of non host resistance.

The fact that a genotype can react differently when seperately inoculated with two or more BLS isolates as observed in this study has also been widely reported. Whereas [15] found the rice varieties FKR19, FKR28, FKR43, NERICA 9, NERICA 12, NERICA 13 and NERICA-L-19 to produce a hypersenstive reaction when challenged with the African *Xoc* strains BAI6 and BAI1, these genotypes were all found to be suceptible to the Asian *Xoc* strains. Similarly, [9] found the rice genotypes FKR 14 and ITA 306 to be highly resistant to African *Xoc* strains but moderate susceptible and highly susceptible to the Philipine strain (BLS 256). They further observed that the genotype TN1 was highly susceptible to all *Xoc* strains tested and that whereas the *Xoc* strain BLS 256 induced large leisons on the genotype ITA, the isolates MA13 and MA11D induced small leisions on the same variety. Whereas [22] found the genotype Morebereckan to be one of the most resistant to Asian *Xoc* strains, this genotype was found to be moderately susceptible to the Namulonge BLS isolate and highly susceptible to the Iganga BLS isolate. In our study, this differential reaction of genotypes to the two *Xoc* isolates suggests that the two isolates could

be genetically diverse and points to a potential large diversity in the pathogen population in the country. [22,23] have indeed reported a large degree of genetic diversity among *Xoc* populations.

The Namulonge *Xoc* isolate was found to produce longer streaks than the Iganga *Xoc* isolate on all the rice genotypes that were susceptible to both isolates save for Kafaci cross 14, GSR IRLL (2015) and IRBN (2014) entry 15 where the Iganga isolate produced longer streaks. Long streaks are associated with high levels of susceptibility as a result of rapid multiplication of the pathogen [9] As obseved by [9] Wonni *et al*. (2015), genotypes with short streaks were resistant because they had the ability to curtail multiplication of bacterial cells in their tissues. Similar observations were made by [24] while working with *Xanthomonas campestris pv. oryzae*.

5. Conclusion

The study indicated that the rice genotypes Nerica 1, Nerica 6 and IURON (2015) Plot 7 were resistant (R) to both the Namulonge and Iganga BLS isolates while the genotypes IURON (2015) Plot 227, Namche 1, Kafaci cross 37 and Nerica 4 x WAC 116 were moderately resistant (MR) to both pathogen isolates. The resistant genotypes Nerica 1, Nerica 6 and IURON (2015) Plot 7 could be used as sources of genes for introgression into susceptible but agronomically desirable genotypes. Screening of genotypes for resistance to BLS in Uganda should continue but with more geographically diverse isolates.

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Statement of Competing Interests

The authors have no competing interests.

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