



Thai Indigenous Lowland Rice Germplasms: Sources of Bacterial Blight Disease Resistance and Agronomic Attributes

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ABSTRACT

Bacterial blight (BB) has caused significant reductions in yield and quality of rice. The use of genetically resistant cultivars has proven to be one of the most effective methods used to address this problem. This study screened a total of 333 Thai lowland indigenous rice germplasms against four *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) isolates under greenhouse conditions in the rainy and dry seasons of 2017. The ten varieties demonstrating the greatest BB resistance in the lower five centimeters of the lesion lengths in both experiment years were further investigated and validated for their agronomic performances in field conditions at the Udon Thani Rice Research Center in 2018. Our findings revealed that of the ten BB resistant lowland rice varieties, five varieties; LLR023, LLR134, LLR137, LLR205 and LLR207, exhibited high performances of agronomic traits in field conditions; as found in the plant height, tiller number, panicle number, panicle length, seeds per panicle, grain yield and harvest index when compared with the KDML105 check varieties. These five selected rice varieties may further serve as new genetic resources for future BB resistance and agronomic trait improvement programs.

INTRODUCTION

Rice (*Oryza sativa* L.) is a staple daily energy source for one-third of the world's population (Noroozi, Beheshtizadeh, & Sattari, 2015). Most rice consumers and producers are located in the Asia-pacific regions of South Asia and Southeast Asia (Gumma, Nelson, Thenkabail, & Singh, 2011; Redfern, Azzu, & Binamira, 2012). Thailand has remained one of the region's top five rice producers and has led the area in rice exportation (FAO, 2018), due to the strength of its remarkable fragrant and tasty rice cultivars. The demands of today's fast-growing world population have resulted in increased rice consumption over the past several decades; and, therefore, the necessity to examine

rice productivity yields in terms of both quality and quantity to serve future demand.

Rice diseases, developed by viruses, bacteria, or fungi, are significant constraints leading to the reduction of rice yields (Shamim & Singh, 2017). Among all diseases, bacterial blight (BB), caused by several strains of the pathogenic bacterium *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), has been reported as having the most deleterious effect on rice production (Chukwu et al., 2019; Ou, 1985; Swings et al., 1990). Diseased rice plants prominently showed three particular symptoms; kresek (seedling wilt caused by systemic infection), leaf blight, and pale-yellow leaf (Ou, 1985). Leaf blight disease typically proceeds downward from the tips of infected leaves (Chukwu et al., 2019;

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Niño-Liu, Ronald, & Bogdanove, 2006). In addition to vegetative damage, this pathogen also causes the maldevelopment of tillers and, thus, the number of seeds (Ou, 1985; Shanti et al., 2010). BB has been estimated to diminish rice yields from 20 to 80 percent, depending on the plant's developmental stage (Yasmin et al., 2017) or the geographical environment; as evidenced in the 60%, 70%, and 80% yield losses in Niger, Southeast Asia, and Mali, respectively (Awoderv, Bangura, & John, 1991; Mew, 1993; Sere et al., 2005; Verdier, Vera Cruz, & Leach, 2012). It is widespread throughout rice cultivation areas across the world with increasing severity (Chukwu et al., 2019). In Thailand, BB was first recorded in 1963 in the Pathum Thani province (Eamchit, 1982).

Breeding programs through either conventional or molecular approaches have been used for generating rice cultivars resistant to bacterial blight (Chukwu et al., 2019; Rao, Lakshminarasu, & Jena, 2002). However, mutant *Xoo* strains have been found capable of breaking down the bacterial leaf blight resistance of rice cultivars after long-term cultivation (Shanti et al., 2010); suggesting that rice cultivars carrying a single *Xa4* gene were no longer effectively resistant to BB when the mutant *Xoo* race was presented (IRRI, 1989). Moreover, empirical evidence supports the involvement of avirulent gene mutation in the adaptation of *Xoo* strains within rice lines containing *Xa10* (Vera Cruz et al., 2000). Efforts are continually being made to achieve resistance to various *Xoo* genotypes, extend durability, and offer a broad spectrum of defense mechanisms against such pathogens in rice cultivars through the concept of gene pyramiding (Das, Rao, Varier, Prakash, & Prasad, 2018; He et al., 2019; Jiang et al., 2020; Kim & Reinke, 2019; Pradhan et al., 2015). Several pyramided BB resistant genes have revealed successful resistance to various *Xoo* strains; however, failures from combined resistance genes have also been reported (Das, Rao, Varier, Prakash, & Prasad, 2018; Yugander et al., 2018), as such resistance mechanisms were governed by multiple genes associated with the genetic diversity of the *Xoo* or rice cultivar (Vera Cruz et al., 2000).

The simultaneous loss of BB resistant genes in new rice varieties might be a result of hybridization and selection for particular agronomic traits. Ullah et al. (2012) for example, determined that grain quality and aroma were not compromised with *Xa4* and *Xa7* after gene pyramiding in introgressed rice in

Basmati-385 and Basmati-2000 cultivars. Therefore, the incorporation of total BB resistance and desirable agronomic traits in rice cultivars remains a challenge (Angeles-Shim, Shim, Vinarao, Lapis, & Singleton, 2020). The combined selected resistance genes in favorable rice cultivars, developed through breeding programs, resulted in new broad-spectrum bacterial blight-resistant lines with high yield and quality; as found in the combination of resistance genes *Xa4*, *xa5*, and *Xa21* in Mangeumbyeo (Suh et al., 2013); *xa5*, *xa13*, and *Xa2* in Jalmagna (Pradhan et al., 2015); *Xa4*, *xa5*, *xa13*, and *Xa21* in Tapaswini (Das, Rao, Varier, Prakash, & Prasad, 2018); and the *Xa4*, *xa5*, *Xa7*, *xa13*, and *Xa21* resistance genes in Tainung82 (Hsu, Chiu, Yap, Tseng, & Wu, 2020).

The popular aromatic KDML105 and RD6 varieties, which comprise 87% of the rice cultivation in Thailand's northeastern region, are susceptible to bacterial blight disease (Vanavichit et al., 2018). Few studies have generated broad-spectrum BB resistant RD6 lines via introgression with a single effective resistance gene of another cultivar (Nan et al., 2019; Pinta, Toojinda, Thummabenjapone, & Sanitchon, 2013; Wongkhamchan, Chankaew, Monkham, Saksirirat, & Sanitchon, 2018). Because Thailand is a hotspot of genetic diversity, in which 155 cultivars carry four BB resistance genes (Sombunjitt, Sriwongchai, Kuleung, & Hongtrakul, 2017), introgression of these genes from various indigenous rice varieties to the KDML105 and RD6 varieties may lead to new rice varieties resistant to local *Xoo* strains. Moreover, indigenous rice genotypes in a particular cultivation area, such as Thailand's lowlands, possess excellent agronomic traits that might be used as parental lines. It is important to explore the genetic variation, BB resistance, and agronomic traits in particular, among rice germplasms to broaden the genetic background used in future rice breeding programs.

This study aims to investigate the BB resistant rice varieties from the lowland areas across Thailand that showed significant agronomic trait values. To do so, all collected rice varieties were tested for their resistance ability in greenhouse conditions. Rice varieties that demonstrated high agronomic traits together with high BB resistance ability were further validated through field experimentation. Additionally, the correlation between BB resistant ability and each particular agronomic trait was examined to explore the significance of the formulated traits within selected rice varieties.

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MATERIALS AND METHODS

Plant Materials

The 333 indigenous lowland rice (LLR) varieties used in the bacterial leaf blight resistance ability tests were collected from twenty-one provinces across Thailand. Five known BB resistant rice cultivars (Azucena, IR62266, IR64, IRBB21, and IRBB5) and three known susceptible rice cultivars (KDML105, RD6, SKN) (Korinsak et al., 2009; Sribunrueang, Chankaew, Thummabenjapone, & Sanitchon, 2017) were added as negative and positive controls, respectively (Fig. 1). Within the evaluation of the BB resistance ability and agronomic traits, the ten rice varieties which showed the highest resistance ability (minimal BB lesion lengths) in the greenhouse experiments were also examined in the field.

Bacterial Isolates and Bacterial Inoculum

The *Xoo* isolates used in all experiments were independently isolated from naturally infected rice leaves in four of Thailand's provinces; CM 3-1

(Chiang Mai), MS 1-2 (Maha Sarakham), NY 1-1 (Nakon Nayok), and NB 7-7 (Nonthaburi) (Fig. 1). Each bacterial isolate was further cultured on nutrient agar and then incubated in a chamber at 29-30°C for 48-72 hours. In the BB resistance ability test, the bacterial inoculum was prepared by mixing four bacterial isolates adjusted with distilled water to an optical density (OD) of 0.3 at 600 nm (approximately 10^9 CFU/ml) by spectrophotometer (Sribunrueang, Chankaew, Thummabenjapone, & Sanitchon, 2017). In the BB resistance validations and agronomic trait evaluations conducted in the field, the bacterial inoculum was prepared from infected leaves of KDML105 and RD6 rice mixed with the four bacterial isolates. Leaves with yellow or greenish-brown lesions were cut into 6 cm pieces before incubation in one liter of distilled water at room temperature for two to three hours. After that, the pieces were crushed to extract the bacterial pathogen utilized within the experiment three hours after preparation (Lamo et al., 2015; Sharma & Pandey, 2012).

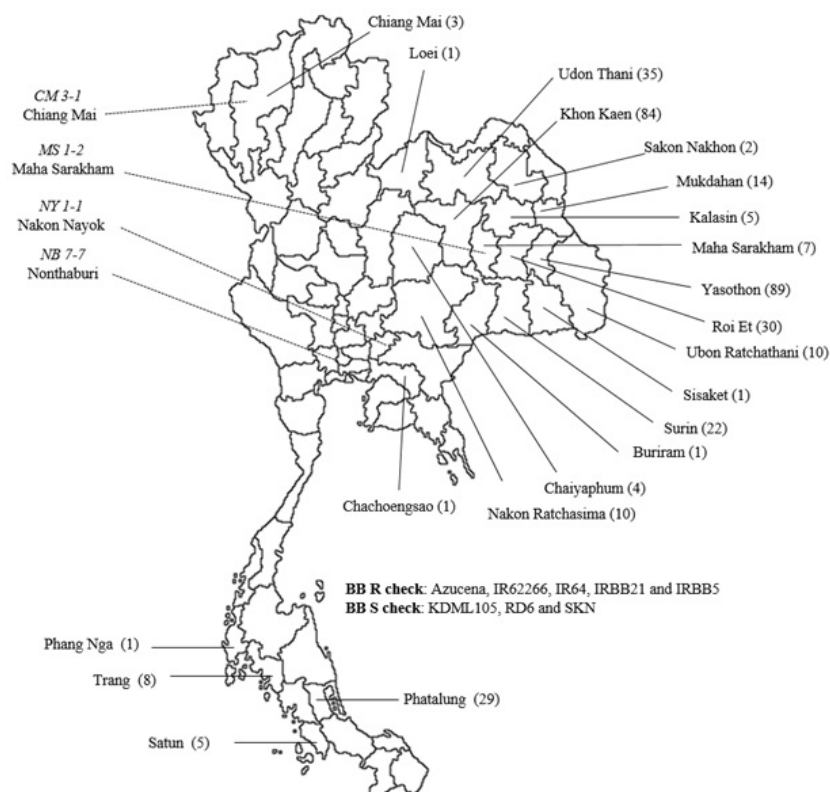


Fig. 1. Sources of Thai indigenous lowland rice germplasm and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) isolates used in this study

Bacterial Inoculation Method and Disease Development Conditions

Greenhouse Experiment

The greenhouse experiments were conducted in the 2017 rainy season (September) and dry season (November) at the Agronomy Field Crop Station, Khon Kaen University, Khon Kaen, Thailand, to explore the variations of disease incidence under different atmospheric conditions. Seeds of each rice cultivar were soaked in sterile water for three days and then sown in randomized planting trays with 4.7 x 4.7 x 5.0 cm³ holes filled with sterilized sandy loam soil. Three seeds of each cultivar were sown per experimental unit. The experiment was assigned in a completely randomized design (CRD) with three replications. The moisture in the greenhouse was maintained via a fogger system, three times daily. Fertilizer was applied at 15 days after sowing (DAS) with 15-15-15 NPK fertilizer (187.5 kg/ha) (Chumpol, Chankaew, Saepaisan, Monkham, & Sanitchon, 2018). Bacterial inoculation was conducted via the leaf clipping method following Kauffman, Reddy, Hsieh, & Merca (1973). The uppermost and lowermost leaves of each plant were clipped with scissors that were dipped into the bacterial suspension at 5 cm downward from the leaf tip. In the BB resistance ability test, the seedlings of all rice germplasms (21 DAS) were prepared for bacterial inoculation. Inoculated rice plants were grown in muddy soil in the greenhouse at 27-28°C and 85-90% relative humidity. Water was maintained at 5 cm from the soil surface throughout the experiment.

Field Experiment

The field experiment for BB resistance ability validation and agronomic trait evaluation was conducted in the rainy season (August) of 2018 at the Udon Thani Rice Research Center, Udon Thani, Thailand. Seeds of the ten selected indigenous lowland rice varieties and the five check varieties (both resistant and susceptible to BB) were soaked for three days and then nursed via the drilling method in paddy plots in single rows at 26 DAS. The rows of ten selected varieties, the BB resistant checks (IRBB21, SPT, TN1), and the BB susceptibility checks (KDML105 and SKN) varieties were randomly grown at 25 x 25 cm (between plants and rows). The KDML105 variety was added in every two trails and completely trapped the surrounding area. Bacterial inoculation was conducted at the 30-day

tilling stage via the leaf clipping method prescribed by Kauffman, Reddy, Hsieh, & Merca (1973). The inoculated plants were grown naturally in the field and the agronomic traits were examined. Note that the data of only five infected plants were recorded.

Evaluation of Bacterial Blight Resistance

The inoculated rice plants in all greenhouse experiments were examined at 8 and 15 days after inoculation (DAI), whereas the field experiments were carried out at 18 DAI. The BB symptoms of each genotype, evidenced by the lesion lengths (cm), were recorded following the standard evaluation measurement system proposed by the International Rice Research Institute (IRRI, 1989) and classified into five categories: 0-5 cm = resistant; 5-10 cm = moderately resistant; 10-15 cm = moderately susceptible; 15-20 cm = susceptible; and >20 cm = highly susceptible.

Investigation of Agronomic Traits

Eight agronomic traits of the ten select cultivars were observed in the field experiments at 18 DAI, involving both vegetative (plant height, number of tillers) and reproductive aspects (number of panicles, panicle length, number of seeds per panicle, thousand-seed weight, biological yield, and grain yield) (Nan *et al.*, 2019).

Data Analysis

The combined BB lesion length data from the greenhouse experiments in both the rainy and dry seasons of 2017 were examined for the correlations between them and visualized for resistance ability to BB via scattered plot analysis (Stöckl, Dewitte, & Thienpont, 1998). Of the ten cultivars, those demonstrating the greatest BB resistance ability through their lesion lengths and agronomic traits were compared to known resistant and susceptible cultivars using the analysis of variance (ANOVA). The least significant difference (LSD) was used to determine the difference of treatment means (Saville, 2003), and the Harvest index (HI) examined (Yang & Zhang, 2010).

RESULTS AND DISCUSSION

Wild and indigenous rice cultivars within specific areas were investigated to explore the disease resistance abilities and agronomic traits in order to generate new and improved lines through rice breeding programs. To date, many rice cultivars have undergone improvements in disease

resistance, especially bacterial leaf blight resistance caused by various *Xoo* races (Vera Cruz et al., 2000), and productive yields (Das, Rao, Varier, Prakash, & Prasad, 2018; He et al., 2019; Kim & Reinke, 2019). In this study, we screened the bacterial blight resistance abilities of indigenous lowland rice varieties collected across Thailand and examined the relevant agronomic trait performances.

Evaluation of Bacterial Blight Resistance in the Greenhouse

Bacterial blight disease results from the interaction between susceptible rice cultivars and the virulent *Xoo* race under favorable growing environments. Only the rice cultivars that contain a resistance gene(s) specific to the avirulent *Xoo* race will exhibit disease resistance. However, genetic variability in both plant and pathogen populations led to a gradient of compatibility and specificity (Vera Cruz et al., 2000). Thus, disease incidence and severity vary within plant host populations, as well as in pathogen populations. This research found that each plant of the 333 indigenous lowland rice cultivars, as well as the five resistant and three susceptible plants in the greenhouse experiment, were infected (data not shown). Data frequency revealed that in the rainy season of 2017, 22 varieties were classified as resistant with lesion lengths less than 5 cm, and 319 varieties were classified as susceptible, with lesion lengths greater than 5 cm (Fig. 2a). Contrastingly, in the dry season, 25 varieties were categorized as resistant and 316

were deemed susceptible (Fig. 2b). The lesion lengths of the infected plants in the dry season as a function of the values from those in the rainy season demonstrated a linear relationship with a positive correlation ($r = 0.486^{**}$) (Fig. 3). This analysis generated a range of resistance ability. The findings presented that ten of the 333 tested cultivars (LLR137, LLR131, LLR205, LLR134, LLR207, LLR277, LLR140, LLR264, LLR023, and LLR191) appeared resistant, indicated by lesion lengths of less than 5.00 cm, and that both the known resistant and susceptible cultivars maintained their disease response properties (Fig. 3 and Table 1).

Here, four *Xoo* isolates were able to infect different indigenous rice varieties from various cultivated areas. However, within the greenhouse experiment, lesion lengths indicating disease severity on infected plants appeared heterogeneous among various rice varieties, ranging from highly resistant to highly susceptible (Fig. 1 and Fig. 2). This implies dissimilar specificity between resistance and avirulence genes in compatible rice cultivars (*Xoo* isolate) according to its gene-for-gene interaction (Flor, 1971). If four isolates of *Xoo* proved identical, the *Xoo* genotype was, therefore, virulent to all susceptible rice varieties. In contrast, different isolates present within the mixed inoculum would suggest variations in either avirulence genes among *Xoo* isolates or in the resistance genes among rice varieties; however, isolates were not determined within a mixed inoculum.

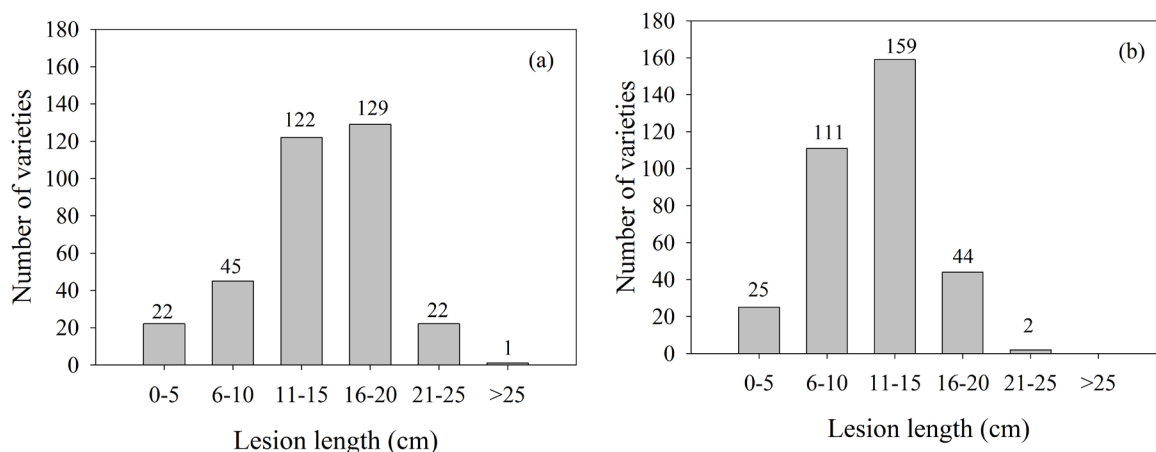
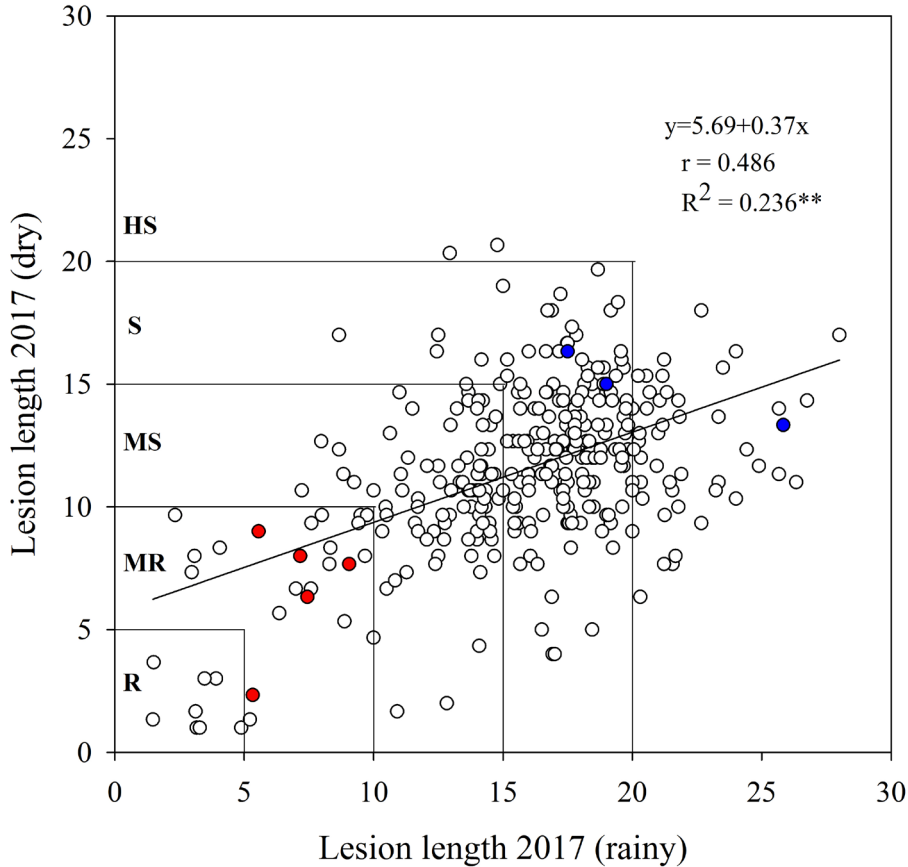


Fig. 2. The frequency of BB disease reaction (in lesion length) of 341 rice varieties in both test seasons; (a) rainy season 2017, and (b) dry season 2017; where resistant = 0-5 cm, moderately resistant = 6-10 cm, moderately susceptible = 11-15 cm, susceptible = 16-20 cm, and highly susceptible >20 cm



Remarks: R = resistance, MR = moderate resistance, MS = moderate susceptible, S = susceptible, HS = highly susceptible

Fig. 3. The combined analysis of each variety based on BB lesion length (rainy and dry season, 2017, KKU). The top ten resistance varieties (LLR023, LLR131, LLR134, LLR137, LLR140, LLR191, LLR205, LLR207, LLR277, and LLR264) presented lesion lengths of less than 10 cm. The resistant check varieties (Azucena, IR62266, IR64, IRBB21, and IRBB5) are shown with a red circle; and the susceptible varieties (KDML105, RD6, and SKN) are shown with a blue circle

Field Screening at the Udon Thani Rice Research Center

In addition to specificity between rice variety and Xoo, the environment might play an important role in disease severity (Swords, Dahlbeck, Kearney, Roy, & Staskawicz, 1996). The BB infections measured herein varied between variety based on the seasonal screening conditions (Fig. 2). Because this pathogen favors rainy conditions, large-scale field tests limit the success of breeding

programs, due to difficulties in field management (Sribunrueang, Chankaew, Thummabenjapone, & Sanitchon, 2017). However, large scale screening is capable under greenhouse conditions with multiple methods and seasons that can minimize the number of germplasms for further field validation (Sribunrueang, Chankaew, Thummabenjapone, & Sanitchon, 2017). Such interaction might be considered for an extensive evaluation of germplasms to identify resistant genotypes.

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Table 1. The lesion lengths of ten selected rice varieties with the check varieties after inoculation with four mixed *Xoo* isolates under greenhouse conditions in the rainy and dry seasons of 2017

Varieties	Lesion length (cm)	
	Rainy season	Dry season
Test varieties		
LLR023	1.28 de	3.18 f
LLR131	0.86 e	1.22 fg
LLR134	0.99 e	1.45 fg
LLR137	1.00 e	1.08 g
LLR140	1.67 de	1.32 fg
LLR191	0.97 e	4.95 e
LLR205	0.79 e	1.33 fg
LLR207	0.64 e	1.92 fg
LLR264	0.98 e	1.85 fg
LLR277	1.02 e	1.76 fg
Resistance checks		
Azucena	3.03 cd	6.44 de
IR62266	2.36 cde	8.94 c
IR64	4.06 c	7.62 cde
IRBB21	2.09 cde	7.82 cd
IRBB5	1.42 de	2.21 fg
Susceptible checks		
KDML105	20.00 a	16.26 a
RD6	20.94 a	14.95 b
SKN	17.61 b	13.49 b
Mean	5.53	5.62
F-test	**	**
CV%	23.15	31.11

Remarks: ** = significant different at $P < 0.01$. The different letter after mean within column showed significant different. CV= the coefficient of variation

The research filed screening experiments revealed infection success on all inoculated plants. The lesion lengths of the ten selected indigenous lowland rice varieties were not significantly different, nor did they differ from the known resistant cultivars. The recognized susceptible cultivars showed consistent BB susceptibility in the field conditions (Table 2). The results indicated that the ten selected indigenous lowland rice varieties were consistently resistant to BB in both seedling (greenhouse) and tillage (field) stages. Importantly, there was a consistency in BB resistance of the ten selected cultivars conferring their simultaneous resistance against the four mixed *Xoo* isolates under both

greenhouse and field conditions. This suggests that there are fewer environmental constraints on disease severity in artificial conditions, thereby placing a greater emphasis on the genetic control of plant-pathogen interaction for disease resistance development. The ten selected genotypes demonstrated greater resistance than the known resistance variety; especially in the IRBB21 and IRBB5 varieties which possess the *Xa21* and *xa5* genes (Korinsak *et al.*, 2009), indicating that the resistant varieties identified herein represent a potential reservoir of initial material, and can serve directly as donor parents in future rice breeding programs.

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Table 2. The mean and standard error (SE) of lesion lengths of ten selected rice varieties with the check varieties after inoculation with four mixed *Xoo* isolates under field conditions at the Udon Thani Rice Research Center in 2018

Varieties	Lesion length (cm)
	Mean \pm SE
Test varieties	
LLR137	0.12 \pm 0.20
LLR131	0.15 \pm 0.24
LLR134	0.14 \pm 0.22
LLR277	1.00 \pm 0.00
LLR205	0.15 \pm 0.33
LLR023	0.25 \pm 0.42
LLR264	0.05 \pm 0.15
LLR191	1.05 \pm 0.49
LLR140	0.41 \pm 0.44
LLR207	0.19 \pm 0.34
Resistance checks	
IRBB21	1.65 \pm 0.94
SPT	0.65 \pm 0.66
TN1	1.50 \pm 1.35
Susceptible checks	
KDML105	20.4 \pm 4.27
SKN	14.2 \pm 2.85
CV (%)	42.3

Remarks: CV= the coefficient of variation

Investigation of Agronomic Traits

In rice breeding programs, disease resistance ability plays a crucial role in rice cultivar improvement; however, enhancing the productive yields within their agronomic traits is still needed. Therefore, identifying novel rice varieties capable of achieving disease resistance with the desirable agronomic traits is needed to minimize the genetic linkage of exotic germplasms introduced. In this pursuit, we comprehensively investigated the agronomic traits of ten selected cultivars which presented significant BB resistance ability in comparison with the currently popular varieties (Table 2).

The resulting agronomic traits of rice plants in the field experiments are summarized in Table 3 and Table 4. Compared with the well-known KDML105 cultivar, the LLR023, LLR131, LLR134, LLR 91, LLR205, and LLR207 varieties did not significantly differ in plant height (Table 3). Similarly, the high tiller and panicle number of the LLR023, LLR205, and LLR207 varieties were not different from that of

KDML105, and only the LLR277 differed in panicle length (25.8 cm) (Table 3). Additionally, the number of seeds per panicle in the LLR023, LLR131, LLR137, and LLR207 were also not significantly different from that of the KDML105 (149 seeds). Note that the field experiments were conducted on only ten plants in a single row for each variety due to the limited seed number. The traits of the LLR023 and LLR207 varieties appeared to closely resemble those of the KDML105 traits.

A summary of the reproductive yield measurements is presented in Table 4, in which a variation was observed in each tested variety. In comparison to the KDML105 cultivar and the susceptible checks, the reproductive yields of several selected varieties were greater than that of the KDML105, yet remained relatively similar to those of the resistant checks. Remarkably, the harvest indices of all tested varieties were higher than that of the KDML105 (Table 4).

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Table 3. Mean and standard error (SE) of plant height, tiller number, panicle number, panicle length, and the number of seed/panicle of 15 rice varieties tested under field conditions at the Udon Thani Rice Research Center

Genotype	Plant height (cm)	Tiller no.	Panicle no.	Panicle length (cm)	Seed/panicle
	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
Test varieties					
LLR023	134.4±10.3	9.4±0.89	9.4±0.89	26.0±0.70	149.00±10.03
LLR131	140.0±4.84	6.0±0.70	5.2±0.44	25.6±2.30	150.00±8.16
LLR134	140.8±3.56	7.8±0.83	7.4±1.14	25.6±0.54	97.50±2.08
LLR137	119.4±3.78	7.0±1.58	6.8±1.48	26.4±0.89	151.25±8.53
LLR140	152.2±7.91	6.4±0.54	6.0±0.70	25.8±0.83	125.00±4.08
LLR191	138.4±8.38	8.2±1.78	6.8±1.78	23.6±1.51	123.00±5.71
LLR205	136.4±5.02	9.0±2.44	8.0±1.87	24.6±1.14	114.75±13.30
LLR207	133.4±5.17	11.6±1.67	10.4±1.5	25.2±0.44	143.20±16.60
LLR264	153.6±3.43	8.0±0.70	7.0±0.70	27.0±0.70	137.50±18.92
LLR277	84.4±6.80	6.2±0.83	4.4±0.54	20.2±1.09	103.25±5.37
Resistance checks					
IRBB21	134.2±1.64	11.2±1.64	10.0±1.87	25.8±0.83	125.50±12.15
SPT	117.6±1.14	10.2±0.83	13.0±2.34	24.8±0.44	141.00±13.44
TN1	108.0±5.43	16.2±2.28	15.0±4.08	25.2±0.83	145.25±24.01
Susceptible checks					
KDML105	138.6±1.81	11.2±1.09	9.6±1.14	25.8±0.83	149.00±2.00
SKN	129.2±3.42	9.4±1.14	9.4±1.14	24.6±0.54	145.25±5.67

Table 4. Grain width, grain length, grain length/grain width ratio, thousand-seed weight, biological yield, grain yield, and the harvest index of the 15 rice genotypes, Udon Thani Rice Research Center

Genotypes	1000 seed weight (g)	Biological yield (g/ four plants)	Grain yield (g/ four plants)	Harvest index
Test varieties				
LLR023	28.70	240.81	75.79	0.31
LLR131	30.02	210.63	74.10	0.35
LLR134	25.20	267.93	80.70	0.30
LLR137	27.00	154.41	60.18	0.39
LLR140	27.80	195.58	45.21	0.23
LLR191	27.90	212.61	74.35	0.35
LLR205	28.50	238.65	81.12	0.34
LLR207	25.60	232.94	74.92	0.32
LLR264	29.10	254.72	66.27	0.26
LLR277	28.20	61.81	13.38	0.22
Resistance checks				
IRBB21	31.70	166.12	66.42	0.40
SPT	33.30	278.91	84.71	0.30
TN1	24.50	202.43	79.39	0.39
Susceptible checks				
KDML105	22.80	199.10	34.90	0.18
SKN	24.00	238.18	52.97	0.22

Correlation between Lesion Lengths and Agronomic Traits of All Tested Varieties

The correlation analyses between lesion lengths and agronomic traits of all tested varieties are summarized in Table 5. When determining the agronomic traits as a function of the lesion length, there was a significantly negative correlation for both 1,000-seed weight and the harvest index, at $r = -0.590^*$ and -0.597^* , respectively (Table 5). Moreover, significant correlations between yield components were determined; including panicle length and plant height ($r = 0.719^{**}$), panicle length and seed per panicle ($r = 0.514^*$), tiller number and panicle number ($r = 0.923^{**}$), seed per panicle and biological yield ($r = 0.649^{**}$), and grain yield and harvest index ($r = 0.669^*$) (Table 5).

Higher values of the desirable agronomic traits, including plant height, tiller number, panicle length, and the number of grains per panicle; resulted in higher product yields in rice plants (Ibrahim, Ramalingam, & Subramanian, 1990;

Lee, 1980), as evidenced in our experiment results (Table 3 and Table 4). The main objective of our evaluation was to identify desirable resistance genotypes to BB disease resulting in a combination of higher yields with the desired quality parameters. We observed large variations in the agronomic traits and reproductive yields among the tested varieties, as well as in the resistant and susceptible checks. We may deduce that genetics of the various rice varieties play an important role in this expression, in variations of both the environment and severity of BB infection. Our study revealed, successfully, an increase in resistance abilities of the tested varieties, which presented smaller lesion lengths with greater seed weights and harvest indices (Table 5). The LLR023, LLR131 LLR137, LLR205, and LLR207 cultivars expressed significant performances in terms of productive yield, suggesting their further application in lowland rice breeding programs as prospective donor parents.

Table 5. Correlation coefficients of lesion lengths and agronomic traits of the 15 rice varieties evaluated in field conditions at Udon Thani Rice Research Center in the rainy season of 2018

Traits	LL	PH	TN.	PN	PL	SPP	1000SW	BY	GY	HI
LL	1.000									
PH	0.053	1.000								
TN	0.235	-0.181	1.000							
PN	0.168	-0.174	0.923**	1.000						
PL	0.030	0.719**	0.168	0.240	1.000					
SPP	0.308	0.118	0.328	0.397	0.514*	1.000				
1000SW	-0.590*	-0.001	-0.282	-0.089	-0.018	-0.090	1.000			
BY	0.100	0.359	0.296	0.426	0.380	0.649**	0.234	1.000		
GY	-0.449	0.350	0.323	0.456	0.486	0.161	0.279	0.424	1.000	
HI	-0.597*	-0.064	0.268	0.258	0.234	0.107	0.346	0.032	0.669**	1.000

Remarks: LL= lesion length, PH = plant height, TN = tiller number, PN = panicle number, PL = panicle length, SPP = seed per panicle, 1000SW = thousand seed weight, BY = biological yield, GY = grain yield, HI = harvest index. * = significant different at $P < 0.05$. ** = significant different at $P < 0.01$

CONCLUSION

In these two experiments, conducted under both greenhouse and field conditions, 345 rice varieties were evaluated for BB resistance against four mixed *Xoo* isolates, in which ten lowland rice accessions (LLR023, LLR131, LLR134, LLR137, LLR140, LLR191, LLR205, LLR207, LLR264, and LLR277) were identified as resistant. Additionally, five of the ten selected varieties (LLR023, LLR131, LLR137, LLR205, and LLR207) also exhibited high performances in specific agronomic traits. These ten varieties may, therefore, be considered as emerging sources of BB resistant varieties in future rice breeding programs in Thailand. This study also recognize, however, the need for further study to identify and examine the resistance genes in each of these accessions.

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