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Reaction of introduced Korean rice genotypes for resistance to rice blast in Uganda

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Rice blast caused by *Magnaporthe grisea* is an economically important disease which distributed in most rice growing areas of the world. Yield losses up to 100% are attributed to the blast disease in different rice growing regions of Uganda. In order to combat this disease screening of forty-six introduced Korean rice accessions and two checks IR-64 (resistant) and NERICA-1 (susceptible) were done in a 6 by 8 alpha lattice design in two replications under natural infestation in field conditions, and three replications in the screen house at National Crops Resources Research Institute (NaCRRI) of Uganda in 2015, A and B seasons. Final leaf blast severity, lesion size, area under disease progress curve (AUDPC) values, panicle blast and grain yield were highly significant among genotypes. Genotypes SRHB-133, SRHB-93 and SRHB-78 were resistant to rice blast in both field and screenhouse conditions and showed a lower lesion size. Therefore, these genotypes that consistently showed resistance to rice blast disease can be used as a source of resistance gene for rice blast. This leads to conclude that screening in both the field across seasons and confirming their resistance in the screen house helps the breeder to identify the genotypes that are truly resistant for further utilization as resistant sources.

Key words: Rice blast, screening, *Magnaporthe grisea,* Uganda.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important stable foods for more than half of world's population. It provides up to 50% of the dietary caloric supply and a substantial part of the protein intake in Asia (Muthayya et al., 2014). In Sub-Saharan Africa rice consumption among urban dwellers has steadily been grown. From 2002 to 2007, rice production in Africa had increased by an average of 3.2% per year, and from 2007 to 2012 by 8.4% per year (CGIAR, 2013). In Uganda rice production from year 2010 to 2014 increased from 93 to 95 thousand hectares, with a yield increment of 214 to 237 thousand tonnes (FAO, 2014). But, the production and productivity of the crop is hampered by a number of biotic and abiotic factors.

Rice blast, caused by *Magnaporthe grisea*, is one of the most devastating diseases, especially in susceptible

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Table 1. List of selected rice genotypes used for the study in Kampala, Uganda in the two cropping seasons of 2015.

Genotype	Designation	Genotype	Designation	Genotype	Designation
1	SRHB-75	17	SRHB-73	33	SRHB-196
2	SRHB-80	18	SRHB-78	34	SRHB-228
3	SRHB-93	19	SRHB-86	35	SRF3-125
4	SRHB-108	20	SRHB-90	36	SRF3-135
5	SRHB-133	21	SRHB-95	37	SRF3-147
6	SRHB-142	22	SRHB-64	38	SRF3-57
7	SRHB-2	23	SRHB-54	39	SRF3-182
8	SRHB-8	24	SRHB-65	40	SRF3-13
9	SRHB-12	25	SRHB-67	41	SRF3-32
10	SRHB-37	26	SRHB-105	42	SRF3-42
11	SRHB-66	27	SRHB-108	43	SRF3-75
12	SRHB-70	28	SRHB-118	44	SRF3-29
13	SRHB-35	29	SRHB-120	45	SRF3-3
14	SRHB-44	30	SRHB-139	46	SR-7
15	SRHB-56	31	SRHB-170	47	NERICA-1
16	SRHB-71	32	SRHB-182	48	IR-64

susceptible varieties, causing yield losses of 50 to 90% (Hai et al., 2007; Hajano et al., 2011; Chuwa et al., 2015). It is becoming severe under high temperature, high relative humidity (85 to 89%), presence of dew, drought stress and excessive nitrogen fertilization. This disease is a major problem in most of the rice-growing regions of the world (Onasanya et al., 2008). Since the variability of the pathogen from year to year and place to place makes its management difficult, it becomes important to give great attention to resistance breeding (Sharma et al., 2012; Kihoro et al., 2013). It is a serious concern in temperate areas as well as in tropical uplands. Even though the disease affects all the plant parts above ground, seedlings and young or tender tissues are more vulnerable than those of older ones. At optimum temperatures, new blast lesions appear within 4 and 5 days after they fall on the leaf surface. In warm and wet weather conditions, new conidia are produced within hours after the appearance of the lesions, and this continues for several days (Greer and Webster, 2001). Yield reductions due to blast are drastic when panicle itself and the panicle base are infected shortly after heading (Shim et al., 2005).

Geneticaly diversified genotypes play a vital role in any breeding program for resistance to both biotic and abiotic stresses. The use of resistant varieties can not only ensure protection against diseases, but also save the time, energy and money spent on other measures of control (Sharma et al., 2012). The genetics of host-pathogen interactions are of considerable biological interest and great importance in developing disease-control strategies in efforts of resistance breeding (Ribot et al., 2008). Therefore, the present study was conducted to identify rice blast resistant genotypes from a set of introduced Korean rice accessions in Uganda conditions.

MATERIALS AND METHODS

Description of study area and genotypes used

In this study, the first forty-six rice genotypes introduced from South Korea though the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI) were screened with one resistant (IR-64) and one susceptible (NERICA-1) checks at the National Crops Resources Research Institute (NaCRRI) in Kampala, Uganda during the two rainy seasons of 2015 (Table 1). NaCRRI is located at 0° 31' N, 32° 35' E, with a mean altitude of 1150 m above the sea level. The soils are ferralitic (red sandy and clay loams) and have a pH range of 4.9 to 5.0. The average annual rainfall is 1300 mm and maximum and minimum temperature of 28.5 and 13.0°C, respectively.

Screening under field conditions

A nursery was raised for each genotype and the seedlings were transplanted to the main field. Twenty-one days old seedlings of 48 genotypes were transplanted in the swamp field in a 6 by 8 alpha lattice design with two replications. The spacing of 20 cm between rows and between plants and 40 cm between plots and between blocks with 1 m between replications were used. Four susceptible varieties (NERICA-1, Basimati-370, Sindano and K-85) used as spreader rows were planted between plots two weeks before raising the nursery. This helped to enhance natural infection and to minimize the chance of escape from infection (IRRI, 2014; Vasudevan et al., 2014). In order to promote development of the disease, high humidity was promoted by irrigation twice a day on rain-free days, so that soil of the field experiment was always wet. Other agronomic practices were done as recommended (Asea et al., 2010).

Screening under controlled conditions

Field screened 48 rice genotypes were further evaluated in the screen house using a single isolates of the pathogen to confirm their resistance. Seeds of test lines and the two checks (IR-64 and

NERICA-1) were planted in 25 and 30 cm diameter buckets filled with forest soil (using 4 seeds/pot) in 6 × 8 alpha lattice design in three replications.

Inoculum preparation and inoculation

Blast-infected plants were collected from rice fields at NaCRRI. The infected rice plants were selected by observing the symptoms on the leaves based on the rice blast identification guide (Phadikar et al., 2012). The infected parts were cut into small pieces (0.5-1.0 cm) and then surface sterilized with 2% sodium hypochlorite for three minutes. These pieces were then washed with distilled water and placed on plates of 19.5 g L^{-1} Potato Dextrose Agar (PDA). The PDA plates were then incubated at 25°C for 5 days until sporulation (Hajano et al., 2011). Thereafter, single spores from sporulating lesions were transferred on 4% water agar with the use of an inoculating needle under stereomicroscope for further multiplication for 24 h and the emerging fungus was purified by isolating a single hyphal tip using a sterile needle under a stereo microscope. The resulting pure cultures were incubated at room temperature (25°C) under darkness. After four weeks, the aerial mycelia were slightly washed off by gentle rubbing with a water soaked tooth brush and spore suspension concentration of 1×10^6 spores/ml was prepared using a Neubauer haemacytometer under a compound microscope (Khan et al., 2001). Before inoculation, 0.05% Tween 20 was added to the suspension to increase the adhesion of the spores to the plants. The plants were inoculated with a hand sprayer until run off at the 3 to 4 leaf stage of the plant. High humidity was maintained by covering the area with a white plastic sheet to facilitate infestation. In addition to this, water was sprinkled on the leaves at mid-day for one week, in order to facilitate blast development (Koutroubas et al., 2009).

Data collection

Data on leaf blast severity, lesion size, AUDPC for leaf blast severity and lesion size, panicle blast and yield were collected on five randomly selected plants in the field and on three plants in the screenhouse from each plot according to the standard evaluation system of rice (IRRI, 2014). In addition to these frequency distributions for leaf and panicle blast severity were calculated. Disease evaluations for leaf blast was done four times for each test line at an interval of one week after inoculation in the screenhouse and when the first symptom was observed on the susceptible lines in the field. According to IRRI (2014) standard evaluation system, severity score 0 = no lesions observed, 1 = small brown specks of pin-point size without sporulating center, 3 = small roundish to slightly elongated, necrotic grey spots, 1-2 mm in diameter, 5 = typical susceptible blast lesions 3mm or longer, infecting less than 10% of leaf area, 7 = typical susceptible blast lesions infecting 11-50% of the leaf area and 9 = more than 75% leaf area affected.

$$\text{Blast severity}(\%) = \frac{\text{Sum of all numerical rating}}{\text{Total number of rating x maximum disease rating}} \text{x}100$$

Genotypes were classified according to Shrestha and Misra (1994), for their reaction to leaf blast as 0-15% resistant, 15.1-30% = moderately resistant, 30.1-50% = moderately susceptible and 50.1-100% = susceptible.

To compare relative levels of resistance in the genotypes, weekly assessments of disease severity was done four times. Area under the disease progress curves (AUPDC) was calculated as described by Madden et al. (2008) as; AUDPC = $\sum_{i=1}^{n}\left[\frac{X_{i+1}+X_i}{2}\right]\left[t_{i+1}-t_i\right]$ in which x_i = blast severity at the i^{th} observation, t_i = the time in days after appearance of the disease at the i^{th} day, and n = total number of observations.

Data analysis

The data were subjected to alpha lattice restricted maximum likelihood (ReML) analysis in GenStat 12th edition software package. The genotypes were considered fixed while blocks, replications and season were random effects. However, the randomized complete block analysis was used when the block mean square is greater than the residual mean square. Variance components due to genotypes σ^2_G and genotype by season interactions σ^2_{GXS} and heritability were determined.

The linear model for the across season analysis was as follows:

$$y_{ijkl} = u + s_i + g_j + s/r_{ik} + s/r/b_{ikl} + (s\,x\,g)_{ij} + e_{ijkl}$$

Where, y_{ijkl} = observed value from each experimental unit, u =grand mean, s_i= effect of the i^{th} season, g_j= effect of k^{th} genotype, s/r_{ik} = effect of the k^{th} replication nested within the i^{th} season, $s/r/b_{ikl}$ = effect of r th replication and b th block nested within the i^{th} season, $(s\,x\,g)_{ik}$ = interaction effect of k^{th} genotype and the i^{th} season and e_{ijkl} = the experimental error.

RESULTS

Screening result of genotypes under field conditions

Across season analysis of variance of traits showed significant differences (P≤0.05) among genotypes for final leaf blast severities, lesion size and their respective AUDPC values, panicle blast and yield (Table 2).

The across season analysis result (Table 4) showed that the lowest final leaf blast severity scores (14.3-14.4%) were obtained for three genotypes SRHB-78, SRHB-12 and SRHB-133. Moderately low final leaf blast severities (17.8 - 28.9%) were recorded for ten genotypes which were grouped as moderately resistant. Twenty-four genotypes that had high final leaf blast severities (32.2 - 48.9%) were classified as moderately susceptible. The remaining ten genotypes showed susceptibility levels equal to the susceptible check (Figure 1), NERICA-1 (66.7%) which was followed by SRHB-196 (62.2%).

The genotypes evaluated also showed variation in the AUDPC for leaf blast severity, with seven of them having lower values (120.6 to 182.8%) than the resistant check (IR-64) at 200.3%. Final lesion size ranged from 4.0 mm^2 for genotype SRHB-170 to 63.4 mm^2 for the susceptible check with overall mean of 19.9 mm^2. Low AUDPC values for lesion size were obtained for four genotypes, with mean values ranging from 26.1 to 36.4 mm^2 compared to a value of 43.6 mm^2 recorded on the resistant check (IR-64). The highest lesion size AUDPC was recorded on susceptible check (413.3 mm^2) followed by genotype SRHB-56 (323.8.9 mm^2) (Table 3).

Screening result of genotypes under controlled conditions

The analysis of variance of traits under controlled condition showed significant differences (P≤0.05) among

Table 2. Across season analysis of variance of rice genotypes for leaf and panicle blast severity and lesion under field conditions at NaCRRI, Kampala, Uganda during seasons of 2015A and 2015B.

SOV	df	Severity		Lesion size		PBS	Yield (t/ha)
		FIN	AUDPC	FIN	AUDPC		
Season (S)	1	641.9 ^{ns}	178156**	2276.7**	281720***	441.6**	2.48^{ns}
Rep /Season	2	54.5*	668 ns	21.7**	259^{ns}	4.6 *	0.15^{ns}
Genotype(G)	47	771.9***	158698***	738.1***	35582***	356.5***	1.54***
G x S	47	183.2***	19744 ***	64.2***	5528***	88.2***	0.11^{ns}
Pooled error	76-94	12.3	1157.5	8.5	426	6.6	0.07
Mean		38.8	484	19.9	145	21.9	2.8
GVC		147.2	34738.5	168.5	7513.5	67.1	0.36
VC (G x S)		85.4	9293.3	27.8	2550.9	40.8	0.02
CGD (BH)		0.76	0.88	0.91	0.84	0.77	0.95
CV (%)		9.1	7.0	14.6	14.3	11.7	9.5

*, **, *** significant at 0.05, 0.01 and 0.001 probability respectively, ns = non-significant at > 0.05 probability, SOV = Sources of variation, df = degrees of freedom, Rep = Replication, GVC = Genetic variance component, CGD = Coefficient of genetic determination in broad sense, FIN = Final, AUDPC = Area under disease progress curve, PBS = Panicle blast severity and CV = Coefficient of variation

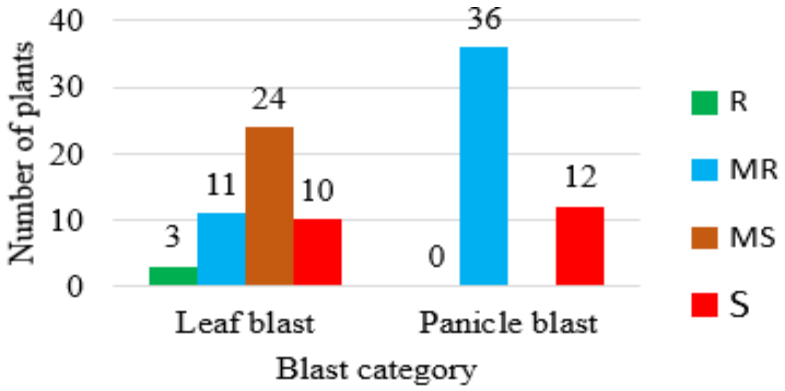

Figure 1. Frequency distribution of rice genotypes for resistance to leaf and panicle blast across seasons under field conditions at NaCRRI, Kampala, Uganda. R = Resistant; MR = moderately resistant; MS = moderately susceptible; S = susceptible.

genotypes for final leaf blast severities, lesion size and their respective AUDPC values, while it showed non-significant for panicle blast and grain yield (Table 4).

The frequency distribution of genotypes for reaction to leaf and panicle blast in the screen house is presented in Figure 2. In this figure five genotypes were resistant, two moderately resistant, twenty-nine moderately susceptible and twelve susceptible. Ten genotypes were resistant to panicle blast, seventeen moderately resistant and 21 were susceptible.

DISCUSSION

Identifying sources of resistance to rice blast has been a major objective for many researchers involved in rice breeding programs (Rama Devi et al., 2015; Biotica et al., 2014; Vasudevan et al., 2014). In this study, 46 introduced genotypes from KAFACI with two checks were evaluated in order to identify resistant sources. The analysis of results revealed that genotypes were significantly different for final leaf blast severity, lesion size, AUDPC values panicle blast severity and yield in both field and screen house conditions. This indicated that genetic variability exists among the screened genotypes, an advantage for improved breeding for blast resistance in rice. Of the genotypes used in this study, none was immune to leaf and panicle blast either in the field or screen house but there were resistant genotypes in these screening conditions.

In the first season's screening for final leaf blast severity under field conditions, four genotypes (SRHB-

Table 3. Disease reaction of rice genotype for blast under field and screen house conditions at NaCRRI Kampala, Uganda during seasons 2015A and B.

Genotype	Field conditions					Screen house condition				
	LBS (%)			Lesion size (mm^2)		LBS (%)			Lesion size (mm^2)	
	Fin	AUDPC	FLBR	Fin	AUDPC	Fin	AUDPC	FLBR	Fin	AUDPC
18	14.4	120.6	R	5.0	26.1	11.1	108.0	R	3.6	19.2
5	13.3	120.6	R	7.1	36.4	11.1	116.7	R	2.4	11.9
3	17.8	143.9	MR	8.7	45.6	11.1	134.0	R	4.2	21.9
9	14.4	147.8	R	9.3	60.1	18.5	142.6	MR	4.0	18.9
12	17.8	147.8	MR	11.6	61.5	11.1	134.0	R	3.0	13.2
31	17.8	182.8	MR	4.5	30.6	35.8	391.0	MS	20.1	119.1
27	17.8	182.8	MR	5.4	34.1	35.8	527.2	MS	19.4	136
13	22.2	210.0	MR	14.7	123.1	38.3	380.2	MS	10.0	55.2
7	21.1	227.5	MR	10.1	63.4	11.1	99.4	R	1.8	8.6.0
39	34.4	276.1	MS	13.9	69.8	35.8	375.9	MS	18.3	108.1
24	27.8	346.1	MR	4.0	36.6	33.3	466.7	MS	11.9	82.9
29	28.9	386.9	MR	9.2	67.8	36.6	430.6	MS	13.4	61.4
26	38.9	394.7	MS	10.3	65.9	51.9	687.0	S	39.8	204.6
23	32.2	408.3	MS	19.8	202.4	30.9	386.7	MS	9.8	72.9
38	38.9	423.9	MS	9.9	62.3	53.1	499.1	S	37.0	170.2
2	38.9	431.7	MS	23.2	130.9	53.1	656.8	S	24.9	156.7
11	34.4	447.2	MS	18.1	126.5	43.2	579.0	MS	17.8	128.6
21	30.0	464.7	MR	12.5	144.9	50.6	527.2	S	21.3	131.7
22	36.7	486.1	MS	16.7	162.0	33.3	276.5	MS	15.3	89.7
43	30.0	497.8	MR	17.3	97.0	33.3	423.5	MS	12.9	109.0
44	37.8	501.7	MS	8.6	62.8	43.2	419.1	MS	18.7	79.6
28	38.9	505.6	MS	9.1	80.3	32.9	534.3	MS	15.5	127.6
40	35.6	507.5	MS	14.1	91.4	45.7	445.1	MS	33.0	147.5
10	48.9	511.4	MS	21.9	169.9	38.3	319.8	MS	11.6	61.0
32	45.6	534.7	MS	11.1	98.1	30.9	276.5	MS	11.4	51.8
36	51.1	550.3	S	20.7	112.7	53.1	587.7	S	40.0	254.8
19	42.2	561.9	MS	25.8	201.1	30.9	350.0	MS	6.4	49.5
17	42.2	573.6	MS	27.1	203.9	55.6	630.9	S	24.7	170.5
41	44.4	585.3	MS	25.7	166.7	43.2	501.2	MS	23.5	155.4
15	45.6	593.1	MS	39.1	318.9	50.6	488.3	S	17.7	125.5
25	51.1	608.6	S	11.3	110.6	44.4	540.1	MS	25.4	159.4
14	51.1	610.6	S	38.9	265.2	33.3	285.2	MS	10.4	66.0
1	46.7	616.4	MS	29.2	196.1	45.7	479.6	MS	19.3	102.1
37	57.8	618.3	S	54.5	323.8	38.3	367.3	MS	23.0	153.4
6	55.6	618.3	S	37.5	243.8	30.9	350.0	MS	8.9	75.3
4	44.4	633.9	MS	39.8	290.7	53.1	760.5	S	30.2	190.3
45	43.3	635.8	MS	11.2	95.3	43.2	445.1	MS	21.0	99.8
30	45.6	649.4	MS	17.7	129.4	45.7	596.3	MS	34.6	204.7
42	51.1	666.9	S	38.9	241.4	43.2	531.5	MS	28.9	169.5
16	44.4	676.7	MS	34.6	316.4	35.8	401.9	MS	8.1	54.6
46	51.1	705.8	S	11.5	115.2	33.3	263.6	MS	6.9	33.1
34	46.7	711.7	MS	13.8	141.6	53.1	522.8	S	34.9	169.0
20	54.4	717.5	MS	33.2	270.5	33.3	337.0	MS	9.7	45.6
8	52.2	731.1	MS	33.9	259.5	45.7	462.3	MS	19.1	119.1
33	62.2	762.2	S	32.1	199.7	50.6	509.9	S	35.2	134.7
35	58.9	764.2	S	9.0	135.0	53.1	626.5	S	40.4	197.9
RC	20.0	200.3	MR	7.9	43.6	27.2	254.9	MR	4.2	21.6
SC	66.7	824.4	S	63.4	413.3	55.6	682.7	S	41.7	258.7

Table 3. Contd.

Mean	38.8	484.0		19.9	145.0	38.2	423.0	18.6	108.0
LSD (P=0.05)	19.3	199.9		11.4	105.8	5.7	71.3	4.1	17.3
CV	9.1	7		14.6	14.3	9.2	10.4	13.3	9.9

RC = Resistant check, SC = Susceptible check, FIN = Final, AUDPC = area under disease progress curve, FLBR = Final leaf blast reaction, LBS = Leaf blast severity, CV = Coefficient of variation, LSD = least significant difference.

Table 4. Analysis of variance of rice genotypes for leaf and panicle blast severity and lesion size in the screen house conditions at NaCRRI, Kampala, Uganda in season 2015A.

SOV	df	Leaf blast severity		Lesion size		PBS	Yield (g/plot)
		FIN	AUDPC	FIN	AUDPC		
Rep	2	60.7 *	24108**	30.7**	840**	8.1^{ns}	85.9^{ns}
Rep/Block	21	12.3^{ns}	2802^{ns}	-	-	-	-
Genotypes	47	489.3***	80917***	404.4***	12655***	433.7***	197.9***
Residual	71 and 92	12.1	1735	6.2	114	4.9	39.1
LEE	73- 77	12.3	1926	-	-	-	-
Mean		38.2	423	18.6	108	22.8	35.8
GVC		159	26330.5	132.8	4180.3	142.9	52.9
CGD(BH)		0.97	0.98	0.98	0.99	0.99	0.80
CV (%)		9.2	10.4	13.3	9.9	9.7	17.5

*, **, *** significant at 0.05, 0.01 and 0.001 probability respectively, ns = non-significant at p> probability, SOV = Sources of variation, df = degrees of freedom, Rep = Replication, LEE = Lattice effective error, GVC = Genetic variance component, CGD = Coefficient of genetic determination in broad sense, CV = Coefficient of variation, FIN= Final, AUDPC = Area under disease progress curve, and PBS = Panicle blast severity.

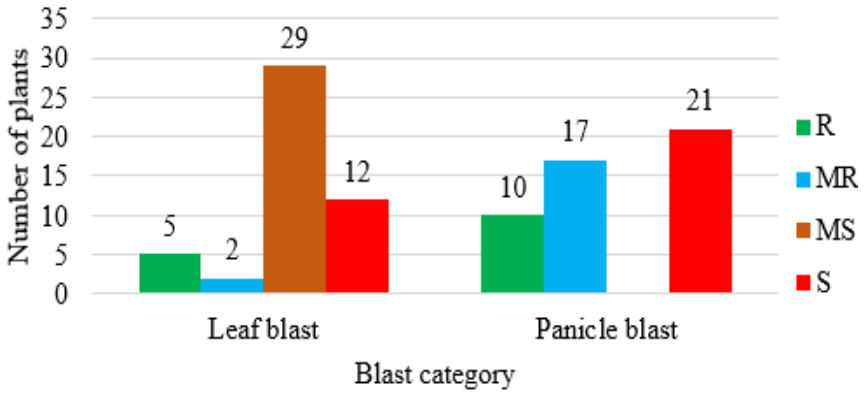

Figure 2. Frequency distribution of rice genotypes for resistance to leaf and panicle blast in the screenhouse at NaCRRI, Kampala, Uganda. R = Resistant; MR = moderately resistant; MS = moderately susceptible; S = susceptible.

133, SRHB-78, SRHB-93 and SRHB-12) were classified as resistant and eight as moderately resistant. In the second season none of the genotypes showed resistance, though 19 that showed moderately resistance were resistant in the first screening. Based on field experiment results across seasons, three genotypes (SRHB-133, SRHB-78 and SRHB-12) showed resistance, and 11 moderate resistances. In the screen house conditions, five genotypes showed resistance (SRHB-93, SRHB-133, SRHB-2, SRHB-70 and SRHB-78) and two moderate resistances. This indicates a difference in performance of the rice genotypes under differing screening conditions and seasons. These results are compatible with the findings of Ghazanfar et al. (2009), Kumar et al. (2012), Pasha et al. (2013a) and Rama Devi et al. (2015) for screening rice genotypes against

resistance to rice blast. Their results revealed that while none of the varieties were immune to blast, genotypes were grouped as resistant, moderately resistant and susceptible. These variations may be attributed variously to genetic difference for resistance to blast, or to variation in environment from season to season and screening conditions. These findings indicate that screening under both field and screen house conditions and in several seasons could be effective for getting genotypes with resistant genes for rice blast disease.

The significant effect of season that produced variation in values for leaf blast, lesion size and their AUDPC values could be due to variable weather conditions. Environmental factors, relative humidity, temperature and amount of rainfall could strongly affect the sporulation, release and germination of blast conidia (Park et al., 2009;Yang et al., 2011).

Variation for panicle blast severity, shown in the analysis of the overall field screening indicates the presence of genetic variation among genotypes. None of the genotypes showed immunity to panicle blast severity, though 36 genotypes were resistant and 12 were found susceptible. However, in the screen house condition 10 genotypes showed resistance, 17 were moderately resistant and the remaining was susceptible. A similar result was reported by Pasha et al. (2013b), Chuwa et al. (2015), Lee et al. (2015). Nagaraju et al. (2008) also reported in screening 265 genotypes, none of them was immune for leaf and panicle blast, eight genotypes were resistant and 138 moderately resistant to leaf blast and 18 genotypes were resistant, and 82 moderately resistant to panicle blast.

Conclusion

In general, this study showed the value of testing the reaction of the introduced Korean rice genotypes to the Ugandan situation, even when they were introduced by the source as being resistant. In this study the across-season field screening results showed that three genotypes were resistant, eleven moderately resistant, 24 moderately susceptible and ten susceptible to rice leaf blast. In the screen house five genotypes were shown to be resistant, two moderately resistant, 29 moderately susceptible and 12 susceptible, again indicating genetic variation among genotypes. Results from the two screening environments showed that genotypes SRHB-133, SRHB-93 and SRHB-78 were more consistent for resistance to rice blast and good performance for yield. So, these genotypes can be either used by farmers after intensive evaluation for production or used to introgress the resistant genes into the locally-adapted elite materials of Uganda. Therefore, genotypes that consistently showed resistance to rice blast disease under both screening conditions can be used as a source for resistance in the rice blast breeding program. From this study, it is possible to conclude that screening in both the field across seasons and in the screen house helps the breeder to identify the genotypes that are truly resistant for further utilization as resistant sources. Additionally, large populations could be screen in the screen house at reduced cost.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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REFERENCES

Asea G, Onaga G, Phiri NA, Karanja DK, Nzioka P (2010). Quality rice seed production manual. CABI Africa and NaCRRI, Nairobi, Kenya.

Biotica C, Rao KK, Chamundeswari N, Bhuvaneswari V, Nagakumari P, Rao PVR, Rani MG, Satyanarayana PV, Suryanarayana Y, Bharatalakshmi M, Reddy AV (2014). Screening of advanced breeding lines for seedling blast resistance in rice (Oryza sativa L.) using microsatellite markers. Curr. Biotica 8(2):125-131.

Consultative Croup for International Agricultural Research (CGIAR) (2013). Africa rice center (AfricaRice). Africa Rice Cent.

Chuwa CJ, Mabagala RB, Reuben MSOW (2015). Assessment of grain yield losses caused by rice blast disease in major rice growing areas in Tanzania. Int. J. Sci. Res. 4(10): 2211-2218.

Food and Agriculture Organization (FAO) (2014). Food and Agriculture Organization of the United Nations Statistics division.

Ghazanfar MU, Habib A, Sahi ST (2009). Blast Disease. Pak. J. Phytopathol. 21: 41-44.

Greer CA, Webster RK (2001). Rice blast disease in California. Plant Dis. 85:1096-1102.

Hai LH, Kim P, Van, Dun P, Van, Thuy TTT, Thanh DN (2007). Grain yield and grain-milling quality as affected by rice blast disease (*Pyricularia grisea*). Omonrice 15:102-107.

Hajano J, Pathan M, Rajput Q, Lodhi M (2011). Rice blast-mycoflora, symptomatology and pathogenicity. Int. J. Agro Vet. Med. Sci. 5(1):53-63.

International Rice Research Institute (IRRI) (2014). Standard evaluation system for rice. International Rice Research Institute. Los Banos, Manila, Philippines.

Khan JA, Jamil FF, Cheema AA, Gill MA (2001). Screening of rice germplasm against blast disease caused by *Pyricularia oryza*, Int. Proc. National Conf. of Plant Pathology. held at NARC. Islamabad, pp. 86-89.

Kihoro J, Bosco NJ, Murage H, Ateka E, Makihara D (2013). Investigating the impact of rice blast disease on the livelihood of the local farmers in greater Mwea region of Kenya. Springerplus 2(1):308.

Koutroubas SD, Katsantonis D, Ntanos DA, Lupotto E (2009). Blast fungus inoculation reduces accumulation and remobilization of pre-anthesis assimilates to rice grains. Phytopathol. Mediterr. 48:240-252.

Kumar S, Singh SS, Singh AK, Elanchezhian R, Sangale UR, Sundaram PK (2012). Evaluation of rice genotypes for resistance to blast disease under rain fed lowland ecosystem. J Pl Dis. Sci.

7(2):175-178.
Lee J, Lee J, Yoon Y, Kim S, Hur Y, Yeo U, Sohn Y, Song Y, Park D, Nam M, Cho J (2015). Enhancement of panicle blast resistance in korean rice cultivar " Saeilmi " by Marker Assisted Backcross Breeding. 2015: 1-10.
Madden LV, Hughes G, van den Bosch F (2008). The study of plant disease epidemics. American Phytopathological Society (APS Press), 2007.
Muthayya S, Sugimoto JD, Montgomery S, Maberly GF (2014). An overview of global rice production, supply, trade, and consumption. Ann. NY Acad. Sci. 1324(1)7-14.
Chandrashekhra MV, Sunkad G, Naik MK, Nagaraju P (2008). Screening of Rice genotypes against blast caused by Pyricularia oryzae. Karnataka J. Agric . Sci. 21(2):305-305.
Onasanya A, Sy AA, Akator SK, Kabore B, Conde CK, Traore M, Kiepe P, Guinee A De (2008). Importance of varietal improvement for blast disease control in Africa. JIRCAS Working Report 70(2011): 77-90
Park J-Y, Jin J, Lee Y-W, Kang S, Lee Y-H (2009). Rice blast fungus (*Magnaporthe oryzae*) infects Arabidopsis via a mechanism distinct from that required for the infection of rice. Plant Physiol. 149:474-486.
Pasha A, Babaeian N, Bagheri N, Nematzadeh G (2013a). Field evaluation of resistance to *pyricularia oryzae* in rice genotypes. Int. J. Agric. Crop Sci. 5:390-394.
Pasha A, Bagheri N, Nematzadeh G, Babaeian-Jelodar N (2013b). Identification of rice genotypes resistant to panicle blast 1346-1350.
Phadikar S, Sil J, Das A (2012). Classification of rice leaf diseases based on morphological changes. Int. J. Geogr. Inf. Sci. 2:460-463.
Rama Devi SJS, Singh K, Umakanth B, Vishalakshi B, Renuka P, Vijay Sudhakar K, Prasad MS, Viraktamath BC, Ravindra Babu V, Madhav MS (2015). Development and identification of novel rice blast resistant sources and their characterization using molecular markers. Rice Sci. 22:300-308
Ribot C, Hirsch J, Balzergue S, Tharreau D, Nottéghem JL, Lebrun MH, Morel JB (2008). Susceptibility of rice to the blast fungus, Magnaporthe grisea. J. Plant Physiol. 165(1):114-124.
Sharma TR, Rai AK, Gupta SK, Vijayan J, Devanna B, Ray S (2012). Rice blast management through host-plant resistance: Retrospect and Prospects. Agric. Res. 1:37-52.
Shim SH (2005). Damage analysis of rice panicle blast on disease occurrence time and severity. Plant Pathol. J. 21(2):87-92.
Shrestha SM, Misra NK (1994). Evaluation of common cultivars of rice against leaf and neck blast in Nepal. J. Inst. Agric. Anim. Sci. 15:101-103.
Vasudevan K, Vera Cruz CM, Gruissem W, Bhullar NK (2014). Large scale germplasm screening for identification of novel rice blast resistance sources. Front. Plant Sci. 5:1-9.
Yang H, Yang X, Wang Y (2011). The correlation analysis between blast resistance and genetic diversity of 39 Yunnan glutinous rice varieties. J. Yunnan Agric. Univ. 26:1-5