

Research Application Summary

Evaluation of the response of rice genotypes to bacterial leaf streak disease in Uganda

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Abstract

Destructive rice diseases like bacterial leaf streak (*Xanthomonas oryzae* pv. *oryzicola*) have been reported to be on the increase. In 2014, researchers in Uganda spotted signs typical of bacterial leaf streak disease (BLS) in rice fields in Butalejja, Namutumba, and Iganga districts in Eastern Uganda. Bacterial leaf streak is one of the devastating diseases of rice in subtropical Asia and parts of Africa, causing yield loss of up to 60% in susceptible varieties. Host plant resistance has been suggested as the most effective way of managing the disease. However, the reaction of rice genotypes to the disease in Uganda is not yet known. A study was conducted with the objective of identifying sources of resistance to bacterial leaf streak disease in Uganda. Thirty five rice genotypes were evaluated for their reaction to the disease using a BLS isolate (BLS 78) collected from Namulonge in Wakiso district in Central Uganda using the infiltration method with a needleless syringe. Inoculation was done at 30 days after planting and data collected 15 days after inoculation. Data was collected on the streak length induced by BLS on the inoculated leaves. The mean streak length per rice genotype was interpreted as; Resistant (R), $0 < SL \leq 1\text{mm}$, Moderately Resistant (MR), $1 < SL \leq 10\text{mm}$, Moderately Susceptible (MS), $10 < SL \leq 30\text{mm}$, Susceptible (S) $SL > 30\text{mm}$. The mean streak length due to BLS varied significantly ($p < 0.001$) among the genotypes. The observations ranged from highly resistant in Nerica1, Nerica 6 and IURON plot 7 to highly susceptible in Du 363. Only three genotypes were found to be resistant, eight were moderately resistant, 11 were moderately susceptible while 12 were found to be susceptible. The resistant genotypes identified could be used as sources of genes for introgression into susceptible but agronomically desirable rice genotypes in the country.

Key words: Bacterial leaf streak, genotype resistance, rice, Uganda

Résumé

Les pathologies destructrices du riz comme la strie bactérienne des feuilles (*Xanthomonas oryzae* pv. *Oryzicola*) ont été reportées être en augmentation. En 2014, les chercheurs en Ouganda ont repéré des signes typiques de la maladie bactérienne des stries foliaires dans des champs de riz dans les districts de Butalejja, Namutumba et Iganga dans l'est de l'Ouganda. La strie foliaire bactérienne est l'une des maladies dévastatrices du riz dans l'Asie subtropicale et dans certaines parties d'Afrique, entraînant une perte de rendement

allant jusqu'à 60% chez certaines variétés sensibles. La résistance des plantes hôtes a été suggérée comme le moyen le plus efficace de gérer la pathologie. Toutefois, la réaction des génotypes de riz à cette pathologie n'est pas encore documentée en Ouganda. Une étude a été menée pour identifier les sources de résistance à la pathologie en Ouganda. Les réactions à la pathologie de trente-cinq génotypes de riz ont été évalués à l'aide d'un isolât BLS (BLS 78) obtenu à Namulonge dans le district de Wakiso en Ouganda, en utilisant une méthode d'infiltration avec une seringue sans aiguille. L'inoculation a été effectuée 30 jours après la plantation et les données recueillies 15 jours après l'inoculation. Les données ont été collectées sur la longueur de la partie infectée sur les feuilles inoculées. La longueur moyenne de la strie par génotype de riz a été interprétée comme suit : Résistant (R), $0 < SL \leq 1$ mm, modérément résistant (MR), $1 < SL \leq 10$ mm, Modérément Susceptible (MS), $10 < SL \leq 30$ mm, Sensible (S) $SL > 30$ mm. La longueur moyenne de la bande variait significativement ($p < 0,001$) suivant les génotypes. Les observations allaient de très « Résistant » pour Nerica 1, Nerica 6 et IURON 7 à « Très sensible » pour Du 363. Seulement trois génotypes ont été résistants, huit modérément résistants, 11 modérément susceptibles, alors que 12 étaient sensibles. Les génotypes résistants identifiés pourraient être utilisés comme sources pour la modification des gènes sensibles mais agronomiquement souhaités.

Mots clés: Strie des feuilles, résistance aux génotypes, riz, Ouganda

Background

Rice has been gathered, consumed, and cultivated worldwide for more than 10,000 years (Kenmore, 2003). It is the principle food grain consumed by almost a half of the world's population (Khush *et al.*, 2004), making it the most important food crop currently produced (Cottyn *et al.*, 2001). Currently, rice is grown in over 75% of the African countries and is the main staple in Egypt, Liberia, Gambia, Guinea, Senegal and the Sierra Leone. In addition, rice has become an important food security crop in Angola, Benin, Burkinafaso, Chad, Ghana and Uganda (MAAIF, 2009). In Uganda, rice is mainly grown by small scale farmers and a few large scale growers, cultivating both upland and lowland genotypes with an estimated annual production of 191,000 metric tonnes (UBOS, 2010). This production is still low and like in many African countries it cannot meet the increasing local demand.

Rice production in Uganda is constrained by many factors. These include, among others, destructive rice diseases like bacterial blight, blast and rice yellow mottle virus. Other constraints include pests like birds, changing weather patterns and declining soil fertility (Musiime *et al.*, 2005). In 2014, signs reminiscent of bacterial leaf streak disease were observed in rice fields in Uganda's Eastern districts of Butaleja, Iganga and Namutumba with an incidence of 80, 40 and 30%, respectively (Afolabi *et al.*, 2014). In Asia, the disease has become a serious threat to rice production and yield losses of 10-20% have been reported but could reach 40-60% in severe cases (Chen *et al.*, 2007). Bacterial leaf streak is considered so important in some areas to the extent that in China and the

United states, the disease is of quarantine importance (Tang *et al.*, 2000; Nino-Liu *et al.*, 2006). Bacterial leaf streak has a potential to destroy rice and jeopardise food and income security in Uganda. Resistant varieties have been suggested to be the most effective means of controlling the disease (Tang *et al.*, 2000; Wonni *et al.*, 2015). Accordingly a study was conducted with the objective of identifying possible sources of resistance to bacterial leaf streak disease of rice in Uganda.

Literature summary

Bacterial leaf streak is endemic to Asia and much of West Africa. It also occurs in Western Australia (Nino-Liu *et al.*, 2006). In Africa, the disease has been reported in Madagascar, Burkina Faso, Mali, Senegal and Nigeria (Wonni *et al.*, 2011) and most recently in Burundi (Afolabi *et al.*, 2014a) and Uganda (Afolabi *et al.*, 2014b). There is a high degree of genetic diversity among *Xanthomonas oryzae* pv. *oryzicola* strains (Wonni *et al.*, 2014). Rice stubble from the previous cropping season is the most important source of primary inoculum. The bacteria may also be disseminated by irrigation water, humans, insects and birds (Nyvall, 1999). Host genetic resistance is the most important control measure for bacterial leaf streak (Tang *et al.*, 2000; Wonni *et al.*, 2015).

Study description

Screening of genotypes for resistance to BLS was conducted in a screen house at the National Crops Resources Research Institute (NaCCRI) which is the leading centre for research on rice in Uganda under the National Research Organisation (NARO). The germplasm comprised of genotypes from NARO's breeding program, released varieties, introductions and farmers' local preferred varieties. A total of 35 genotypes were screened in a completely randomised design using a BLS isolate collected from Namulonge in Wakiso, Central Uganda (BLS 78). Inoculation was done 30 days after planting. Inoculum was prepared by growing bacterial cells on modified Wakimoto media (sucrose 20 g/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 culture was re-suspended in sterile distilled water at an optical density of 0.35 and a wavelength of 600 nm. This was then used to inoculate the three top functioning leaves of each plant. Inoculation was done using the infiltration method with a needleless 10 ml syringe (Poulin *et al.*, 2014; Wonni *et al.*, 2015). Six plants were inoculated per genotype. For the control, plants were inoculated with sterile distilled water. The experiment was repeated once. The length of streaks (SL) induced by BLS on the genotypes was measured 15 days after inoculation and interpreted in accordance to the scale used by Wonni *et al.* (2015) as; Resistant (R), $0 < SL \leq 1\text{mm}$, Moderately Resistant (MR), $1 < SL \leq 10\text{mm}$, Moderately Susceptible (MS), $10 < SL \leq 30\text{mm}$, Susceptible (S) $SL > 30\text{mm}$. Analysis of variance (ANOVA) was done using the mean streak length per genotype data.

Table 1. Rice genotypes screened for resistance to bacterial leaf streak disease

Genotype	Origin	Genotype	Origin
IURON (2015) PLOT 7	IRRI	GSR IRLI	IRRI
SUPA LOCAL	Land race	NAMCHE 1	NaCRRI
IIRON (2015) PLOT 110	IRRI	NAMCHE 3	NaCRRI
IIRON-2-2-24 (2015)	IRRI	IR SUPA 6	IRRI
KAFACI CROSS 37		IIRON-2-2-16 (2015)	IRRI
KAFACI CROSS 39		IR SUPA1	IRRI
KAFACI CROSS 14		AROMA PLOT 5	
NERICA 4 X WAC 116		DU 363	
IIRON-2-2-16 (2015)	IRRI	E22	
SUPA 1052		E20	
IRBN ENTRY 15	IRRI	NERICA 4 X GIGANTE	
KAFACCI CROSS 1	Korea AGORO		
NERICA 1	WARDA/AfricaRice	RUMBUKA	
NERICA 4	WARDA/AfricaRice	JARIBU	
NERICA 6	WARDA/AfricaRice	KOMBOKA	Tanzania
NERICA 10	WARDA/AfricaRice	NAMCHE 5 X SUPA 1052	NaCCRI
K85	Land race	NAMCHE 4	NaCRRI
MOROBEREKAN	Ivory Coast		

IRRI- International Rice Research Institute, NaCRRI- National Crops Resources Research Institute, WARDA- West Africa Rice Development Agency

Table 2. Mean lesion length induced by Bacterial leaf streak on rice genotypes 15 days after inoculation.

Genotype	Mean streak Length (mm)	Disease reaction	Genotype	Mea Streak Length (mm)	Disease reaction
IURON (2015) PLOT 7	1 a	R	GSR IRLI	31 j	S
SUPA LOCAL	21 hi	MS	NAMCHE 1	8 bc	MR
IIRON (2015) PLOT 110	8 b	MR	NAMCHE 3	17 fgh	MS
IIRON-2 -2-24 (2015)	9 bcd	MR	IR SUPA 6	32 jk	S
KAFACI CROSS 37	10 bcde	MR	IIRON-2-2-16 (2015)	35 jk	S
KAFACI CROSS 39	8	MR	AROMA PLOT 5 (2015)	35 jkl	S
KAFACI CROSS 14	34 jk	S	E22	9 bcde	MR
NERICA 4 X WAC 116	9 bcd	MR	AGORO	33 jk	S
IIRON-2-2-16 (2015)	35 jk	S	RUMBUKA	7 b	MR
KAFACI CROSS 1	40 l	S	JARIBU	37 kl	S
NERICA 1	10 a	MR	KOMBOKA	14 ef	MS
NERICA 4	13 cdef	MS	NAMCHE 5 X SUPA 1052	17fgh	MS
NERICA 6	10 a	MR	NERICA 4 X GIGANTE	17 fgh	MS
NERICA 10	17 fgh	MS	IURON PLOT 4	47 m	S
MOREBEREKAN	14 def	MS	IR SUPA 1	31 j	S
DU 363	12.3 n	S	NAMCHE 4	19 ghi	MS
SUPA 1052	16 fg	MS	E20		
K85	25 i	MS			

R-Resistant, MR- Moderately resistant, S- Susceptible, MS- Moderately susceptible. Mean streak lengths followed by different letters are significantly different ($\alpha = 0.05$)

Results

Small water soaked lesions typical of BLS were visible developing along the veins of leaves of inoculated plants four days after inoculation save for Nerica 1, Nerica 6 and IURON plot 7 where a hypersensitive reaction characterised by browning of the inoculated area was observed. The lesions expanded lengthwise along the veins resulting into translucent streaks of varying lengths with yellow exudate on both the upper and under side of the leaves in the susceptible and moderately susceptible varieties.

The lesion length induced by BLS varied from 1 mm in the resistant genotypes to 120 mm in the most susceptible genotype (Table 2). Two Nerica varieties were found to be highly resistant to the pathogen while two were moderately susceptible, the landraces K85 and Super local were moderately susceptible to the pathogen while the highly susceptible genotypes comprised of introductions and crosses.

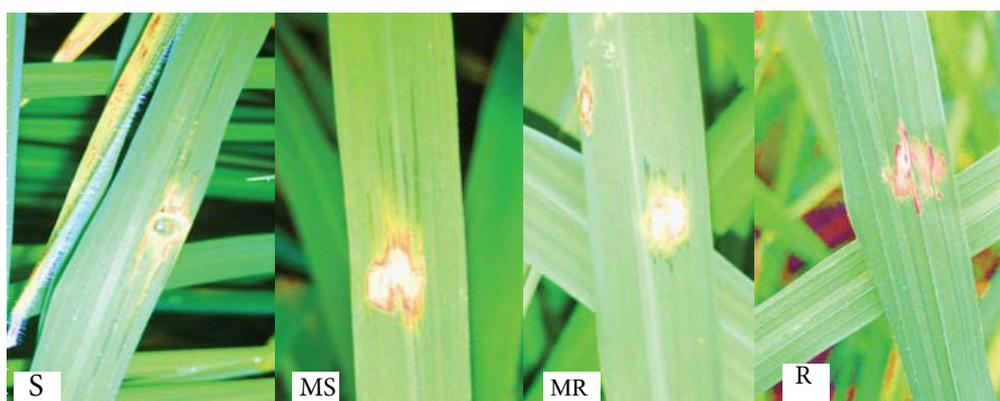


Figure 1. Reaction of the rice genotypes to the BLS 15 days after inoculation S – Susceptible, MS – Moderately Susceptible, MR– Moderately Resistant, R– Resistant.

Table 3. Analysis of variance for the mean streak strength induced by Bacterial leaf streak 15 days after inoculation

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Genotype	34	91.3077	2.6855	8.78	<.001
Residual	35	10.7100	0.3060		
Total	69	102.0177			

Discussion

The mean streak length due to BLS varied significantly ($P < 0.01$) among the genotypes tested (Table 3). The level of resistance of the genotypes to BLS varied, ranging from highly resistant to highly susceptible. This finding is consistent with observations by

Xia *et al.* (1992) of high variability of genotype reaction to BLS. Knowledge of varietal resistance is vital in selecting genotypes with stable resistance (Banitol *et al.*, 2010). In this study, we evaluated 30 genotypes for resistance to BLS. The genotypes Nerica 1, Nerica 6 and IURON plot 7 were highly resistant to the pathogen, inducing a hypersensitive reaction. This is consistent with findings by Wonni *et al.* (2016) who made similar observations on the varieties Nerica 13, Nerica 17, FKR 19 and FKR 43 when challenged with African Xoc strains. With the exception of Namche 1, the Namulonge bred Namche varieties and the landraces Super local and K85 were all moderately susceptible to the pathogen (Table 2). Given the large diversity observed in the BLS population elsewhere (Raymundo *et al.*, 1999; Wonni *et al.*, 2014), it is essential that further studies are done to characterise the diversity of the pathogen in Uganda. As such the rice genotypes in Uganda, including introductions, should therefore be screened against more isolates to test for differential reaction. The stability of the identified resistance should also be evaluated in the major rice growing areas of the country before the advanced breeding lines and introductions can be recommended for adoption by farmers. Since the disease has only been recently reported in the country, it is also essential that the yield loss due to the disease be established so as to estimate the extent of damage of the disease. Nerica 1 and Nerica 6 could be used as a source of genes for introgression into susceptible but agronomically desirable varieties. To hasten the breeding work, it will be imperative to understand the nature of gene action involved in the resistant genotypes.

Research application

The identified resistant genotypes will be recommended for multi-location testing by farmers in areas with high BLS incidence in the country. The resistant genotypes will further be used by breeders as a source of genes for introgression into susceptible by agronomically desirable genotypes. Since no BLS control strategy exists in the country, findings of this study will provide useful insights to the rice breeding program of the National Research Organisation. This is the first effort to identify sources of resistance to BLS in Uganda.

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