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THESIS

MARKER-ASSISTED PYRAMIDING BACTERIAL BLIGHT RESISTANCE GENES (*xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* AND *qBB11*) IN RICE

SIRIPORN KORINSAK

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Bacterial Blight (BB) caused by *Xanthomonas oryzae pv. oryzae* (*Xoo*) is one of the most serious diseases in rice production world wide. Utilization of resistant varieties is considered to be the most effective method to control this disease. Three resistance genes, *xa5, xa33(t)* and *Xa34(t)* were identified in rice cultivars IR62266, Ba7 and Pin Kaset, respectively in this study. These cultivars and a KDML105 introgression line carrying the *Xa21* and *qBB11* were used as the BB resistance donors to construct the pyramiding population. Marker-Assisted Selection (MAS) was carried out to pyramid five BB resistance genes including *xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11* into indica rice genetic background. Pyramiding lines carrying the combination of two, three and four resistance genes were tested for BB resistance against six BB isolates, TB0304, TXO16, TXO34, TXO37, TXO107 and TXO133. The pyramided lines having more than single gene showed broader resistance spectrum and higher level of resistance than parental lines with single gene. *xa5* was the most effective, followed by *Xa34(t), xa33(t)* and *Xa21*. The two new identified resistance genes *xa33(t)* and *Xa34(t)* and closely their liked markers will be useful information to improve broad-spectrum BB resistance in Thai rice breeding programs through MAS. Furthermore, the pyramided lines obtained in this study can be used as genetic resources of BB resistance in breeding programs.

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LIST OF ABBREVIATIONS

AFLP = Amplified Fragment Length Polymorphism
BB = Bacterial blight
bp = Base pair
BSA = Bulk Segregation Analysis
CAPS = Cleaved Amplified Polymorphic Sequence
cm = Centimeter
cM = Centimorgan
°C = Degree celcius
DNA = Deoxyribonucleic Acid
dNTP = Deoxynucleotide Triphosphate
EPS = Bacterial extracellular polysaccharides
FM = Fibular material
FMs = Functional Marker
g = gram
h = Hour
KDML105 = Khao Dawk Mali 105
kb = Kilobase
LL = Lesion Length
LRR = Leucine Rich Repeat
MAS = Marker-Assisted Selection
Mb = Megabase
MBAS = Modified Bulk Segregation Analysis
min = Minute
ml = Milliliter
mM = Millimolar
MR = Moderate resistance
MS = Moderate susceptible
ng = nano gram
PCR = Polymerase Chain Reaction

LIST OF ABBREVIVATION (Continued)

PK = Pin Kaset

R = Resistance

RAPD = Random Amplified Polymorphic DNA

RFLP = Restriction Fragment Length Polymorphism

RGP = Rice Genome Project

S = Highly susceptible

s = Second

SNP = Single Nucleotide Polymorphism

SSR = Simple Sequence Repeat

STS = Sequence-Tagged Site

µl = Microliter

µM = Micromolar

Xoo = *Xanthomonas oryzae* pathovar *oryzae*

MARKER-ASSISTED SELECTION BACTERIAL BLIGHT RESISTANCE GENES (*xa5, Xa21, xa33(t), Xa34(t)* AND *qBB11*) IN RICE

INTRODUCTION

Bacterial leaf blight (BB) caused by the rod-shaped bacterium, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most devastating diseases in rice (*Oryza sativa* L.). Outbreaks of BB usually occur in irrigated and rainfed lowland ecologies throughout Asia and worldwide. The disease was first characterized in Fukuoka, Japan in 1884 (Ou, 1985). The damage of rice crop from BB was first reported in Thailand at Pathum Thani province in 1963 (Tabei and Eamchit, 1974). Leaf blight symptom can occur at all stages of rice plants. The severity of infection is increasing when high amount of fertilizer is applied. Wilting and death are always found in seedling stage. Meanwhile, higher numbers of sterile and immature grains are found in reproduction stage. BB disease can cause yield loss typically ranging from 20-30% but in severe cases, it can cause as high as 80% yield reduction. However, it depends on rice growth stages, geographic locations or seasonal conditions (Singh *et al*., 1977; Ou, 1985).

Control measures for BB include cultural practices, chemical control, biological control, disease forecasting, and most importantly, host genetic resistance. Since the chemical control is not effective, the utilization of resistant varieties carrying resistance genes have been considered to be the most effective way to control the disease (Niño-Lui *et al*., 2006). Most breeders are interested in utilizing BB resistant varieties, and this goal is certainly achievable providing the availability of an easy strategy to identify resistance genes.

At present, biotechnology progress continuously. Identification, cloning, and functional analyses of a gene can be performed relatively rapidly. Up to date, more than 40 disease resistance genes have been identified in dicot and monocot plants (Martin *et al*., 2003). In the case of BB resistance, 35 BB resistance genes have been identified in cultivated rice and the wild relatives (Niño-Lui *et al.*, 2006; Wang *et al.*, 2009; Singh *et al.*, 2007). Eleven of them were recessive resistance genes including *xa5*, *-xa5(t)*, *xa8*, *xa13*, *xa15*, *xa19*, *xa20*, *xa24*, *xa28*, *xa31* and *xa32* (Niño *et al.*, 2006; Singh *et al.*, 2007; Rao, 2003), while six of them have been cloned including *Xa1*, *xa5*, *xa13*, *Xa21*, *Xa26* and *Xa27* (Chu *et al.*, 2006; Gu *et al.*, 2005; Iyer and McCouch, 2004; Song *et al.*, 1995; Sun *et al.*, 2004; Yoshimura *et al.*, 1998).

The majority of BB resistance genes were identified in rice *O. sativa* ssp. indica and wild rice *O. longgistaminata*, *O. rufiprogon*, *O. minuta* and *O. officinalis*, while some of them were identified in *O. sativa* ssp. japonica (Brar and Khush, 1971; Lee *et al.*, 2003). Most of these genes follow the classic gene-for-gene concept for the race-specific interaction between rice and *Xoo* (Flor, 1971). Avirulent gene in bacteria exhibits the specificity for resistance gene in the rice plant. Some resistance genes are effective only in adult plants, while others are effective at all stages of growth. Some genes confer resistance to a broad spectrum of *Xoo* races, whereas others do so against only one or a few races. This observation could be influenced by particular geographical locations (Niño-Lui *et al.*, 2006). The developmental control of disease resistance has been observed in other plant-pathogen systems. Several rice resistance genes are expressed at the highest level only in the adult stage (Century *et al.*, 1999; Panter *et al.*, 2002). *Xa21*-mediated resistance gene was shown to be expressed since the seedling stage but the plants were found susceptible, and *Xa7* gene showed broad resistance only in adult plants (Sidhu and Khush, 1978). On the contrary, *xa5* gene could confer resistance at all growth stages and exhibit a broad spectrum of resistance to *Xoo* isolates in Asia with an exception of South Asia (India and Nepal) (Adhikari *et al.*, 1995).

The first step towards rice improvement via marker-based selection and map-based cloning of the resistance genes is the identification of molecular markers that are tightly linked to the genes of interest. Recent advances in molecular marker technology, has made it easier to identify and introgress resistance genes to desired genetic backgrounds. Several major resistance genes against BB pathogen have been tagged by Restriction Fragment Length Polymorphism (RFLP) and Randomly Amplified Polymorphic DNA Sequence (RAPD) markers (McCouch *et al.*, 1992;

Yoshimura *et al.*, 1992; Zhang *et al.*, 1996). In addition, Simple Sequence Repeat (SSR) markers have been extensively used to identify disease resistance genes in rice (Wu and Tanksley, 1993; Panaud *et al.*, 1996). The SSR markers provide several advantages over the other two types of markers when applied in a plant breeding program. Markedly, they are based on the polymerase chain reaction (PCR) technique, represent single loci, and can detect high levels of polymorphism

Another effective PCR-based marker is Cleaved Amplified Polymorphic sequence (CAPS) and Bi-Directional PCR Amplification of Specific Alleles (Bi-PASA) (Konieczny and Ausubel, 1993; Liu *et al.*, 1997). They are co-dominant genetic markers, but CAPS requires restriction endonuclease digestion to detect polymorphisms (SNP) in the region of interest whereas Bi-PASA can be amplified and directly runned on agarose gel without cutting enzyme. Generally, marker-assisted selection (MAS) requires identified markers tightly linked to the traits of interest and the markers should be cost effective and easy to use, and the functional marker, bi-PASA, was considered to be a suitable and powerful tool for breeding durable resistance in rice breeding program.

Resistant rice cultivars mainly based on a single resistance gene were developed, however, large-scale and long-term cultivation of those varieties and the rapid adaptation of the pathogen race cause the breakdown of disease resistance trait in those cultivars. One of the important strategies to prolong the useful life of major gene resistance is to pyramid many major resistance genes in a single gene resistance cultivar (Khush, 1976). The gene pyramiding technique provided a broad-spectrum of resistant cultivar which is economical and effective method for BB management (Adhikari *et al.*, 1999). However, pyramiding major genes using conventional breeding method based on phenotype alone is perhaps inappropriate because of the difficulty caused by the interference of expression among major genes and it is time consuming. Therefore, molecular breeding dealing with genotypes provides more advantages to detect the transfer of target resistant gene during the breeding program precisely and easily.

Numerous researchers have been interested in *Xa21* and *xa5* genes and many studies on these genes pertaining to disease mechanisms and strategies to control the disease were reported. These genes are effective and broad-spectrum resistance to many resistant disease races. *Xa21* gene, the first successfully cloned gene, was introgressed from a wild species *O. longistaminata* into *O. sativa* background (Khush *et al.*, 1989), conferring resistance to a broad range of highly virulent *Xoo* strains. The *xa5* mediate resistance gene, a recessive resistance gene located on short arm of chromosome 5, (Blair M.W. and McCouch., 1997), was successfully cloned recently (Iyer and McCouch, 2004). Most of those BB resistance genes were analyzed and identified using RFLP, SSR and Sequence Tag Site (STS) techniques and additional markers linked to BB resistance genes were produced.

Rice is often attacked by BB disease which no effective bactericide is commercially available to control this disease. The BB resistant rice variety is an important controlling method against this disease. A very important aspect in resistance breeding programs is the durability of the introduced resistance genes. Therefore, in this study, five BB resistance genes *(xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11*) were pyramided for board-spectrum and durable resistance by using the BB resistance genes which were identified and tagged in rice cultivars ‘IR62266’, ‘Ba7’ and ‘PK’. In this experiment, two new BB resistance genes designated as *xa33(t)* and *Xa34(t)* in rice cultivar ‘Ba7’ and ‘PK’, respectively were found and ‘IR62266’ was found to carrying *xa5* gene. Thus, the closely linked markers which were found in this study are useful in improving BB resistance through MAS in rice breeding programs. The introgression at least four BB resistance genes into one genetic background was successful. Therefore, the rice lines with gene combinations are the best germplasm to improve BB resistance for breeding program in Thailand.

OBJECTIVES

1. To identify and tag the BB resistance genes in rice cultivars IR62266 and Ba7.

2. To develop BB pyramiding rice lines carrying *xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11* using MAS.

3. To validate the BB pyramiding lines for multi-race resistance.

LITERATURE REVIEW

1. Bacterial blight disease in general

Bacterial blight (BB) is one of the most destructive bacterial diseases of rice in irrigated and rainfed lowland ecosystems. BB is widespread throughout Asia. The disease has been reported to occur in Australia, the United States, and several rice-growing countries of Latin America and Africa as well (Mew *et al.*, 1987). Farmers in the Fukuoka area of Japan have first seen BB disease during 1884–1910. The study of the disease started since then. In Thailand, BB was first reported in Pathum Thani province in 1963 (Tabei and Eamchit, 1974). BB can cause damage at vegetative and reproductive stages of rice plants. It can decrease photosynthetic area and reduce photosynthesis system of plant leaves. Rice yield losses in severely infected fields generally range from 20 to 30% and in some areas are reportedly up to 80% (Singh *et al.*, 1977; Ou, 1985). High fertilizer input condition can induce the disease development. Irrigation water is considered to contribute the spread of BB disease, as it carries the bacterial ooze that drop in the rice field water. The pathogen can survives around 15 days in the field water (Ou, 1985).

2. Causal organism and symptoms of BB disease

BB is caused by the short rod-shaped bacterium with round ends 1-2×0.8-1 um, monotrichous flagellum 6-8 µm, gram-negative, non-spore-forming and aerobic bacteria (Ishiyama, 1992). According to the study of its morphology and physiology, the bacterium was first named *Bacillus oryzae* Hori & Bokura (Ou, 1985). Ishiyama (1922) renamed the bacterium to *Pseudomonas oryzae* Uyada & Ishiyama. Later, it was transferred to *Bacterium oryzae* (Uyada & Ishiyama) Dowson. Subsequently has adopted the name to *X. campestris* pv. *oryzae* (Ishiyama) Dye. Lastly, it was named *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) (Swings *et al.*, 1990).

Colonies of *Xoo* are circular, convex, whitish yellow to straw yellow, with smooth surface, entire margin, and opaque against transmitted light (Figure 1). *Xoo* can survive on rice stubbles, straw and weed hosts. The over wintering of bacterium occurs in two forms: i) the dry form, *Xoo* is found in the vascular vessel and xylem parenchyma of dried plants. If they are moistened by rain in winter, these dry form bacteria gradually die. ii) the growth form, bacterial cells are found in stubble and in the root system of perennial wild plants, especially *Leesia* spp. The pathogens survive in an inactive stage. The dry form can be activated and turn into the growth form after receiving moisture under favorable conditions (Figure 2).

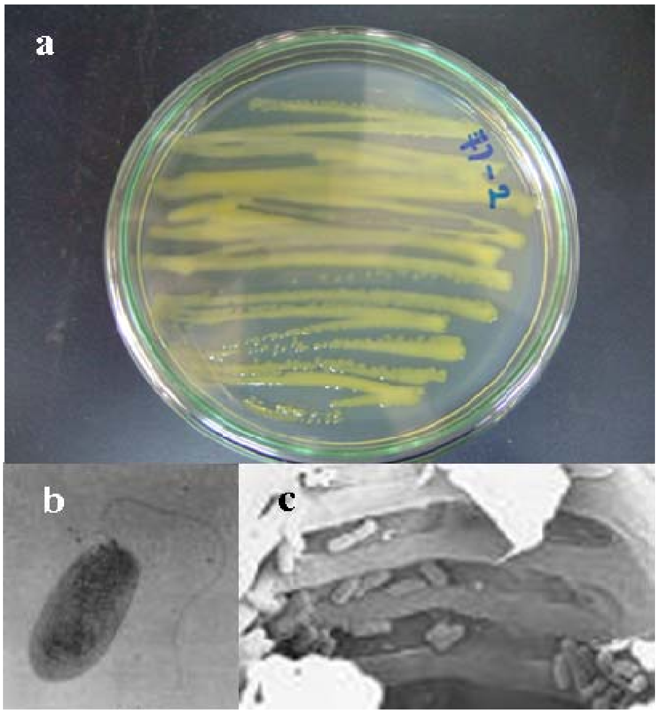
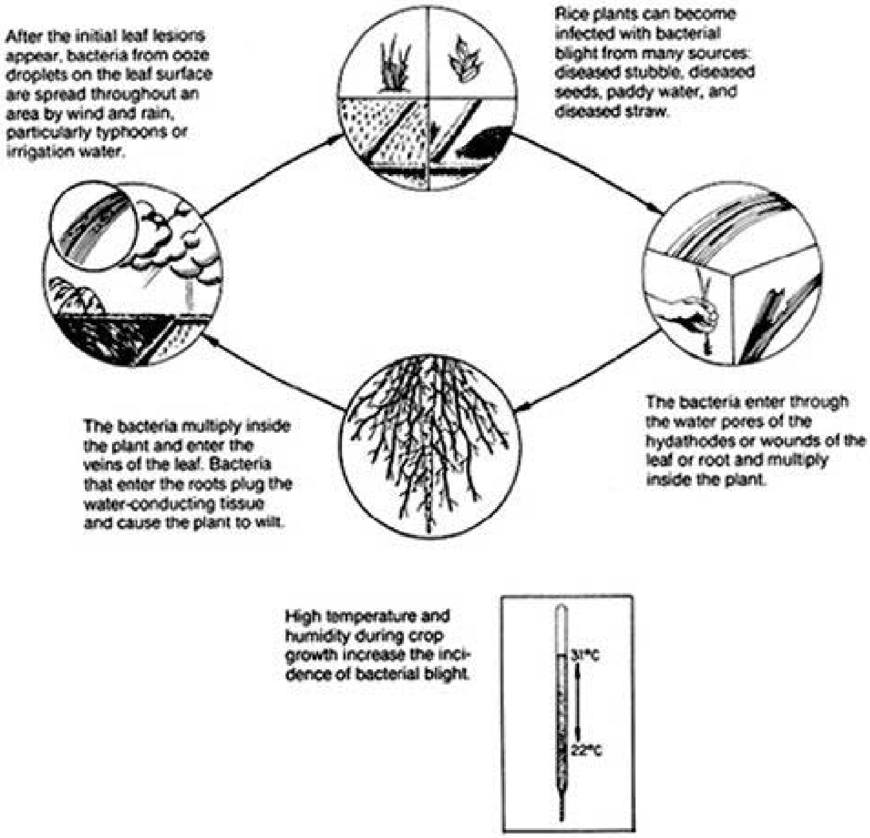


Figure 1 Characteristics of *Xanthomonas oryza* pv. *oryzae* (a) colonies (b) rod shape of pathogen (c) *Xoo* in rice xylem vessel with scanning electron micrograph

Source: www.ceniap.gov.ve and www.apsnet.org



After the initial leaf lesions appear, bacteria from ooze droplets on the leaf surface are spread throughout an area by wind and rain, particularly typhoons or irrigation water.

Rice plants can become infected with bacterial blight from many sources: diseased stubble, diseased seeds, paddy water, and diseased straw.

The bacteria multiply inside the plant and enter the veins of the leaf. Bacteria that enter the roots plug the water-conducting tissue and cause the plant to wilt.

The bacteria enter through the water pores of the hydathodes or wounds of the leaf or root and multiply inside the plant.

High temperature and humidity during crop growth increase the incidence of bacterial blight.

Figure 2 The life cycle of *Xanthomonas oryza* pv. *oryzae*
Source: www.knowledgebank.irri.org

The BB is a vascular disease spreads through the xylem vessels. Lesions usually begin at the margin, a few centimeter (cm) from the tip, as water-soaked stripes. It can occur at all stages of the rice plants. At the seedling stage, the symptom first appeared as tiny water-soaked spots at the margin of the rice leaf blade. Then, it will enlarge and the rice plants turn yellow and wither. The symptom of the disease at the seedling stage is known as kresek (Ou, 1985) (Figure 3). The lesions may start at anywhere on the leaf blade at the site of an injury. The lesions can occur on leaf sheath of susceptible cultivars. The affected leaves will turn yellow, roll up and wilt rapidly. At the tillering and reproductive stages, the symptom is known as leaf blight, a systemic infection that produces tannish-grey to white lesions along the vein. If plant produces panicles, the sterility percentage and number of immature grains will increase. Grains from diseased plants were easily broken during milling. In severely diseased field, grain can be infected appearing on the glumes as discolored spot surrounded by water-soaked margin (Ou, 1985). On resistant cultivars, a yellow stripe appears inside of the margin of the leaf blade with no necrotic lesion for some time but stripes may eventually turn yellow and necrotic. Milky or opaque dewdrops of bacterial exudates on the surface of young lesions can be observed in the early morning. They dry up to form small, yellowish, spherical beads. They are shaken off by wind and drop into the field water. Droplets can be detected by drawing the leaves through the fingers and feeling the stickiness.

Figure 3 The BB disease symptom (a) leaf blight symptom occur on adult plant (b) kresek symptom occur on the seedling plant, (c) and (d) characteristics of BB symptom

3. The infection of *Xoo* in rice plants

Primarily, *Xoo* enters its hosts through hydathodes and wounds. Hydathodes have a structure similar to stomata except that the guard cells. Hydathodes usually occur on the serration of leaves or at the leaf tips of plants belonging to the Gramineae. The bacteria multiplied outside the hydathodes of susceptible rice cultivars and gained entrance through them within 24 hours (h) after spray-inoculation. In contrary, they were trapped and embedded in a thin layer of exudate secrete from the water pores of resistant cultivars (Huang and Cleene, 1989). The water pore has been related to resistance to hadathodal invasion by *Xoo*. On the other hand, the hydathode apertures in susceptible rice plants are much larger due to the reduced growth of the outer ledges, allowing *Xoo* to pass through freely. In many cases, infection through wound seems more successful than natural opening. Outbreaks of BB on rice have been correlated with wounds caused by rainstorm (Ou, 1985).

In the resistance varieties, bacterial cells were irregular in shape and enveloped by abundant fibrillar material (FM) and apparently dead. Bacterial extracellular polysaccharides (EPS) have been implicated as determinants of virulence in a number of plant pathogenic bacteria. Three days after inoculation, bacteria of virulent EPS^+ strains were surrounded by electron transparent zones in a matrix of FM in xylem vessels by the clipping method. While, bacteria of avirulent EPS^- strains were not protected by electron-transparent zones. They were embedded in FM and lost their structural integrity. *Xoo* was able to multiply for awhile on seedling leaf surfaces of maize, a nonhost, suggesting that nonhosts may serve as alternate inoculum sources of the pathogen for nearby host plants (Figure 4). FM was constantly observed in rice xylem vessels following inoculation with *Xoo*. This FM is believed to originate from host cell walls. However, its chemical nature has not been determined (Huang and Cleene, 1989).

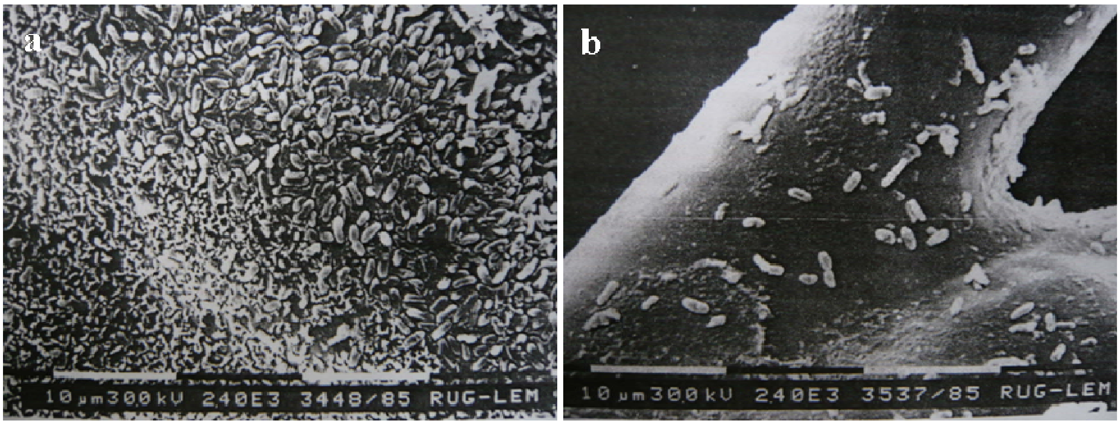


Figure 4 *Xoo* on nonhost plant using scanning electron micrograph. Bar = 10 µm (a) *Xoo* on unwound leaf of maize (b) *Xoo* on a trichome of leaf of maize

Source: Huang and Cleene (1989)

4. Identification and molecular mapping of bacterial blight resistance genes

The identification and characterization of major genes for resistance and related factors have a great deal to the success in plant breeding programs. To date, more than 30 BB resistance genes have been identified from rice plants as shown in Table 1 are currently reported and identified from cultivated rice and wild rice (Rao *et al.*, 2002). All of them have been considered to follow the gene-for-gene theory. Eleven are recessive genes including *xa5*, *-xa5(t)*, *xa8*, *xa13*, *xa15*, *xa19*, *xa20*, *xa24*, *xa28*, *xa31* and *xa32* (Niño-Lui *et al.*, 2006; Rao, 2003; Singh *et al.*, 2007). Three resistance genes, *xa15*, *xa19*, and *xa20*, were induced by mutagenesis (Lee *et al.*, 2003). Six resistance genes, *Xa21*, *Xa1*, *xa5*, *xa13*, *Xa26* and *Xa27*, had already been cloned (Chu *et al.*, 2006; Gu *et al.*, 2005; Iyer and McCouch, 2004; Song *et al.*, 1995; Sun *et al.*, 2004; Yoshimura *et al.*, 1998).

Table 1 Genes conferring resistance to different races of bacterial blight pathogen

Gene	Chr.	Cultivar/Variety	Isolate/race	Reference
Xa1	4	Kogyku	Japanese race I and II	Sakaguchi, 1976
Xa2	4	Tetep	Japanese race I and II	Sakaguchi, 1976
Xa3	11	Wase Aikoku, Chukogu-45	Japanese race II and III	Ezuka *et al.*, 1975
Xa-4	11	IR20, IR22, IR1529-680-3, TKM6	Philippine race I	Petpisit *et al.*, 1977 Sidhu *et al.*, 1978
xa5	5	IR1545-248, BJ-1, IR291-7, DV85	Japanese races	Blair and McCouch, 1997 Petpisit *et al.*, 1977 Sidhu *et al.*, 1978 Singh *et al.*, 1983
xa5(t)	5	Ajaya	Indian races	Rao, 2003
Xa6	not determined	Malaget sunsong, IR994-102, IR1698-241, Zenith	Philippine race I	Sidhu *et al.,* 1978
Xa7	6	DV85, DV87	Philippine race I	Sidhu *et al.*, 1978; 1979
xa8	7	PI231129	Philippine isolates	Sidhu *et al.*, 1978; 1979
xa9	11	Sateng	Philippine isolates	Singh *et al.*, 1983
Xa10	11	Cas209	Philippine and Japanese isolates	Yoshimura *et al.*, 1983
Xa11	not determined	IR8, RP9-3	Japanese isolates	Ogawa and Yamamoto, 1986
Xa12	4	Kogyoku and Java 14	Japanese and Indonesian isolates	Ogawa *et al.*, 1978a; b
xa13	8	BJ1	Philippine isolates	Zhang *et al.*, 1996b
Xa14	4	TN1	Japanese isolates	Taura *et al.*, 1989
xa15	not determined	M41	Japanese isolates	Noda, 1989
Xa16	not determined	Tetep and IR24	Japanese isolates	Noda, 1989

Table 1 (continued)

Gene	Chr.	Cultivar	Isolate/race	Reference
Xa17	not determined	Asominori	Japanese isolates	Ogawa, 1989
Xa18	not determined	Toyonishiki	Burmese isolates	Ogawa and Yamamoto, 1986
xa19	not determined	XM5	Japanese isolates	Taura *et al*., 1991
xa20	not determined	XM6	Japanese isolates	Taura *et al*., 1992
Xa21	11	*O. longistaminata*	Philippine and Japanese isolates	Khush *et al*., 1990
Xa22	11	Zhachanglong	Chinese isolates	Lin *et al*., 1996
Xa23	11	*O. nivara*	Indian isolates	Kumar, 1999
Xa23		*O. rufipogon*	PXO99	Wang et al., 2006
xa24	2	DV85, DV86, Aus295	Philippine race 6	Mir and Khush, 1990 Krush and Angeles, 1999 Lee *et al.,* 2001
Xa25	12	Minghui63	Philippine race 9	Gao *et al*., 2002 Chen *et al*., 2002
Xa26	11	Nep Bha Bong To, Minghui63	Philippine race 1, 2, 3, and 5	Lee *et al*., 2003 Sun *et al*., 2004
Xa-27	6	*O. minuta*, Arai Raj	Philippine race 2	Amante-Bordeos *et al*., 1992 Lee *et al.,* 2003
Xa28	not determined	Lota Sail	Philippine race 2	Lee *et al*., 2003
Xa29	1	*O. officinalis*	-	Tan *et al*., 2004
Xa30	11	CB30	Phillipine race 6	Jin *et al*., 2007
Xa30	4	*O. nivara*		Singh *et al*., 2007
Xa31	4	Zhachanglong	PXO61 and OS105	Wang *et al*., 2009
xa31	5	*O. glaberrimar*		Singh *et al*., 2007
xa32	6	*O. barthii*		Singh *et al*., 2007

xa5, a recessive resistance gene was first reported by Murty and Khush (1972). It was naturally found only within the *Aus* subpopulation of rice (Garris *et al.*, 2003). This recessive R gene was mapped to the telomeric region on short arm of chromosome 5 (Blair and McCouch, 1997). RFLP markers RG556, RG207, RZ390 and SSR markers RM122 and RM390 were closely linked to *xa5* gene (Yoshimura et al., 1995; Blair and McCouch, 1997). Subsequently, *xa5* gene was positionally cloned and found to encode the gamma subunit of transcription factor IIA (TFIIAγ). Resistant and susceptible isolines reveal two nucleotide substitutions resulting in an amino acid change between resistant and susceptible lines (Iyer and McCouch, 2004). Rice cultivars containing *xa5* gene can provide resistance in parts of Southeast and Northeast Asia but not in South Asia (Adhikari *et al.* 1995). This result indicating that the *xa5* gene might be useful for many countries in Asia. The *xa5* is particularly strong and has broad resistance to all BB isolates in Korea (Jeung *et al.*, 2006). Moreover, Iyer-Pascuzzi and McCouch (2007) presented a set of CAPS markers for easy, quick and direct identification of cultivars or progeny carrying *xa5*-mediated resistance and provide evidence that these markers are 100% predictive of the presence of the *xa5* allele.

-*xa5(t)* was identified form rice cultivar Ajaya (IET8585). This variety is highly resistant to all pathotypes in India. The F_2 population was screened with RAPD and SSR markers. Two SSR markers RM39 and RM31 on long arm of chromosome 5 were tightly linked to the resistance gene (Rao, 2003). In the same way, *xa31*(t) was identified in wild rice *O. glaberrima* using SSR analysis. This recessive gene was also located on chromosome 5. The flanking markers were RM548 and RM593 with the distance of 1.7 and 1.1 cM, respectively (Singh *et al.*, 2007).

Xa7 is a dominant resistance gene directed against *Xoo* located on chromosome 6 and originally identified in rice cultivar DV85. The resistance gene conveys resistance at flowering stage (Sidhu *et al.*, 1978). It was the most resistant to BB in Indonesia (Kadir *et al.*, 2004) and expressed low level of susceptibility to Korean BB races (Jena *et al.*, 2007). This resistance gene was resistance to Philippine races 2 and 3 (Ezuka and Sakaguchi, 1978). Kaji and Ogawa (1995) determine a recombinant value of 8.8% between *Xa7* and RG1091, with was located at 107.5 cM on RGP rice map. Later, Yoshimura *et al.* (1996) reported the positions of *Xa7* at 107.3, 103.0 and 90.5 cM using RFLP markers. Subsequently, Porter *et al.* (2003) studied about development and mapping of markers linked to the rice BB resistance gene *Xa7* and found that *Xa7* was also mapped to position 107.3 cM on RGP map with various molecular markers including AFLP, SSR and STS. Recently, the high-resolution mapping and the genetic prediction of resistance gene *Xa7* have been reported (Chen *et al.,* 2008). *Xa7* was mapped to the 0.21 cM interval between the STMS and SSR markers GDSSR02 and RM20593, respectively.

Xa27 was identified in wild rice *O. minuta* Acc. 101141 (Amante-Bordeos *et al.*, 1992). It was reportedly located between RFLP markers RG424 and RG162 (70.4-104.6 cM) on the long arm of chromosome 6, which is about 22.1 cM away from *Xa7*. The fine genetic mapping of this resistance gene was carried out. *Xa27* was tightly linked with markers M964 and M1197 and co-segregated with markers M631, M1230 and M449 (Gu *et al.*, 2004). The resistance reaction of *Xa27* showed semi-dominant or a dosage effect in the cv. CO39 genetic background (Gu *et al.*, 2004). Cloning of the *Xa27* gene from rice and cognate avr gene avr*Xa27* from *Xoo* were successful. The resistant and susceptible alleles of *Xa27* encode the identical proteins (Gu *et al.*, 2005).

xa32(t) was identified in wild rice *O. barthii*. It was mapped with SSR markers using bulk segregation analysis (BSA). BSA indicated presence of *O. barthii* on the terminal region of chromosome 6 at a distance of 9.3 cM proximal to RM588 (Singh *et al.*, 2007).

Many BB resistance genes, i.e. *Xa3*, *Xa4*, *Xa6*, *xa9*, *Xa10*, *Xa21*, *Xa22*, *Xa23*, *Xa26* and *Xa30*, have been reported to locate on chromosome 11. Most of them are multigene family and tightly link together. *Xa21* gene was introgressed from a wild species *O. longistaminata* into *O. sativa* background (Khush *et al.*, 1989). It confers resistance to a broad range of *Xoo* strains. This resistance gene was first tagged with RAPD marker (Ronald *et al.*, 1992). Later, the RFLP marker RG103 had found to be tightly linked to this gene at a distance of 1.2 cM. Then, a PCR-base STS marker pTA248 was developed and can be used in MAS and can be adopted in a map-based cloning strategy. *Xa21* was the first BB resistance gene successfully cloned. It was isolated using map-based cloning and found to be a member of a complex locus located on long arm of chromosome 11. The predicted structure of *Xa21* indicates that the protein has a cytoplasmic domain containing a serine-threonine kinase, a transmembrane domain, and an extracellular domain with leucine rich repeat (LRR) receptor kinase like proteins (Song *et al.*, 1995). Currently, PB7/8, a functional marker derived from *Xa21* gene has been very effective for selecting BB resistance *Xa21* gene in rice (Chunwongse *et al.*, 1993).

Xa3/Xa26 locus was mapped to a region of about 1.68 cM. This locus co-segregated with marker R1506 and between R1506 had two flanking markers, RM224 and Y6855RA. These two flanking markers were 0.21 cM and 1.47 cM, respectively from marker R1506 (Yang *et al.*, 2003). *Xa26* encodes a leucine-rich repeat (LRR) receptor kinase-like protein. The gene belongs to a multigene family consisting of four members (Sun *et al.*, 2004). *Xa3* had the same copy numbers of *Xa26* family members from the rice line Minghui 63 (Xiang *et al.*, 2006). Many reports concluded that *Xa3*, *Xa4*, *Xa6*, *xa9* and *Xa26* were the same gene (Ogawa *et al.*, 1986b, c; Sun *et al.*, 2004; Xiang *et al.*, 2006). Another resistance gene from the rice line IR1188 was also identified and mapped in the same region on the chromosome 11. (Jantaboon *et al.*, 2004)

The resistance gene *Xa10* was identified from rice cultivar Cas 209 (Mew *et al.*, 1982; Yoshimura *et al.*, 1983). It confers race-specific resistance to only a few Philippines races of BB pathogen. The *Xa10* locus was initially mapped between the RAPD marker $O07_{2000}$ and RFLP marker CDO365 on the long arm of chromosome 11 (Yoshimura *et al.*, 1995). The resistance gene locus was later integrated to the region between RFLP markers RG103 and RG1109 on the rice genetic map of double haploid lines (IR64/Azucena). *Xa21* and *Xa23* were located at the middle region of chromosome 11. *Xa21* co-segregated with RG103 (Ronald *et al.*, 1992) while *Xa23* was mapped to a region between markers RG1091 and G1465 (Zhang *et al.*, 1998). Therefore, *Xa10* locus is flanked by *Xa21* and *Xa23*. Fine mapping of *Xa10* revealed that the resistance gene was flanked between markers M491 and M419 on Nipponbare genome which consisted of six candidate genes (Gu *et al.*, 2008).

5. DNA markers and marker-assisted selection (MAS)

DNA markers or molecular markers are typically derived from a small region of DNA that show sequence polymorphism. DNA markers are tools for simultaneously advancing our understanding of plant genome and increasing the efficiency of plant breeding. They can be used to dissect the genetic basis of complex phenotypes in to Mendelian components in order to obtain information about gene dosage, epitasis, pleiotropy and genotype×environment interaction (Toojinda, 1999). The use of DNA markers, which permit the genetic dissection of the progeny at each generation, increases the speed of selection process (Babu *et al.*, 2004). The closely linked DNA markers to the target genomic regions can be used to accelerate fixation of favorable alleles in the next selection step. Molecular markers could also increase the efficiency of backcrossing by allowing selection of genotype with the maximum percentage of recurrent parent genome (Hospital, 2005).

Common four types of markers are often used in applied plant genomics and implement in rice including RAPD, RFLP, Amplified fragment length polymorphism (AFLP) and Simple Sequence Repeats (SSR). However, RAPD and RFLP markers have limitations. RFLP using southern analysis is laborious, time-consuming, costly and involves the use of radiochemical. So far, RFLP and RAPD are difficult to re-amplify while SSR marker is simple, rapid, accurate, efficient, cost-effective and complementary to existing breeding protocols. Furthermore, SSR has several advantages apply to plant breeding program based on polymerase chain reaction (PCR) amplification, represent single-loci, and can detect high levels of polymorphism (McCouch and Doerge, 1995).

SSR marker is tandem repetitions of mono-, di-, tri-, or tetranucleotide units. The PCR base SSR is co-dominant and highly polymorphic. The polymorphism in the length of the amplified SSR can be revealed either by agarose gel electrophoresis, if the differences in length between alleles are high enough, or more often in acrylamide gels. SSR can be used as molecular markers which have wide-ranging applications in crops (Vienne *et al.*, 1998). It constitutes excellent genetic markers with locus identity and can be multiplexed to achieve higher throughput (Mitchell *et al.*, 1997). The disadvantages of SSR are the high cost of discovery and lack of transferability across genera and even distantly-related species (Roder *et al.*, 1995).

A new generation of molecular markers based on the detection of single nucleotide polymorphisms (SNP) promises high-throughput assays at relatively low costs, along with the potential for high levels of multiplexing (Dubcovsky, 2004). CAPS and Bi-PASA (Konieczny and Ausubel, 1993; Liu *et al.*, 1997) are co-dominant genetic markers and can be use for MAS but CAPS require restriction endonuclease digestion to detect SNP in an interesting region. Whereas, Bi-PASA is easier to use than CAPS. It can be amplified and directly run on agarose gel.

Progress in molecular genetics has resulted in the development of DNA tags, which can be used in MAS strategies for cultivar development (Dubcovsky, 2004). One of the major applications of molecular markers to rice breeding is using MAS or marker-assisted backcrossing (MAB). MAS is a tool for genetic improvement of crop, livestock, forestry, and fish gaining considerable importance. It would improve the efficiency of plant breeding through precise transfer of genomic regions of interest and accelerating the recovery of the recurrent parent genome. In the same way, backcross breeding is a procedure for the introgression of a target gene from a donor into the genetic background of a recipient. In backcross breeding, DNA markers can be used to control the target gene and the genetic background (Hospital, 2005). Hence, breeding with MAS/MAB has major advantages compared with traditional phenotype-dependent breeding in terms of convenience and efficiency. Therefore, MAS strategy is a way to capitalize on available markers and to incorporate valuable traits into elite lines that are suitable for cultivar release (Dubcovsky, 2004). Consequently, MAS require identified marker with a high level of accuracy and efficiency, cost effective and easy to use. Dubcovsky (2004) has proposed that the success of a marker-based breeding system depends on four main factors including (i) A genetic map with an adequate number of uniformly-spaced polymorphic markers to accurately locate desired QTLs or major gene(s); (ii) Close linkage between the QTL or a major gene of interest and adjacent markers; (iii) Adequate recombination between markers and rest of the genome; and (iv) An ability to analyze a larger number of plants in a time- and cost- effective manner.

Conventional breeding is primarily based on phenotypic selection of superior individuals among segregating progenies resulting from hybridization. Combining the favorable resistance genes/QTL located on different chromosome in one background following repeated backcross breeding is a difficult task. Moreover, transfer of recessive genes through conventional breeding requires additional selfing generations after every backcross, a procedure that is prohibitively slow for most commercial breeding purpose thus, MAS has been used to transfer favorable alleles of genes/QTL for biotic and abiotic stress resistance/tolerance into the desired rice genetic background (Babu *et al.*, 2004; Toojinda *et al.*, 2005).

6. Molecular breeding for BB resistance

More than 30 BB resistance genes have been identified and some of them have been incorporated into the modern rice varieties through conventional breeding. However, the pathogen can easily breakdown a single gene. The breakdown of resistance in modern and high-yielding rice varieties after a few years of cultivation was attributed to fast-changing pathogens. One way to delay the breakdown is to pyramid multiple resistance genes into rice varieties. It is very difficult or nearly impossible with conventional breeding approach.

The successful of BB resistance gene pyramiding using MAS has been reported from several rice breeding programs, for examples, Abenes *et al.* (1993) pyramided four BB resistance genes, *Xa4*, *xa5*, *xa13*, and *Xa21*, using MAS. The pyramiding lines with two, three, and four resistance genes had shown a wider spectrum and a higher-level of resistance than lines with only single gene according to Huang *et al.* (1997) and Sanchez *et al.* (2000). Jena *et al.* (2007) also reported that *Xa4+xa5+Xa21* pyramiding lines expressed high levels of resistance to all races in Korea. Singh *et al.* (2001) used MAS to improved BB resistance in indica rice cultivar PR106 with *xa5*, *xa13* and *Xa21*. They found that *Xa21* was the most effective followed by *xa5*, whereas *xa13* gene was the least effective against *Xoo*. These three resistance genes were also introgressed into Samba Mashuri and the pyramid lines exhibited high levels of resistance to *Xoo* (Sundarum *et al.*, 2008). *Xa21* and *Xa4* from IRBB60 were introgressed into a hybrid rice line, Shunhui527 using MAS. The improved lines expressed high level of resistance to the *Xoo* strain CI-C VIII (Haung *et al.* 2003). In addition, *Xa21* and *Xa7* were pyramided into Minghui 63 background and the improved lines showed high level of resistance to BB (Zhang *et al.*, 2006). Moreover, TGMS rice was introgressed with *Xa4*, *Xa7* and *Xa21* for the development two-line hybrids. The plants carrying gene combinations exhibit highly resistance phenotype (Perez *et al.*, 2008).

METERIALS AND METHODS

Materials

1. Plant materials for gene identification and pyramiding

1.1 Identification of BB resistance in IR62266

Two *indica* rice cultivars, IR62266 and Khao Dawk Mali 105 (KDML105 were used to develop a 190 F_3 population. IR62266 introduced form IRRI was used as a donor parent whereas, KDML105 an aromatic rice cultivar with the best eating qualities of Thailand was used as a recipient parent. IR62266 and KDML105 were identified as highest resistance and highly susceptible to BB isolates collected from rice field in Thailand. The 190 $F_{2:3}$ individuals were inoculated with three different *Xoo* isolates to identify number and location of BB resistant gene possessed by IR62266.

1.2 Identification of BB resistance in Pin Kaset and Ba7

Two *indica* rice cultivars, Pin Kaset (PK) and Ba7 were crossed to develop segregating population used for identify BB resistance genes possessing by PK and Ba7. Ba7 and PK were used as male and female recurrent parents respectively. F_2 and BC_2F_3 populations were used to identify BB resistance gene in Ba7. These two populations consisted of 139 and 161 progenies. Linked markers and genomic location of a BB resistance gene were determined by genotypic-phenotypic association, while a BB resistance gene in PK was studied in the BC_2F_2 population. A total of 436 BC_2F_2 individuals were used to identify the relationship between BB resistant phenotype and linked DNA markers. IRBB7 was used to compare the resistance reaction pattern with Ba7. On the other hand, IRBB21 and IR1188 were used to compare the DNA banding pattern and the resistance reaction pattern with PK.

1.3 Pyramiding of BB resistance genes

Four indica rice cultivars including IR62266, Ba7, Pin Kaset and 104-4-1-19-7 were used as genetic sources of BB resistance genes *xa5*, *xa33(t)(t)*, *Xa34(t)*, and *Xa21*/*qBB11*, respectively. The list of indica rice cultivars and their origins were as following:

1) IR62266 IRBB7 and IRBB21were developed by International Rice Research Institute (IRRI) and introduced to Thailand by Rice Research Center.

2) Ba7 was not known for the origin but it was used as differential variety by the staff of Rice Research Center.

3) Pin Kaset (PK) was developed by Rice Gene Discovery Unit (RGDU). It derived from the cross between KDML105 and CT9993. PK also had a cooking quality profile the same as KDML105.

4) KDML105 is a Thai local cultivar. It has the best cooking quality and been the most popular grown rice variety in the North and Northeast of Thailand. KDML105 is very susceptible to BB disease.

5) 104-4-1-19-7 was a KDML105 backcross introgression line developed by Rice Gene Discovery Unit. It was identified to carry *Xa21* and *qBB11* derived from IR1188 (Jantaboon *et al.*, 2004).

1.4 Validation of pyramiding lines

Twenty eight F_4 pyramid lines derived from the cross between 3 BC_2F_2 lines carrying *xa5/Xa21/qBB11* and 4 BC_2F_1 lines carrying *xa33(t)/Xa34(t)* were selected based on the combination of BB resistance gene indicating by genetic markers. All of them have a good plant-type and homozygous alleles at the target BB resistance genes. The parental lines which used to develop all population were used as reference for single BB resistance genes (Table 2).

Table 2 List of materials including pedigree and BB resistance genes used for BB evaluation. + = presence of resistance gene

Entry	**Pedigree**	**Resistance gene**				
		xa5	***Xa21***	***xa33(t)***	***Xa34(t)***	***qBB11***
	KDML105					
	IR62266	+				
	Ba7			+		
	PK				+	
	IR1188		+			+
	104-4-1-19-7		+			+
1	RGDU07099-2-9M-18M					+
2	RGDU07097-1-1M-5M	+				+
3	RGDU07099-2-9M-8M	+				+
4	RGDU07097-15-26M-8KPS	+			+	
5	RGDU07099-8-21M-5KPS	+			+	
6	RGDU07097-28-3M-1KPS		+			+
7	RGDU07097-28-3M-3KPS		+			+
8	RGDU07097-15-12M-3		+		+	
9	RGDU07097-15-12M-4		+		+	
10	RGDU07099-5-51M-23M			+		+
11	RGDU07097-28-14M-4KPS			+	+	
12	RGDU07099-6-8M-5KPS			+	+	
13	RGDU07097-1-17M-1KPS	+	+			+
14	RGDU07097-1-17M-2KPS	+	+			+
15	RGDU07097-1-26M-9M	+	+		+	
16	RGDU07097-1-26M-6M	+	+		+	
17	RGDU07099-1-17M-2M	+		+		+
18	RGDU07097-1-26M-10M	+		+		+
19	RGDU07097-1-27M-1KPS	+		+	+	
20	RGDU07097-1-30M-1KPS	+		+	+	
21	RGDU07097-26-8M-1KPS		+	+		+
22	RGDU07099-2-25M-4KPS		+	+		+
23	RGDU07099-2-12M-5M		+	+	+	
24	RGDU07099-2-12M-9M		+	+	+	
25	RGDU07099-5-3M-23KPS	+	+	+		+
26	RGDU07097-1-8M-9KPS	+	+	+		+
27	RGDU07099-2-12M-10M	+	+	+	+	
28	RGDU07099-2-12M-13M	+	+	+	+	

2. *Xoo* isolates

Nine *Xoo* isolates from the collection of Rice Gene Discovery Unit were used to test resistance reaction in this study. Three *Xoo* isolates TXO1, TXO2 and TXO5 were used to identify BB resistance gene in IR62266 while TXO16 and TB0304 were used to identify BB resistance genes Ba7 and PK, respectively. Out of nine, six *Xoo* isolates including TB0304, TXO16, TXO34, TXO37, TXO107 and TXO133 which selected based on the resistant specificity to each resistance gene in parental lines were used for BB evaluation in the pyramiding population (Table 3).

3. Molecular markers

3.1 Identification of BB resistance in IR62266

Thirty four SSR markers closely linked to BB resistance genes which reported previously were chosen to genotype in parental lines, KDML105 and IR62266. Nineteen SSR markers were selected based on polymorphism between parents. These polymorphic markers were used to genotype the F_3 population to identify a BB resistance gene. List of SSR markers were shown in Appendix Table 1.

3.2 Identification of BB resistance in in PK and Ba7

One hundred and forty four SSR markers that distributed all 12 rice chromosomes were chosen. Sixty two SSR markers shown polymorphic between PK and Ba7 were used to genotype the BC_2F_2 and BC_2F_3 populations to identify a BB resistance gene in PK and Ba7 respectively. List of SSR markers were shown in Appendix Table 2.

3.3 Pyramiding of BB resistance genes

Table 4 showed SSR, STS and SNP markers used for MAS selection to pyramid the BB resistance genes including *xa5*, *Xa21*, *xa33(t)*, *Xa34(t)*, and *qBB11*.

Table 3 Resistance reaction of seven *Xoo* isolates used in BB resistance gene identification and pyramiding. R, MR, MS and S mean resistance, moderate resistance, moderate susceptible and susceptible, respectively.

Entry	**Activities/plant materials**	**Isolate code**	**-**	***xa5***	***Xa21/qBB11***		***xa33(t)***	***Xa34(t)***
			KDML105	**IR62266**	**104-4-1-19-7**	**IR1188**	**Ba7**	**PK**
1	Identification/IR62266	TXO1	S	R	R	R	R	R
2	Identification/IR62266	TXO2	S	R	R	R	R	R
3	Identification/IR62266	TXO5	S	R	R	R	R	R
4	Identification/PK and Pyramiding gene	TB0304	S	R	R	R	S	R
5	Identification/Ba7 and Pyramiding gene	TXO16	S	R	R	R	R	MS
6	Pyramiding gene	TXO34	S	R	MS	R	R	MR
7	Pyramiding gene	TXO37	S	R	S	MR	MR	MS
8	Pyramiding gene	TXO107	S	R	R	R	MR	MR
9	Pyramiding gene	TXO133	S	R	R	R	MS	MR

Table 4 Type, chromosomal location and primer sequences of molecular markers for MAS to pyramid 5 BB resistance genes. F= forward primer, R = reward primer.

Gene	Marker	Type of marker	Chr.	Primer sequence (5'->3')	Remark
xa5	RM507	SSR	5	F- CTT AAG CTC CAG CCG AAA TG R- CTC ACC CTC ATC ATC GCC	www.gramene.org
	RM153	SSR	5	F- GCC TCG AGC ATC ATC ATC AG R- ATC AAC CTG CAC TTG CCT GG	www.gramene.org
	RM122	SSR	5	F- GAG TCG ATG TAA TGT CAT CAG TGC R- GAA GGA GGT ATC GCT TTG TTG GAC	www.gramene.org
	PAxa5	SNP	5	F1- GGC CAC CTT CGA GCT CTA CC F2- GCT CGC CAT TCA AGT TCT TGT C R1- CAG ATA CCT TAT CAA ACT GCT C R2- CAA CAT TGC AACTCC TGT ATA AG	unpublished
Xa21	PB7-8	STS	11	7F- AGA CGC GGA AGG GTG GTT CCC GGA 8R- AGA CGC GGT AAT CGA AAG ATG AAA	Chunwongs (1993)
xa33(t)	RM7243	SSR	6	F- TGT GGT GGA CCA CGG AAG ATG G R- GCA CTC TGC ACT GAG AGC AAC AGG	www.gramene.org
	RM5509	SSR	6	F- GAT GAT CCA TGC TTT GGC C R- TTC CAG CAG AAA GAA GAC GC	www.gramene.org
	RM400	SSR	6	F- ACA CCA GGC TAC CCA AAC TC R- CGG AGA GAT CTG ACA TGT GG	www.gramene.org
Xa34(t) and *qBB11*	RM224	SSR	11	F- ATC GAT CGA TCT TCA CGA GG R- TGC TAT AAA AGG CAT TCG GG	www.gramene.org

Methods

1. Development of segregating and pyramiding populations

1.1 Identification of BB resistance in IR62266

IR62266 was crossed with KDML105 to produce 2 F_1 plants. The F_1 plants were self-pollinated to produce 190 F_2 plants and then single seed descent method was carried out to generate 190 $F_{2:3}$ population that was used to identify a BB resistance gene and its genomic location. The process of population development was illustrated in Figure 5.

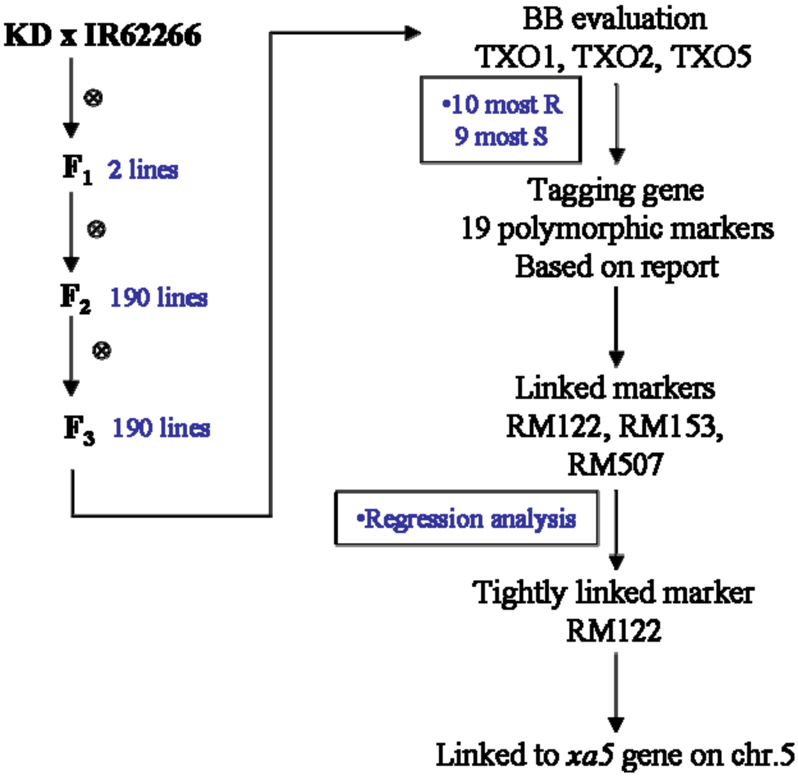


Figure 5 Scheme of population development and identification of BB resistance gene in IR62266

1.2. Identification of BB resistance in PK and Ba7

Ba7 used as a male parent was crossed with PK to develop 139 F_2 population. This population was used to identify linked markers of the BB resistance gene possessed by Ba7 by the meant of gene tagging. Backcrossing and MAS were then used to develop the backcross populations that used to validate the accuracy of linked markers and to confirm the location of BB resistance gene. The F_2 resistant plant (RGDU04040-130) was crossed with PK to generate 98 BC_1F_1 individuals. RM7243, RM5509 and RM400 indentified as linked markers in the F_2 population, were used to select BC_1F_1 plants carrying the resistance gene, and 10 selected BC_1F_1 plants were chosen and crossed to PK to generate 122 BC_2F_1 individuals. Same markers were carried out and identified 52 BC_2F_1 plants carrying the resistance gene. One heterozygous plant (RGDU05228-18) was self-pollinated to produce 838 BC_2F_2. After that, four heterozygous BC_2F_2 plants were chosen and then self-fertilized to produce 161 BC_2F_3 plants. 161 BC_2F_3 individuals were used to evaluate the effect of the resistance gene and the relationship with linked DNA markers.

On the other hand, 4 BC_2F_1 lines were selected and then self-pollinated to produce 436 BC_2F_2 individuals. This population was used to identify the BB resistance gene carried by PK. 10 most resistance and 10 susceptible BC_2F_2 individuals were used for gene tagging to determine the linked markers. The population development and MAS were illustrated in Figure 6.

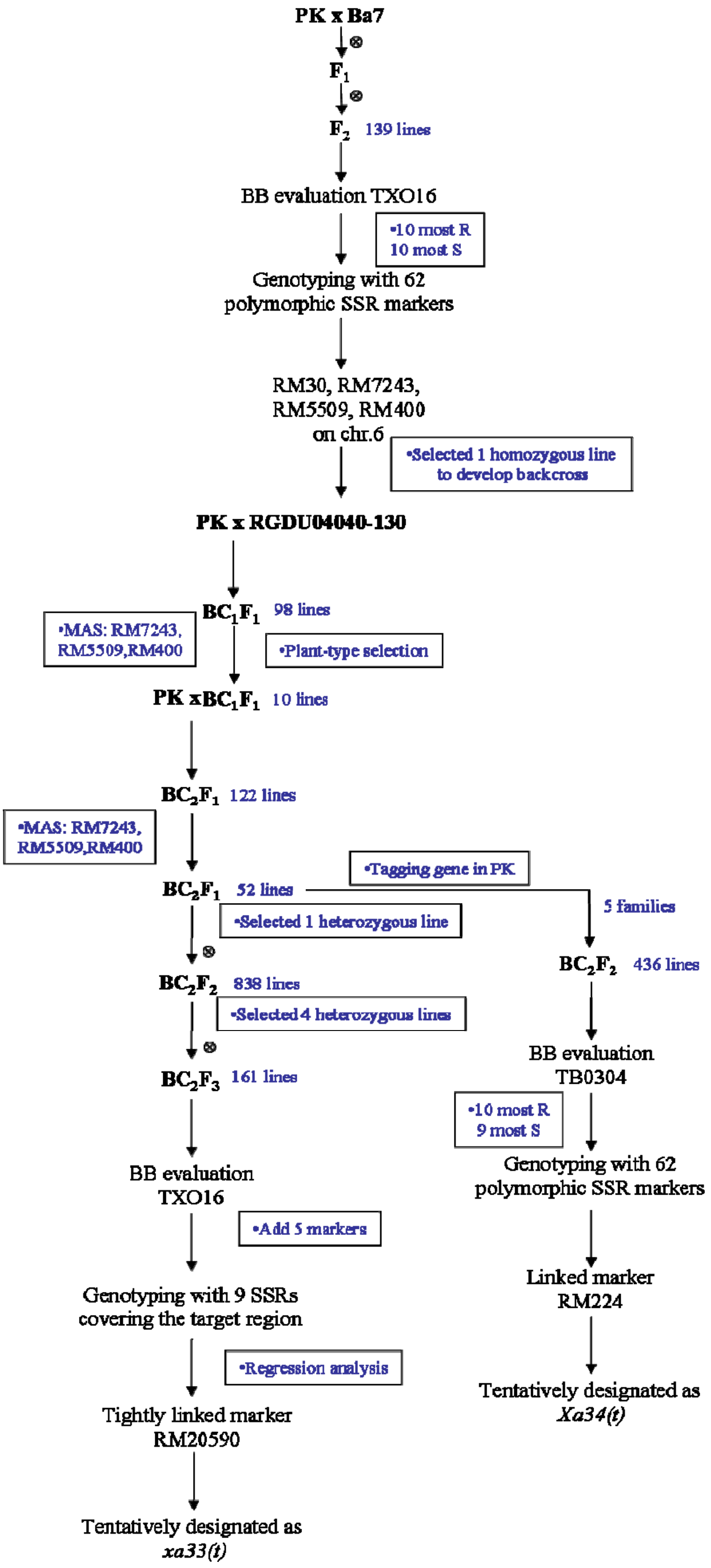


Figure 6 Scheme of identify BB resistance gene in rice cultivars Ba7 and PK.

2. Determination of BB resistance genes

2.1 Identification of BB resistance in IR62266

Average LL of 190 F_3 individuals against three *Xoo* isolates, TXO1, TXO2, and TXO5 were examined. Twenty F_3 plants consist of eleven most resistant and nine most susceptible were selected based on the LL against three isolates. 34 SSR markers selected based upon the location of BB resistance genes that previously reported were screened in parental lines to identify the polymorphic markers and 19 polymorphic SSR markers were selected. The modified bulk segregation analysis was carried out in 20 F_3 individuals using these polymorphic markers to identify the linked markers. These liked markers were then genotype in the 190 F_3 population. The phenotype and genotype were analyzed for relationship.

2.2 Identification of BB resistance in in Ba7

A *Xoo* isolate, TXO16 showed an incompatible reaction to Ba7 and a compatible reaction to PK was used to assay a resistance reaction in F_2 and BC_2F_3 populations (Figure 6). 139 F_2 plants were inoculated at seedling stage, while 161 BC_2F_3 plants were inoculated at tillering stage. One hundred and fourteen rice SSR markers covering the 12 linkage groups were analyzed for polymorphism between 'Ba7' and PK. To determine BB resistance gene in Ba7, 10 most resistant and susceptible F_2 plants were selected based on their LL and were genotyped with 62 polymorphic SSR markers. Four identified flanking SSR markers, RM30, RM7243, RM5509 and RM400, were used for MAS to develop BC_2F_2 and BC_2F_3 generations used for validate the resistance gene. To determine the tightly linked markers, five SSR markers, RM20523, RM20536, RM3430, RM20590 and RM340, were added into the BC_2F_3 genotyping.

A rice variety 'IRBB7' carrying *Xa7* which located in the same location of BB resistant gene in Ba7 was used to identify whether or not *Xa7* and identified gene is the same. Sixty three *Xoo* isolates, collected from various parts of Thailand, were used to inoculate these two variety and the resistance reaction and pattern were compared.

2.3 Identification of BB resistance in PK

The compatible and incompatible reaction of TB0304 was opposite with its of TXO16. Four hundred and thirty six BC_2F_2 individuals were inoculated with TB0304 at seedling stage (Figure 6). LL was taken and used to classify resistance and susceptible in ten most resistant and nine most susceptible BC_2F_2 plants. These materials were genotyped with 62 polymorphic SSR markers (Table 3). One identified flanking SSR marker RM224 was used for MAS to develop F_2 and F_3 pyramiding population.

3. Pyramiding of BB resistance genes

3.1 Pyramiding of *xa5*, *Xa21* and *qBB11*

A F_3 line no. 60-0-0 was selected from the cross between KDML105 and IR62266 and used as male parent (Figure 5). This line was identified to carry *xa5*. Line 104-4-1-19-7 was the backcross progeny derived from cross between KDML105 as recipient and IR1188 as donor. This line carries *Xa21* and *qBB11*. These two lines were crossed and 6 F_1 plants were produced. These F_1 plants then crossed to line 104-4-1-19-7 to produce 70 $BC_1F_{1.}$ MAS with four markers, RM122, RM153, PB7/8 and RM224 were applied to select the BC_1F_1 carrying *xa5, Xa21* and *qBB11*. Eighteen BC_1F_1 lines carrying heterozygous alleles at *xa5*/*Xa21*/*qBB11* were identified and used to develop 103 $BC_2F_{1.}$ The same set of markers was applied to select the BC_2F_1 carrying *xa5, Xa21* and *qBB11* genes. Fifty lines carrying heterozygous at all three targets were selected and self pollinated to produce 1,350 BC_2F_2 individuals. 213 BC_2F_2 individuals were selected based on marker profile and plant-type. In this generation, a new developed primer ‘PAxa5’ was used with RM122, RM153 and RM507 to identify the plants carrying homozygous *xa5* allele. Finally, forty one BC_2F_2 were identified as homozygous at *xa5/Xa21*/*qBB11* loci. Three of them were chosen as genetic source to pyramid *xa5*, *Xa21* and *qBB11* with *xa33(t)* and *Xa34(t)*. The pyramiding process was illustrated in Figure 7.

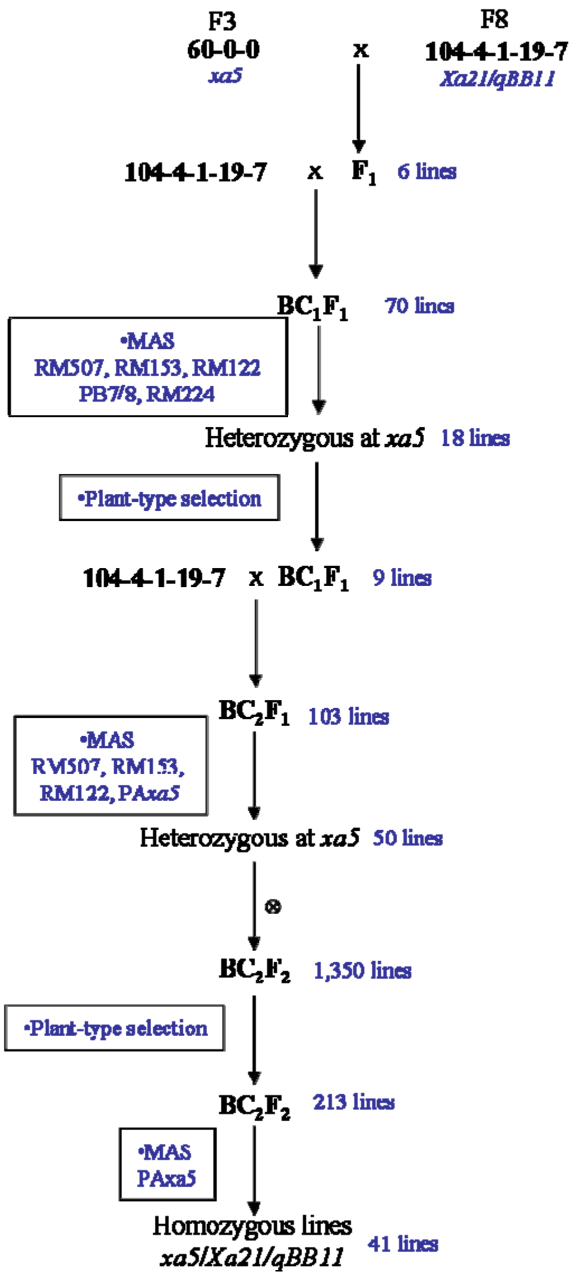


Figure 7 The development of pyramiding population to combine 3 BB resistance genes *xa5*, *Xa21* and *qBB11*.

3.2 Pyramiding of *xa5, Xa21, xa33(t), Xa34(t)* and *qBB11*

Three BC_2F_2 plants carrying homozygous alleles of *xa5/Xa21/qBB11* were crossed with 4 BC_2F_1 lines derive from PK/Ba7, which carrying heterozygous allele of *xa33(t)* and homozygous allele of *Xa34(t)*, to generate 16 F_1 plants. Subsequently, self-pollination was done to produce 500 F_2 plants that were used to identify the combinations of BB resistance genes. All combination was discovered in this F_2 population but some of the genes were still heterozygous phase. Therefore, F_3 generation were generated and subjected to MAS again. Molecular markers used for MAS in F_2 and F_3 generations were described in Table 2. Finally, BB resistance was evaluated using F_4 pyramid lines consisted of various combinations of BB resistance genes. The breeding strategy is given below in Figure 8.

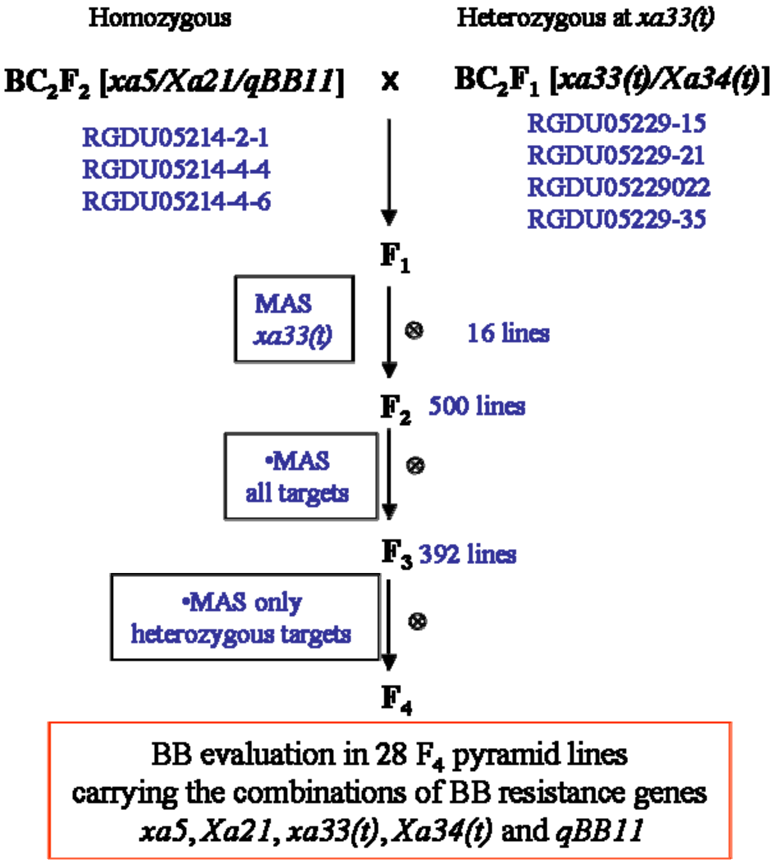


Figure 8 The development of pyramiding population to combine 5 BB resistance genes: *xa5, Xa21, xa33(t), Xa34(t)* and *qBB11*.

4. Assessment of BB resistance

4.1 Culturing

All *Xoo* isolates were grown in peptone sucrose agar medium (5g peptone, 20g sucrose, 3g beef extract and 15g agar, adjusted to 1 liter with dH_2O) for 72 hours at 28^oC. The bacterial cells were suspended in sterile water adjusted to 10^9 CFU/ml.

4.2 Inoculation

The artificial inoculation was conducted in all experiments under greenhouse condition at Kasetsart University, Kampaeng Saen Campus. Eight seeds of each line were sowed in the plastic plate and then Five days old seedlings were transplanted into plastic tray (four plants per pit). Plants were kept in a greenhouse, watered two times per day, fertilized weekly with 46-0-0 and 15-15-15 NPK fertilizers. In the final week, the fertilizer 46-0-0 formula was applied before inoculation three days. BB inoculation was done by using the leaf-clipping method (Kauffman *et al.*, 1973). Two to four fully expanded leaves of each plant were inoculated. The inoculated plants were kept in a greenhouse without water one night. After that the water was applied to these plants five times per day until the inoculated plants ready to score (12-18 days after inoculation). The inoculation was performed at two growth stage of the rice plant *i*) seedling stage (30 days after sowing) and *ii*) tillering stage (60 days after sowing). Lesion length (LL) from the cut leaf tips were measured in centimeter after inoculation about 12-18 days depend on the susceptible control show symptoms sufficiently (Table 5).

4.3 Data record

The resistance reactions were recorded as lesion length (LL) from the cut leaf tips. The classification of BB resistance was based on the LL as following:

1) Identification of BB resistant genes in KDML105/IR62266 and PK/Ba7 populations was scored as R when the LL was less or equal to that of the donor parent and as S when it was longer.

2) Pyramiding of BB resistance genes population was classified as R, moderate resistance (MR), moderate susceptible (MS), and highly susceptible (S) when the LL was 0-3 cm, 3.1-6.0 cm, 6.1-9.0 cm and more than 9.0 cm, respectively (Yang *et al.*, 2003; Chen *et al.*, 2001). The descriptions of all experiments conducted in this study were summarized in Table 5.

Table 5 Description of experiments conducted in this study and the classification of resistance and susceptible.

Population	**Generation**	**Amount of lines**	**Activities**	**Growth stage assessment**	**Classification of R/S based on LL (cm)**
KDML105/ IR62266	F_3	190	Identification of gene in IR62266	Seedling	R = based on donor, S = based on recipient
PK/Ba7	F_2	139	Identification of gene in Ba7	Seedling	R = based on donor, S = based on recipient
	BC_2F_3	161		Tillering	
	BC_2F_2	463	Identification of gene in PK	Seedling	R = based on donor, S = based on recipient
Pyramiding 5 BB resistance genes	F_4	28	BB evaluation for broad resistance	Seedling	R = 0-3 , MR = 3.1-6, MS = 6.1-9, S > 9

4.4 Data analysis of LL in pyramiding population

All of the genetic associations were analyzed based on simple linear regression and ANOVA in STATGRAPHIC 2.1 program. Least Significant Difference (LSD) in STATGRAPHIC 2.1 program was used to compare mean of LL among the pyramid lines.

5. DNA extraction and PCR amplification

Total genomic DNA form young leaves of progenies and parental lines were extracted using DNA trap® (DNA Technology Laboratory). The PCR amplification reactions for SSR markers were carried out in a total volume of 10 µl containing 20 ng of genomic DNA, 0.02 µM of each primer, 0.2 mM each of dNTPs, 2.5 mM $MgCl_2$, 0.2 unit Taq polymerase and 1X PCR buffer. Amplification was initially at 3 min 94°C and performed for 35 cycles of 30 sec at 94°C, 30 sec at 55°C and 2 min at 72°C followed by 5 min at 72°C. The amplification products were separated on 4.5% denaturing acrylamide gel electrophoresis and were detected by silver staining method.

RESULTS

1. Determination of BB resistance genes

1.1 Identification of BB resistance in IR62266

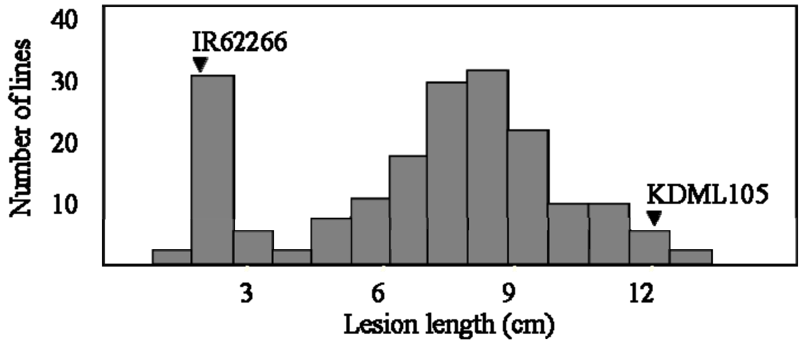
1.1.1 Phenotypic distributions

IR62266 expressed strong resistant interaction (R) to three *Xoo* isolates TXO1, TXO2 and TXO5, whereas KDML105 showed susceptible reaction (S). LL of IR62266 and KDML105 were ranged from 2.0 - 2.3 cm and 6.0 - 14.3 cm, respectively (Figure 9). LL of $F_{2:3}$ population showed a continuous distribution against all three isolates. The segregation ratios fitted well with the expected ratio of 3S:1R against three *Xoo* isolates, TXO1, TXO2 and TXO5 at $\chi2=1.27$, p=0.26; $\chi2=0.83$, p=0.36; $\chi2=1.39$, p=0.24, respectively.

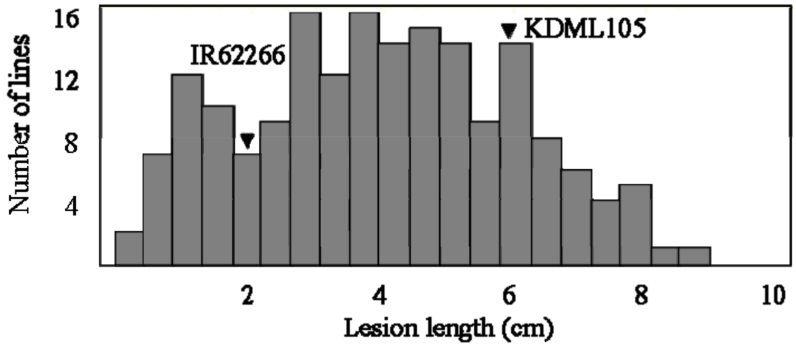
1.1.2 Tagging of BB resistant gene with SSR markers

The ten resistant plants and nine susceptible plants selected based on their mean and standard deviation (Figure 10) were genotyped with 19 SSR markers. Their genotypes and their parental genotypes were showed in Table 6. Two SSR markers RM122 and RM153 located on the short arm of chromosome 5 were clearly discriminated the R and S F_2 plants (Figure 11).

a) TXO1



b) TXO2



c) TXO5

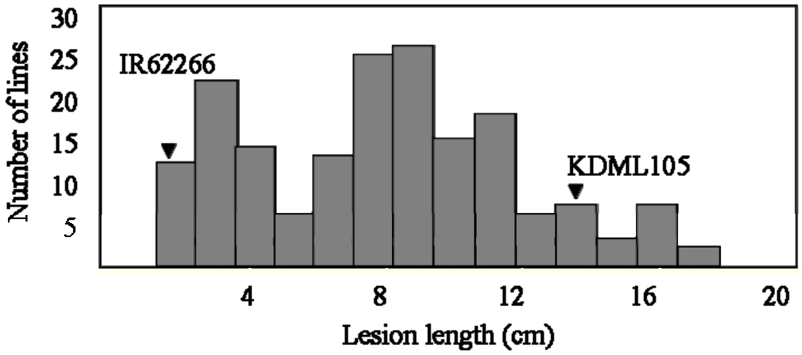


Figure 9 Distribution of LL after inoculation with *Xoo* isolates in a set of F_3 population derived from a cross between KDML105 and IR62266. a) TXO1, the average LL of KDML105 and IR62266 were 12.5 ± 3.4 cm and 2.0 ± 1.0 cm, respectively. b) TXO2, the average LL of KDML105 and IR62266 were 6.0 ± 2.1 cm and 2.1 ± 2.0 cm, respectively. c) TXO5, the average LL of KDML105 and IR62266 were 14.3 ± 3.5 cm and 2.3 ± 0.5 cm, respectively.

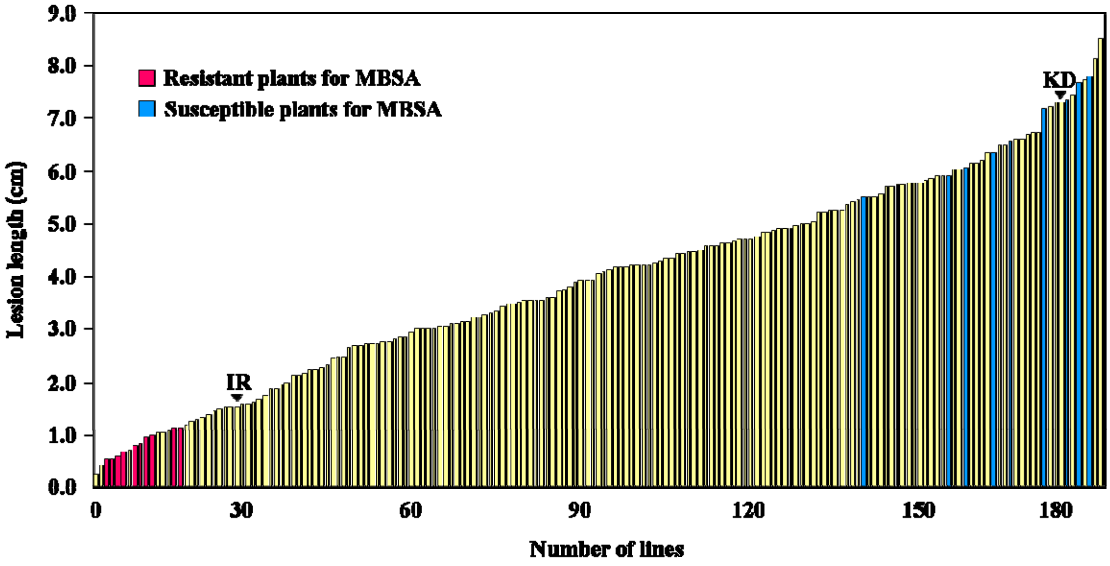


Figure 10 Distribution of F_3 population for LL when inoculated with *Xoo* isolate TXO2. The blue and red bars were F_3 that chosen for gene tagging.

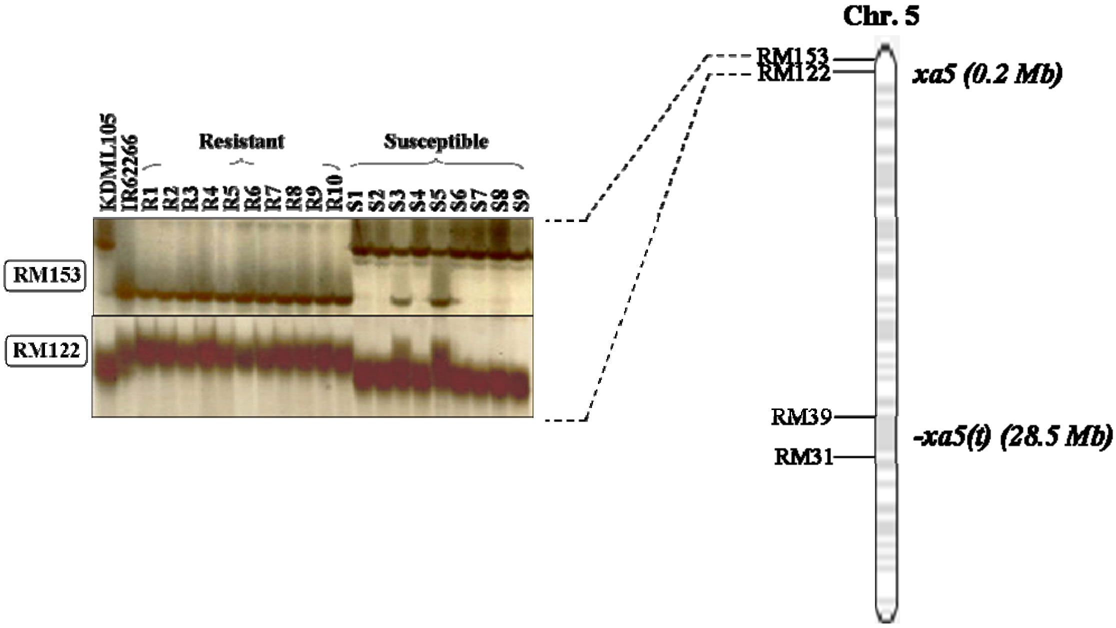


Figure 11 Banding pattern of two SSR markers RM122 and RM153 in R and S plants derived from a cross between IR62266 and KDML105. These markers located in the vicinity of reported *xa5*.

Table 6 Genotypes of R and S F_2 plants with 19 SSR markers, RM507, RM153 and RM122 showed clearly separated R and S plants as shown with highlight. KD = homozygous KDML105, IR = homozygous IR62266 and H = heterozygous.

Entry	**Resistant reaction against TXO1, TXO2 and TXO5**	**Chr.**	**2**	**4**	**4**	**4**	**4**	**5**	**5**	**5**	**5**	**5**	**8**	**9**	**9**	**9**	**9**	**11**	**11**	**11**	**11**
		cM	**103.9**	**35.4**	**94.4**	**118.3**	**152.3**	**3.0**	**5.4**	**10.1**	**30.0**	**111.3**	**90.3**	**73.3**	**81.2**	**99.4**	**114.7**	**85.7**	**102.9**	**110.0**	**115.1**
		Line no	**RM263**	**RM261**	**RM273**	**RM317**	**RM280**	**RM507**	**RM153**	**RM122**	**RM13**	**RM26**	**RM210**	**RM242**	**RM201**	**RM215**	**RM205**	**RM21**	**RM206**	**RM254**	**RM224**
1	R	10	IR	IR	H	H	KD	**IR**	**IR**	**IR**	KD	IR	KD	KD	KD	KD	H	H	KD	H	KD
2	R	17	H	KD	IR	IR	H	**IR**	**IR**	**IR**	IR	IR	IR	KD	KD	KD	IR	H	H	H	H
3	R	57	KD	KD	H	KD	H	**IR**	**IR**	**IR**	IR	KD	KD	H	H	IR	H	KD	H	H	H
4	R	58	IR	H	H	H	H	**IR**	**IR**	**IR**	IR	KD	H	KD	H	IR	IR	H	H	H	H
5	R	60	KD	KD	IR	IR	H	**IR**	**IR**	**IR**	IR	IR	H	IR	H	IR	H	KD	H	H	H
6	R	113	H	H	H	H	IR	**IR**	**IR**	**IR**	H	KD	KD	H	H	H	H	KD	KD	H	KD
7	R	115	H	H	H	H	KD	**IR**	**IR**	**IR**	IR	IR	H	KD	KD	H	KD	H	H	H	H
8	R	136	H	H	H	H	H	**IR**	**IR**	**IR**	IR	IR	IR	H	H	IR	H	KD	KD	H	KD
9	R	222	IR	H	H	H	KD	**IR**	**IR**	**IR**	H	KD	KD	IR	H	KD	KD	IR	H	H	H
10	R	242	KD	H	H	IR	IR	**IR**	**IR**	**IR**	H	IR	H	IR	H	IR	IR	H	H	H	KD
11	R	243	IR	IR	H	H	H	**IR**	**IR**	**IR**	H	IR	H	KD	KD	KD	H	H	H	H	KD
12	S	3	IR	H	H	IR	IR	**KD**	**KD**	**KD**	KD	H	IR	KD	KD	KD	KD	H	H	H	H
13	S	92	IR	KD	H	H	KD	**KD**	**KD**	**KD**	KD	KD	IR	IR	IR	IR	H	IR	IR	IR	IR
14	S	109	H	IR	H	H	IR	**H**	**H**	**H**	KD	KD	KD	H	KD	H	H	KD	KD	H	KD
15	S	112	IR	H	IR	-	IR	**KD**	**KD**	**KD**	KD	IR	KD	H	KD	H	H	IR	IR	IR	IR
16	S	164	KD	IR	IR	IR	H	**H**	**H**	**H**	H	H	KD	H	KD	KD	KD	IR	IR	H	H
17	S	206	KD	KD	H	H	KD	**KD**	**KD**	**KD**	H	KD	IR	IR	IR	IR	H	KD	KD	H	KD
18	S	229	KD	H	-	-	IR	**KD**	**KD**	**KD**	KD	IR	H	IR	IR	IR	H	KD	KD	H	IR
19	S	237	KD	H	KD	H	H	**KD**	**KD**	**KD**	KD	H	H	H	H	H	H	KD	KD	H	KD
20	S	267	KD	IR	H	KD	H	**KD**	**KD**	**KD**	KD	KD	H	IR	IR	IR	IR	H	H	H	H

1.1.3 Determination of closely linked markers by phenotype-genotype association

Two linked SSR markers and RM507 were used to genotype in 190 F_3 individuals. All markers were located at the terminal region on the short arm of chromosome 5. Phenotype-genotype association was analyzed using ANOVA and regression analysis. The result indicated that LL was highly significant associated with three SSR markers. Multiple regression analysis showed convincing evidence that RM122 was probably the closest marker linked to this BB resistance gene in IR62266. This marker explained 66.03% of LL variation in $F_{2:3}$ population as shown in Table 7.

Table 7 Phenotype-genotype association analysis using ANOVA and regression analysis in the F_3 population from the cross between KDML105 and IR62266. Mean of LL was highly significant associated with three SSR markers. IR = homozygous IR62266, H = heterozygous and KDML105 = homozygous KDML105.

Isolate	**Marker**	R^2	**Mean of LL**			
			IR	**H**	**KDML105**	
TXO1	RM507	47.39**	2.51a	7.71b	9.5c	**
	RM153	65.09**	2.53a	7.64b	9.34c	**
	RM122	66.03**	2.39a	7.67b	9.38c	**
TXO2	RM507	30.62**	1.52a	4.14b	5.54c	**
	RM153	53.56**	1.53a	4.12b	5.54c	**
	RM122	53.85**	1.44a	4.20b	5.50c	**
TXO5	RM507	27.90**	3.15a	8.96b	9.89b	**
	RM153	32.95**	3.18a	8.88b	9.65b	**
	RM122	60.75**	3.15a	8.96b	9.89b	**

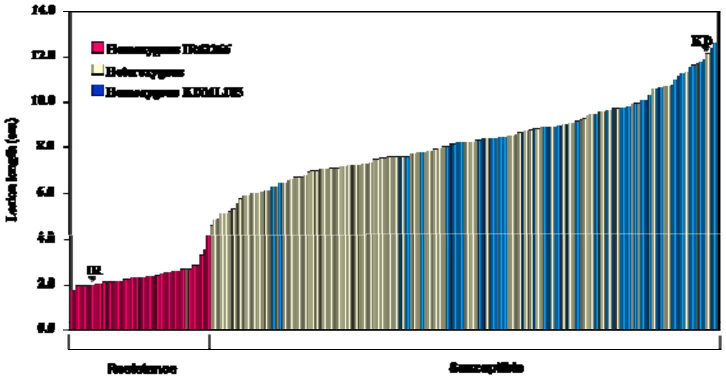
** Significant at *P* = 0.01

a, b and c stand for the clustering value on traits which are significant or not significant

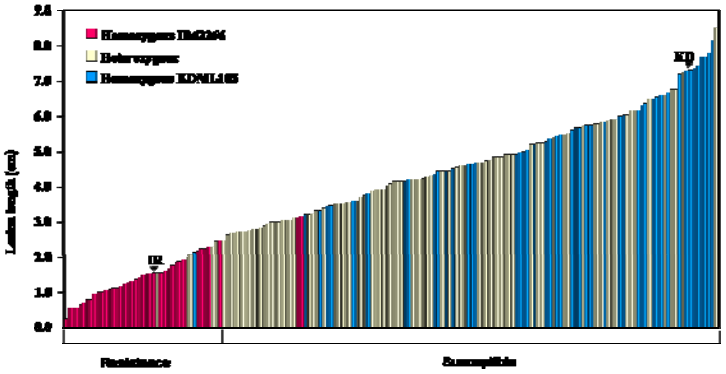
1.1.4 Resistant gene action

The LL of F_2 population showed a continuous distribution (Figure 11). The tightly linked markers RM122 classified F_2 individuals into three genotypic groups, IR62266/IR62266 (39 plants), IR62266/KDML105 (101 plants) and KDML105/KDML105 (50 plants). The genotypic groups IR62266/IR62266 conferred to resistance, IR62266/KDML105 and KDML105/KDML105 conferred susceptible phenotypes as shown in Figure 12. This evidence illustrated that resistance gene behave in complete gene action.

a) TXO1



b) TXO2



c) TXO5

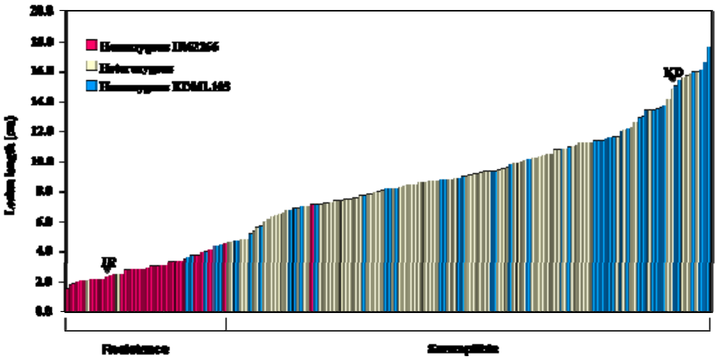


Figure 12 Distribution of F_2 population for LL after inoculated with TXO1 (a), TXO2 (b) and TXO5 (c). The red, yellow and blue bars represented for homozygous IR62266 plants, heterozygous plants and homozygous KDML105 plants, respectively. Based on RM122 genotypes, IR62266 homozygotes showed resistant phenotype, while the heterozygotes and KDML105 homozygotes showed susceptible phenotypes.

1.2 Identification of BB resistance in Ba7

1.2.1 Phenotypic distributions

Ba7 was resistant to TXO16 whereas PK was susceptible. Continuous distributions of LL were observed in F_2 and BC_2F_3 populations (Figure 13-14). Averages LL of 'Ba7' and PK ranged from 0.9 - 2.2 cm and 5.8 - 8.6 cm, respectively. When the cut off of classifying resistant and susceptible was based on the LL mean and standard error of 'Ba7', the numbers of resistant and susceptible were 37 and 102 in F_2 and 38 and 124 in BC_2F_3 population, respectively. These segregation ratios fit well with the expected ratio of 1R:3S at $\chi^2 = 0.19$, $p = 0.65$ and $\chi^2 = 0.21$, $p = 0.65$, respectively. The results suggested that BB resistance in 'Ba7' might be governed by a dominant gene. Inoculations of plants in two different growth stages, seedling (30 days old plants) and tillering stages (60 days old plants), were conducted in this study. Average LL in the seedling stage was a little bit longer than LL in the tillering stage.

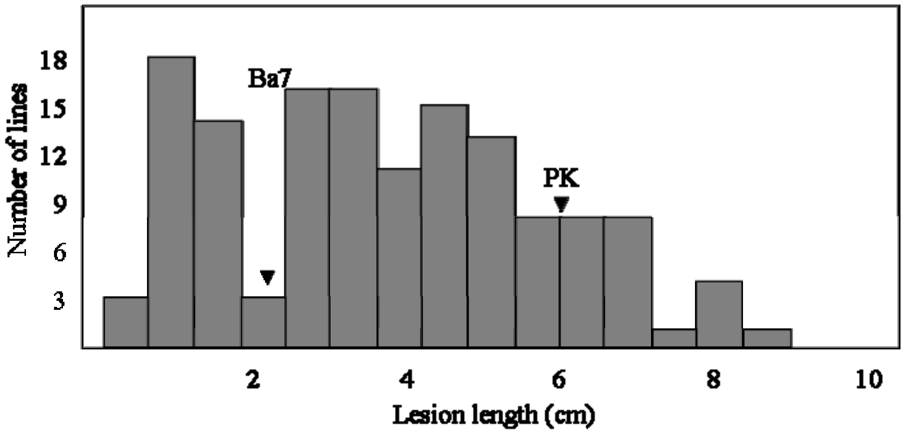


Figure 13 Distribution of F_2 population and range of parents for LL after inoculation with Thai *Xoo* strain, TXO16 at seedling stage. The average LL of 'Ba7' and PK were 2.2 ± 1.4 cm and 6.0 ± 1.6 cm, respectively.

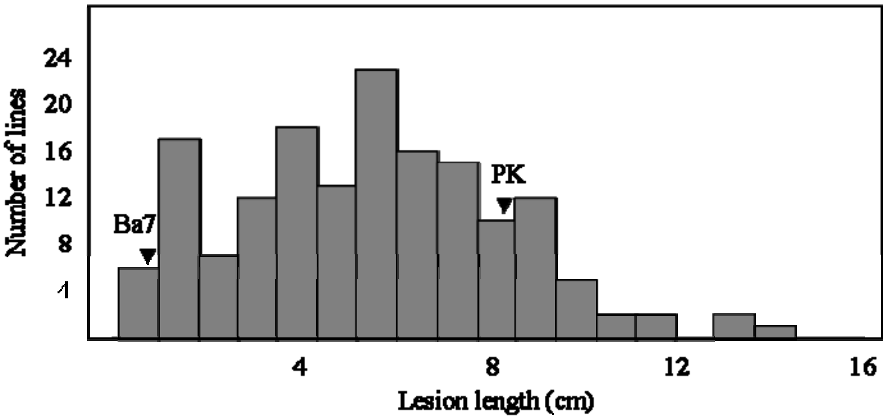


Figure 14 Distribution of BC_2F_3 population and range of parents for LL after inoculation with Thai *Xoo* strain, TXO16 at tillering stage. The average LL of 'Ba7' and PK were 0.9 ± 0.8 cm and 8.6 ± 1.7 cm, respectively.

1.2.2 Resistant reactions of Ba7 and IRBB7 against Thai *Xoo* isolates

Ba7 and IRBB7 were inoculated with 63 Thai *Xoo* isolates collected from various parts of Thailand at seedling stage (30 days old). Ba7 was resistant to 44 isolates whereas IRBB7 was resistant to 41 isolates. Out of 63, 12 isolates showed the different patterns or degrees of resistance between Ba7 and IRBB7 (Table 8). For example, Ba7 was resistant to TXO56, while IRBB7 was susceptible to TXO56. In contrast, Ba7 was susceptible to TB0096 but IRBB7 was resistant to TB0096. This result indicated that resistance gene possessing by Ba7 and IRBB7 were different genes and their resistant reaction were difference against Thai *Xoo* isolates.

Table 8 Resistant reactions (R = resistance, MR = moderate resistance, MS = moderate susceptible and S = susceptible) of Ba7 and IRBB7 against 29 Thai *Xoo* isolates collected from all part of Thailand.

Entry	**Isolate code**	**location**	**Resistance pattern**	
			Ba7	**IRBB7**
1	TB0096	Phitsanulok	S	R
2	TB0304	Chiang Rai	S	MS
3	TB9602	Chiang Mai	R	MR
4	TXO53	Phare	S	MS
5	TXO55	Chiang Rai	MR	S
6	TXO56	Chiang Rai	R	S
7	TXO103	Ubon Ratchathani	MS	MR
8	TXO111	Ubon Ratchathani	MR	MS
9	TXO114	Khon Kaen	MR	R
10	TXO116	Khon Kaen	MS	S
11	TXO121	Udon Thani	R	MR
12	TXO122	Udon Thani	MR	MS

1.2.3 Tagging *xa33(t)* gene with SSR markers

The resistance gene possessed by Ba7 was designed as *xa33*. Ten resistant F_2 plants and ten susceptible F_2 plants were selected for gene tagging. The resistant and susceptible were classified based on their mean and standard deviation of F_2 population (Figure 15). Of 114 SSR markers screened, 62 showed very clear polymorphisms between Ba7 and PK. These markers were used to genotype twenty F_2 plants (10 resistant and 10 susceptible) and their parents. Four SSR markers, RM30, RM7243, RM5509 and RM400, showed distinguishable banding patterns between resistant and susceptible plants as shown in Table 9 and Figure 16. All of them are located on the long arm of rice chromosome 6.

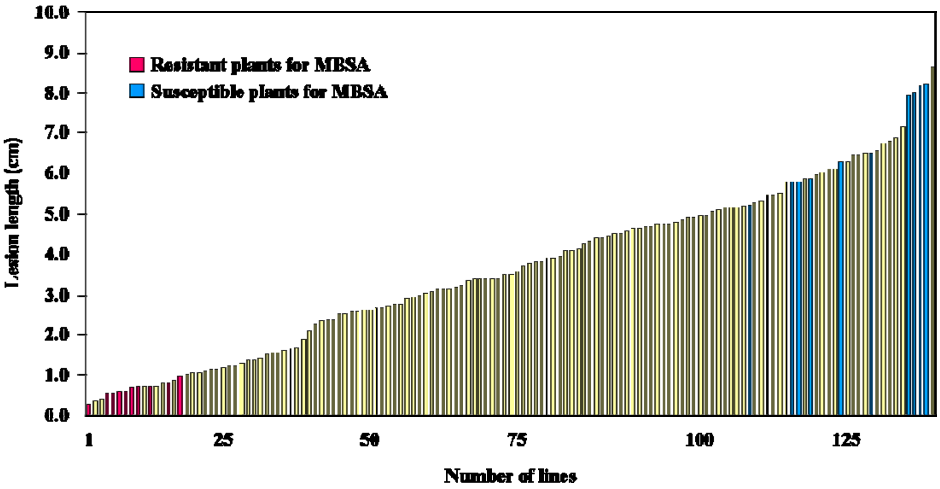


Figure 15 Distribution of BC_2F_3 population for LL when inoculated with *Xoo* isolate TXO16. The blue and red bars were F_2 that chosen for gene tagging.

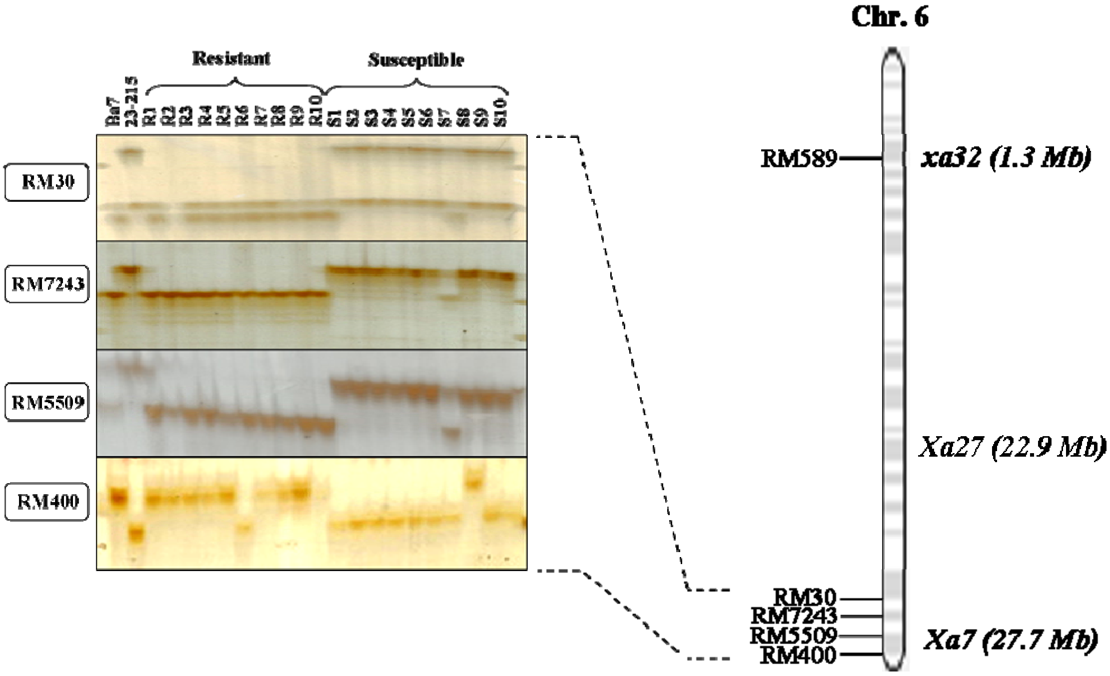


Figure 16 Banding pattern of four SSR markers RM30, RM7243, RM5509 and RM400 in R and S plants derived from a cross between PK and Ba7. These markers located in the vicinity of reported *Xa*7.

Table 9 Genotypes of twenty BC_2F_3 screening with 7 SSR markers on chromosome 6. Five SSR markers could clearly separate between R and S plants. Ba7 = homozygous Ba7, PK = homozygous Pin Kaset and H = heterozygous.

Entry	**Resistant reaction against TXO16**	**Genome position (Mb)**	**26.8**	**27.2**	**27.5**	**27.4**	**27.8**	**28.4**	**28.5**
		Line no	**RM3**	**RM30**	**RM7243**	**RM3430**	**RM5509**	**RM400**	**RM340**
1	**R1**	37	Ba	Ba	Ba	Ba	**Ba**	Ba	Ba
2	**R2**	71	Ba	Ba	Ba	Ba	**Ba**	Ba	Ba
3	**R3**	91	H	Ba	Ba	Ba	**Ba**	Ba	Ba
4	**R4**	117	PK	Ba	Ba	Ba	**Ba**	Ba	Ba
5	**R5**	123	Ba	Ba	Ba	Ba	**Ba**	Ba	Ba
6	**R6**	130	Ba	Ba	Ba	Ba	**Ba**	PK	PK
7	**R7**	132	PK	Ba	Ba	Ba	**Ba**	Ba	Ba
8	**R8**	148	H	Ba	Ba	Ba	**Ba**	Ba	Ba
9	**R9**	197	H	Ba	Ba	Ba	**Ba**	Ba	Ba
10	**R10**	363	H	Ba	Ba	Ba	**Ba**	Ba	Ba
11	**S1**	24	PK	PK	PK	PK	**PK**	PK	PK
12	**S2**	62	PK	PK	PK	PK	**PK**	PK	PK
13	**S3**	65	Ba	PK	PK	PK	**PK**	PK	PK
14	**S4**	102	PK	PK	PK	PK	**PK**	PK	PK
15	**S5**	110	PK	PK	PK	PK	**PK**	PK	PK
16	**S6**	154	Ba	PK	PK	PK	**PK**	PK	PK
17	**S7**	214	Ba	H	H	Ba	**H**	PK	PK
18	**S8**	262	PK	PK	PK	PK	**PK**	Ba	Ba
19	**S9**	276	PK	PK	PK	PK	**PK**	PK	PK
20	**S10**	383	Ba	PK	PK	PK	**PK**	PK	PK

1.2.4 Determination of closely linked markers by phenotype-genotype association

Four BC_2F_2 plants carrying heterozygous alleles of the linked markers were selfed to generate BC_2F_3 population. 161 BC_2F_3 were evaluated for BB resistance against TXO16. Nine SSR markers RM20523, RM20536, RM3430, RM30, RM7243, RM5509, RM400, RM20590 and RM340 were screened to determine the genotypes of BC_2F_3 individuals. LL of BC_2F_3 individuals was subjected to ANOVA and regression analysis. The result confirmed the location of the resistance gene. LL was highly significantly associated with eight SSR markers including RM20523, RM20536, RM3430, RM30, RM7243, RM5509, RM20590 and RM400 (27.15-28.43

Mb). Multiple regressions indicated that RM20590 was the closest markers to the resistance gene. The RM20590 explained 59.12 % of LL variation in the BC_2F_3 population as shown in Table 10.

Table 10 Phenotype-genotype association analysis using ANOVA and regression analysis in the BC_2F_3 population from the cross between PK and Ba7. Mean of LL was highly significant associated with eight SSR markers. Ba7 = homozygous Ba7, H = heterozygous and PK = homozygous Pin Kaset.

Marker	**Genome position (Mb)**	**R^2**	**Mean of LL (cm)**			
			Ba7	**H**	**PK**	
RM20523	27.15	58.20**	1.6a	5.1b	8.3c	**
RM20536	27.16	48.88**	1.7a	5.0b	8.0c	**
RM30	27.25	58.20**	1.65a	5.09b	8.34c	**
RM3430	27.43	52.00**	1.94a	5.04b	8.24c	**
RM7243	27.56	57.16**	1.48a	5.11b	8.16c	**
RM5509	27.82	58.33**	1.53a	5.17b	8.31c	**
RM20590	28.01	59.12**	1.49a	5.13b	8.41c	**
RM400	28.43	52.23**	1.60a	5.28b	8.30c	**
RM340	28.59	ns	4.48a	5.27a	5.59a	ns

** significant at $P = 0.01$

ns = not significant

a, b and c stand for the clustering value on traits which are significant or not significant

1.2.5 Resistant gene action

The resistant gene possessed by Ba7 was designed as *xa33(t)*. The LL of BC_2F_3 population showed a continuous distribution (Figure 17). The tightly linked markers RM20590 classified BC_2F_3 individuls into three genotypic groups, Ba7/Ba7 (27 plants), Ba7/PK (99 plants) and PK/PK (35 plants). The genotypic groups Ba7/Ba7, Ba7/PK and PK/PK conferred to resistance, moderate resistance and susceptible phenotypes, respectively as shown in Figure 15 and Table 10. This evidence illustrated that resistance gene behave in semi-dominant gene action or incomplete gene action.

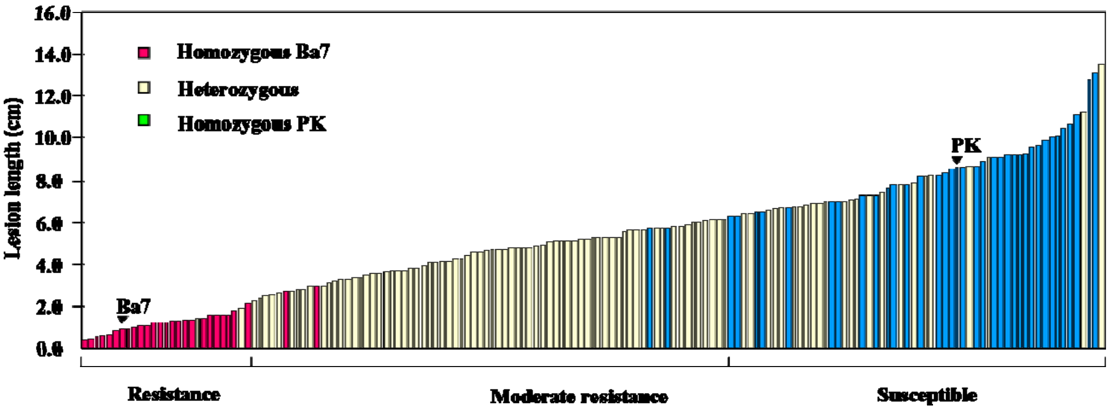


Figure 17 Distribution of BC_2F_3 population for LL after inoculated with TXO16. The red, yellow and blue bars represented for homozygous Ba7 plants, heterozygous plants and homozygous PK plants, respectively. Based on RM20590 genotypes, Ba7 homozygotes, the heterozygotes and PK homozygotes showed resistant, moderately resistant and susceptible phenotypes, respectively.

1.3 Identification of BB resistance in PK

1.3.1 Phenotypic distribution

PK was resistant to *Xoo* isolates TB0304 whereas Ba7 was very susceptible. Frequency distribution of BC_2F_2 population for LL showed continuous skewing toward a lower LL. Figure 18 showed LL of 436 BC_2F_2 plants inoculated with the *Xoo* isolate, TB0304 at seedling stage. LL of PK and Ba7 was 1.5 ± 0.7 cm and 6.7 ± 1.9 cm, respectively. When LL of equal or less than LL of PK was used to classify BC_2F_2 plants, numbers of resistant and susceptible plants were 389 and 47, respectively. The ratio was fit with 8R:1S ($\chi^2 = 1.18$, $p = 0.28$) as it expected that single gene might be responsible for resistant segregating in the BC_2F_2 generation.

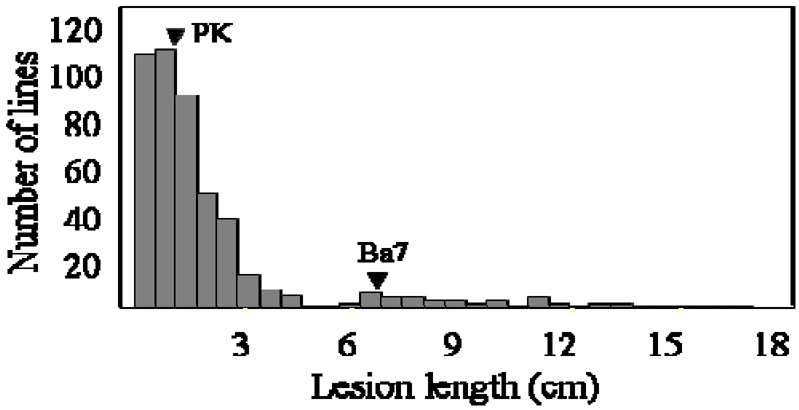


Figure 18 Distribution of BC_2F_2 population for LL after inoculated with the TB0304 isolate. The average LL of PK and Ba7 were 1.5 ± 0.7cm and 6.7 ± 1.9 cm, respectively.

1.3.2 Tagging *Xa34(t)* gene by SSR markers

The resistant gene possessed by PK was designed as *Xa34(t).* LL of BC_2F_2 population was ranged from 0.1-17.3 cm. The ten resistant plants and nine susceptible plants were selected for gene tagging (Figure 19) based on their mean and standard deviation. Of 114 SSR markers, 62 showed very clear polymorphisms between PK and Ba7. These markers were used to genotype 19 BC_2F_2 individual plants (10 resistant and 9 susceptible) and their parents. A SSR marker, RM224 located on the long arm of rice chromosome 11 showed distinguishable banding patterns between resistant and susceptible plants as shown in Figure 20 and Table 11. This marker was located on chromosome 11 in the vicinity of reported *Xa26.*

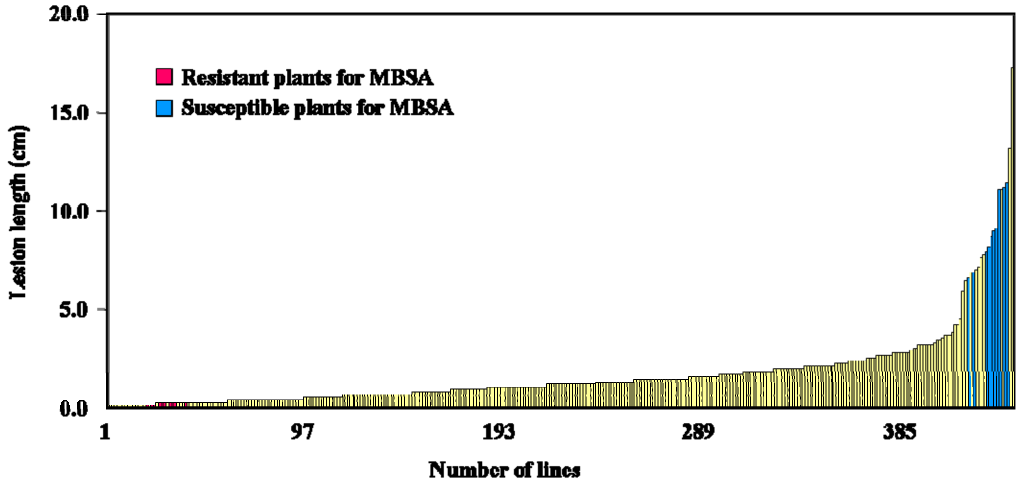


Figure 19 Distribution of 436 BC_2F_2 population for LL inoculated with *Xoo* isolate TB0304. The blue and red bars were BC_2F_2 that using in gene tagging.

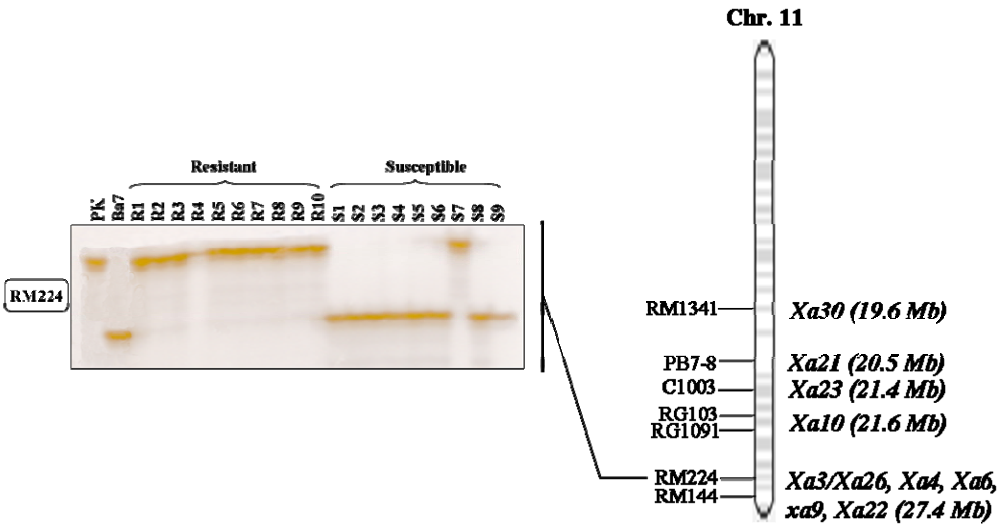


Figure 20 SSR marker RM224 linked to BB resistance gene. This marker was identified resistant and susceptible lines in the BC_2F_2 population. Partial linkage map showed the location of marker and the reported *Xa* genes located in this region.

Table 11 Genotypes of 19 BC_2F_2 lines screened with 15 SSR markers located on chromosome 11, RM224 showed clearly separated between R and S plants as shown with highlight. Ba7 = homozygous Ba7, PK = homozygous Pin Kaset and H = heterozygous.

Entry	**Resistant reaction against TB0304**	**Genome position (Mb)**	**0.4**	**2.3**	**2.7**	**2.7**	**2.8**	**2.8**	**5.7**	**16.6**	**17.7**	**18.3**	**18.8**	**20.5**	**21.6**	**23.7**	**26.7**
		Line no	**RM286**	**RM26071**	**RM26096**	**RM26102**	**RM332**	**RM26108**	**RM120**	**RM287**	**RM209**	**RM229**	**RM21**	**PB78**	**RM206**	**RM254**	**RM224**
1	R	167	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
2	R	180	PK	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
3	R	244	PK	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
4	R	259	Ba7	Ba7	Ba7	Ba7	Ba7	Ba7	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
5	R	298	PK	PK	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**PK**
6	R	307	H	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
7	R	373	PK	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
8	R	419	H	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
9	R	362	PK	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
10	R	377	PK	Ba7	H	H	H	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
11	S	25	PK	-	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**Ba7**
12	S	28	PK	PK	PK	PK	PK	PK	Ba7	PK	PK	PK	PK	PK	PK	PK	**Ba7**
13	S	30	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	**Ba7**
14	S	156	PK	-	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**Ba7**
15	S	184	PK	PK	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**Ba7**
16	S	200	PK	PK	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**Ba7**
17	S	88	H	Ba7	H	H	PK	H	PK	PK	PK	PK	PK	PK	PK	PK	**PK**
18	S	251	PK	PK	PK	PK	PK	PK	H	PK	PK	PK	PK	PK	PK	PK	**Ba7**
19	S	261	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	PK	**Ba7**

1.3.3 DNA banding pattern of IRBB21 and PK using PB7-8

The functional marker PB7-8 was used to identify whether or not PK is carrying *Xa21* gene. IRBB21 (carrying *Xa21*) and PK were screened with PB7-8. The result showed that the amplified fragments of IRBB21 and PK were different in size. IRBB21 carried 1 kb resistant allele of *Xa21*, whereas PK carried 0.7 kb susceptible allele (Figure 21). This indicated that *Xa34(t)* and *Xa21* are not allelic.

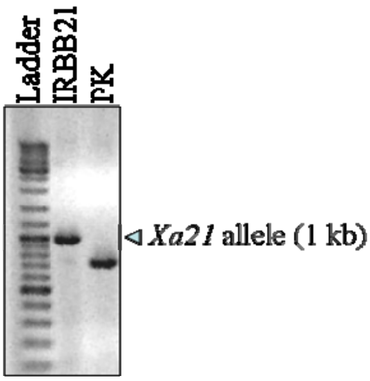


Figure 21 IRBB21 and PK showed different size of amplified fragments of PB7-8 markers.

1.3.4 Resistance reaction pattern among three resistance genes, *Xa21*, *Xa34(t)* and *qBB11*

Three rice varieties, PK, IR1188 and IRBB21 carrying difference genes were evaluated for resistant reaction using 24 *Xoo* isolates. .They showed a race-specific resistance against each isolate except TB0304, TXO103 and TXO109. *Xa21/qBB11*, *Xa34(t)* and *Xa21* were highly resistant against 5, 11 and 6 *Xoo* isolates, respectively. IR1188 carrying *Xa21/qBB11* and IRBB21 carrying *Xa21* had almost the same pattern of resistance against 24 *Xoo* isolates. However, levels of resistance were varied between them. IR1188 and IRBB21 were resistant to TXO7 and TXO16 whereas PK was moderately susceptible to both isolates. In contrary, IR1188 and IRBB21 were susceptible to TXO34, TXO113 and TXO136 whereas PK was resistant to them. This result suggested that *Xa34(t)* and *qBB11* could not be the same gene (Table 12).

Table 12 Resistant reactions (R = resistance, MR = moderate resistance, MS = moderate susceptible and S = susceptible) of PK, IR1188 and IRBB21 against 24 Thai *Xoo* isolates collected from all part of Thailand.

Entry	**Code**	**Location**	**IR1188**	**PK**	**IRBB21**
			Xa21/qBB11	***Xa34(t)***	***Xa21***
1	TB0304	Chiang Rai	R	R	R
2	TXO7	Nakhon Pathom	R	MS	MR
3	TXO16	Phitsanulok	R	MS	MR
4	TXO33	Udon Thani	MR	R	MR
5	TXO34	Udon Thani	S	R	MS
6	TXO37	Phitsanulok	MS	S	MR
7	TXO61	Ubon Ratchathani	MR	R	R
8	TXO73	Kalasin	MR	R	R
9	TXO77	Chiang Rai	MR	R	R
10	TXO85	Surin	R	MR	MR
11	TXO87	Surin	R	MR	MR
12	TXO101	Ubon Ratchathani	MR	R	MR
13	TXO102	Ubon Ratchathani	MR	R	MS
14	TXO103	Ubon Ratchathani	MR	MR	MR
15	TXO107	Ubon Ratchathani	MR	MR	S
16	TXO109	Ubon Ratchathani	MR	MR	MR
17	TXO113	Khon Kaen	MS	MR	MS
18	TXO116	Khon Kaen	MR	MR	MS
19	TXO120	Udon Thani	MR	R	MS
20	TXO134	Roi Et	MR	MR	R
21	TXO136	Ubon Ratchathani	MS	MR	S
22	TXO137	Ubon Ratchathani	MR	R	MR
23	TXO139	Udon Thani	MR	R	R
24	TXO140	Udon Thani	MR	MR	S

2. Pyramiding of BB resistance genes

2.1 Polymorphism of DNA markers in parental lines

RM122, RM153, RM507 and PAxa5 can identify the presence of *xa5* gene. These markers gave the amplified product of 240, 190, 265 and 134 bp respectively in IR62266. Functional marker of the *Xa21* gene, PB7-8, can identify positive allele of *Xa21* (the amplified product of 1,000 bp in IR1188 and 104-4-1-19-7). RM224 can identify the presence of *Xa34(t)* and *qBB11* in the pyramiding population. This marker produced 148 bp and 142 bp amplified products in PK and IR1188/104-4-1-19-7 respectively. RM7243, RM5509 and RM400 were used to identify the *xa33(t)* gene carried by Ba7. Amplified products of Ba7 were 151, 230 and 210 bp fragments respectively. All of linked markers except RM400 showed very clear banding pattern among the pyramiding parents and can be used to identify the resistant allele of *Xa* genes as shown in Table 13.

Table 13 Amplified products of DNA markers among parental lines that used for MAS * indicated the resistance allele, bp = base pair.

Cultivar/gene	Amplified products (bp)								
	RM122	**RM153**	**RM507**	**PAxa5**	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
KDML105	235	207	259	192	700	158	160	249	200
IR62266/xa5	240*	190*	265*	134*	700	158	160	255	205
IR1188/*Xa21+qBB11*	230	210	259	192	1,000*	142*	160	265	210
104-4-1-19-7/*Xa21+qBB11*	235	207	259	192	1,000*	142*	160	249	200
Ba7/*xa33(t)*	230	210	259	192	600	135	151*	230*	210*
PK/*Xa34(t)*	235	207	259	192	700	148*	160	249	200

2.2 Pyramiding of *xa5*, *Xa21* and *qBB11*

Six F_1 plants derived from the cross between line no. 60-0-0 carrying *xa5* and 104-4-1-19-7 carrying *Xa21* and *qBB11* were backcrossed to 104-4-1-19-7 to produce 70 BC_1F_1. Of 70 $BC_1F_{1,}$ 33, 18 and 18 were heterozygous for *xa5* and homozygous for *Xa21* and *qBB11* respectively. Finally, 18 BC_1F_1 were identified carrying all three *Xa* genes. Number of each genotypes was fitted with the expected number in BC_1F_1 generation (35 for heterozygous at *xa5*, 17.5 for homozygous for *Xa21* and *qBB11*. Nine of the eighteen BC_1F_1 plants were selected based on plant-type and backcrossed to 104-4-1-19-7 to develop BC_2F_1 population. Of 103 $BC_2F_{1,}$ 50, 103 and 103 were heterozygous for *xa5* and homozygous for *Xa21* and *qBB11* respectively. In this generation, 50 BC_2F_1 were identified carrying all three *Xa* genes. These BC_2F_1 plants were selfed to generate 1,350 BC_2F_2 population.

In the BC_2F_2, we applied plants-type selection to reduce the population size before subjected to MAS. 213 BC_2F_2 plants were genotyped. Of 213 $BC_2F_{2,}$ 41, 213 and 213 were homozygous for *xa5* and homozygous for *Xa21* and *qBB11* respectively. Finally, 41 BC_2F_2 were identified carrying all three *Xa* genes. The successfully of MAS to discover the target genotypes in BC_1F_1, BC_2F_1 and BC_2F_2 generations were 102, 97 and 77 %, respectively when compared with the theoretic lines (Table 14). These results indicated that molecular marker used in this study were effective.

Table 14 Genotypic and phenotypic selection in pyramiding of *xa5*, *Xa21* and *qBB11*and percent of discovery target genotype by MAS.

Population	**Numbers of lines**	**Linked marker**	**Selection**		**Number of lines (Expected/Observed)**			**Number of selected lines**	**Discovery of target genotype by MAS (%)**
			1st	**2nd**	***xa5***	***Xa21***	***qBB11***		
F_1	6	-	-	-	Het (6)	Het (6)	Het (6)	6	-
BC_1F_1	70	RM122, RM153, RM507, PB7-8, RM224	MAS	Plant-type (9 lines)	Het (35/33)	Homo (17.5/18)	Homo (17.5/18)	18	102
BC_2F_1	103	RM122, RM153, RM507, PAxa5	MAS	-	Het (51.5/50)	Homo (103/103)	Homo (103/103)	50	97
BC_2F_2	1,350	PAxa5	Plant-type (213lines)	MAS	Homo (53.25/41)	Homo (213/213)	Homo (213/213)	41	77

2.3 Pyramiding of *xa5*, *Xa21, xa33(t), Xa34(t)* and *qBB11*

All of F_1 was heterozygous for *xa5 Xa21* and *qBB11*. RM7243, RM5509 and RM400 identified 56, 67 and 54 F_1 carrying the positive allele of *xa33(t)*. Out of 54 F_1, 16 were selected to generate 500 F_2 plants. Numbers of each marker genotype were showed in Table 15. In F_2 generation, the expected numbers were 125, 250 and 125 for homozygous resistant, heterozygous and homozygous susceptible for each marker respectively while the observed numbers were ranged from 110-134, 237-265 and 117-146 for homozygous resistant, heterozygous and homozygous susceptible respectively. Thirty two lines consisted of eight combinations of gene pyramiding were selected as shown in Table 16. The discovery target genotypes by MAS in F_1 and F_2 were 31 and 25 %, respectively when compared with the theoretical expectation.

Eleven F_2 lines carrying some heterozygous at the target genes were selected to generate 392 F_3 plants for one more round of MAS to discover more combinations of the pyramiding genes. The number of selected homozygous were agreed with the expected value as shown in Table 17. In this generation, 11 gene combinations were identified however 8 of them were selected. Finally, of 26 expected gene combinations, 16 were identified in our study (Table 18). The rest of the gene combinations that can not be discovered in this experiment due to the closely linked of the *Xa34(t)* and *qBB11*.

Table 15 Genotypic and phenotypic selection in pyramiding of *xa5*, *Xa21*, *xa33(t)*, *Xa34(t)* and percent of discovery target genotype by MAS.

Generation	**Numbers of lines**	**Genotype**	**Number of lines (Expected/Observed)**							**Number of selected lines**	**Discovery of target genotype by MAS (%)**
			xa5	***Xa21***	***xa33(t)***			***Xa34(t)***	***qBB11***		
			PAxa5	**PB7-8**	**RM7243**	**RM5509**	**RM400**	**RM224**	**RM224**		
F_1	104	Homozygous resistance	-	-	-	-	-	-	-		
		Heterozygous	104/104	104/104	52/56	52/67	52/54	-	104/104	16	31
		Homozygous susceptible	-	-	52/48	52/34	52/50	-	-		
		Missing data	-	-	-	3	-	-	-		
F_2	500	Homozygous resistance	125/112	125/134	125/122	125/121	125/110	125/130	125/133	32	25
		Heterozygous	250/265	250/249	250/252	250/253	250/244	250/237			
		Homozygous susceptible	125/123	125/117	125/126	125/126	125/146	-	-		
		Missing data	-	-	-	-	-	-	-		

Table 16 Line numbers, pedigree and genotype of 32 F_2 pyramid lines . + = present of resistance gene.

Entry	**Line no**	**Pedigree**	**BB resistance gene**				
			xa5	***Xa21***	***xa33(t)***	***Xa34(t)***	***qBB11***
1	241	RGDU07099-1-8MKPS	+	+	+		+
2	359	RGDU07099-5-3M	+	+	+		+
3	497	RGDU07099-8-27M	+	+	+		+
4	23	RGDU07097-1-8M	+	+	+		+
5	112	RGDU07097-20-3M	+	+	+		+
6	169	RGDU07097-27-29M	+	+	+		+
7	307	RGDU07099-2-39M	+	+	+		+
8	32	RGDU07097-1-17M	+	+			+
9	214	RGDU07097-28-36M	+	+			+
10	126	RGDU07097-26-8M		+	+		+
11	293	RGDU07099-2-25M		+	+		+
12	330	RGDU07099-3-21M		+	+		+
13	317	RGDU07099-3-8M		+	+		+
14	42	RGDU07097-1-27M	+		+	+	
15	45	RGDU07097-1-30M	+		+	+	
16	57	RGDU07097-1-42M	+		+	+	
17	157	RGDU07097-27-17M	+		+	+	
18	210	RGDU07097-28-32M	+		+	+	
19	181	RGDU07097-28-3M		+			+
20	200	RGDU07097-28-22M		+			+
21	338	RGDU07099-3-29M		+			+
22	344	RGDU07099-3-35M		+			+
23	13	RGDU07096-2-13	+			+	
24	399	RGDU07099-5-43M	+			+	
25	96	RGDU07097-15-26M	+			+	
26	124	RGDU07097-26-6M	+			+	
27	491	RGDU07099-8-21M	+			+	
28	192	RGDU07097-28-14M			+	+	
29	428	RGDU07099-6-8M			+	+	
30	67	RGDU07097-12-1M			+	+	
31	374	RGDU07099-5-18M			+	+	
32	358	RGDU07099-5-2M			+	+	

Table 17 Line numbers, pedigree and genotype of 11 F_2 pyramid lines that used for MAS in F_3 generation. Genotypic and phenotypic selection in F_3 pyramiding population and percent of discovery target genotype by MAS. + = present of resistance gene H = heterozygous.

Entry	**Line no**	**Pedigree**	**BB resistance genes**					**Number of lines**	**Number of lines (Expected/Observed)**				**Number of selected lines**	**Discovery of target genotype by MAS (%)**
									xa5	***Xa21***	***Xa34(t)***	***qBB11***		
			xa5	***Xa21***	***xa33(t)***	***Xa34(t)***	***qBB11***		**PAxa5**	**PB7-8**	**RM224**	**RM224**		
1	12	RGDU07096-2-12M	+				H	20			5/2	5/5	7	70
2	16	RGDU07097-1-1M	+				H	20			5/5	5/5	10	100
3	41	RGDU07097-1-26M	+	H		+		20		5/6			6	120
4	62	RGDU07097-1-47M	+				H	20			5/5	5/5	10	100
5	82	RGDU07097-15-12M		H		+		59		14.75/22			22	149
6	250	RGDU07099-1-17M	+	H	+		+	55		13.75/13			13	95
7	257	RGDU07099-1-24M	+	H		+		40		10/7			7	70
8	277	RGDU07099-2-9M	H				+	60	15/14				14	93
9	280	RGDU07099-2-12M	H	+	+	+		58	14.5/9				9	62
10	439	RGDU07099-6-19M	+	H		+		20		5/3			3	60
11	472	RGDU07099-8-2M	H	+		+		20	5/8				8	160

Table 18 Gene combinations and number of F_2 and F_3 plants carrying homozygous allele of the genes.

Entry	**Combination**	**Gene combinations**	**Homozygous plant**		**Total of homozygous lines**
			F_2	**F_3**	
1	1 gene	*xa5*	-	-	-
2		*Xa21*	-	-	-
3		*xa33(t)*	-	-	-
4		*Xa34(t)*	6	9	15
5		*qBB11*	-	14	14
6	2 genes	*xa5/Xa21*	-	-	-
7		*xa5/xa33(t)*	-	-	-
8		*xa5/Xa34(t)*	5	29	34
9		*xa5/qBB11*	-	34	34
10		*Xa21/xa33(t)*	-	-	-
11		*Xa21/Xa34(t)*	-	27	27
12		*Xa21/qBB11*	6	-	6
13		*xa33(t)/Xa34(t)*	5	23	28
14		*xa33(t)/qBB11*	-	26	26
15		*Xa34(t)/qBB11*	-	-	-
16	3 genes	*xa5/Xa21/xa33(t)*	-	-	-
17		*xa5/Xa21/Xa34(t)*	-	24	24
18		*xa5/Xa21/qBB11*	2	-	2
19		*xa5/xa33(t)/Xa34(t)*	5	-	5
20		*xa5/xa33(t)/qBB11*	-	15	15
21		*Xa21/xa33(t)/Xa34(t)*	-	16	16
22		*Xa21/xa33(t)/qBB11*	4	-	4
23		*xa33(t)/Xa34(t)/qBB11*	-	-	-
24	4 genes	*xa5/Xa21/xa33(t)/Xa34(t)*	-	9	9
25		*xa5/Xa21/xa33(t)/qBB11*	7	13	20
26	5 genes	*xa5/Xa21/xa33(t)/Xa34(t) /qBB11*	-	-	-

2.4 Evaluation of BB resistance in parental lines

The parental lines including IR62266, IR1188, Ba7, KDML105 and PK were evaluated for resistance against 44 *Xoo* isolates. KDML105 was susceptible to all isolates except TXO148. IR62266 carrying *xa5* was resistant to all isolates. IR1188, Ba7 and PK carrying *Xa21/qBB11*, *xa33(t)* and *Xa34(t)* were resistant against 14, 17 and 23 isolates, respectively. IR1188 was moderate resistant against 24 isolates while Ba7 and PK were moderate resistant against 19 and 15 isolates, respectively. These result indicated that *xa5* was the most effective follow by *Xa34(t)*, *xa33(t)* and

Xa21/qBB11. Moreover, the resistance reaction of *Xa21/qBB11* was skewed toward the moderate resistance (Table 19).

Table 19 Resistant reactions (R = resistance, MR = moderate resistance, MS = moderate susceptible and S = susceptible) of KDML105, IR62266, IR1188, Ba7, and PK against 44 Thai *Xoo* isolates collected from all part of Thailand.

Entry	**Isolate code**	**KDML105** **-**	**IR62266** ***xa5***	**IR1188** ***Xa21/qBB11***	**Ba7** ***xa33(t)***	**PK** ***Xa34(t)***
1	TB0304	S	R	R	S	R
2	TXO7	S	R	R	R	MS
3	TXO16	S	R	R	R	MS
4	TXO33	S	R	MR	R	R
5	TXO34	MS	R	S	MR	R
6	TXO37	S	R	MS	R	S
7	TXO54	S	R	MR	S	R
8	TXO60	S	R	MS	MR	S
9	TXO61	S	R	MR	MR	R
10	TXO73	S	R	MR	R	R
11	TXO77	S	R	MR	MR	R
12	TXO85	S	R	R	R	MR
13	TXO86	S	R	R	MR	R
14	TXO87	S	R	R	MR	MR
15	TXO91	S	R	R	R	R
16	TXO93	MS	R	R	R	R
17	TXO95	S	R	R	R	R
18	TXO96	S	R	R	MR	R
19	TXO98	S	R	MR	R	R
20	TXO101	S	R	MR	MR	R
21	TXO102	S	R	MR	MR	R
22	TXO103	S	R	MR	MR	MR
23	TXO104	S	R	MS	MR	MR
24	TXO105	S	R	R	R	R
25	TXO107	S	R	MR	MR	MR
26	TXO108	S	R	MR	MS	MR
27	TXO109	S	R	MR	R	MR
28	TXO113	S	R	MS	MR	MR
29	TXO116	S	R	MR	R	MR
30	TXO120	S	R	MR	R	R
31	TXO133	S	R	R	MS	MR
32	TXO134	S	R	MR	MS	MR
33	TXO136	S	R	MS	S	MR
34	TXO137	S	R	MR	MR	R

Table 19 (Continued)

Entry	**Isolate code**	**KDML105** **-**	**IR62266** ***xa5***	**IR1188** ***Xa21/qBB11***	**Ba7** ***xa33(t)***	**PK** ***Xa34(t)***
35	TXO139	MS	R	MR	R	R
36	TXO140	S	R	MR	S	MR
37	TXO141	S	R	MR	R	MS
38	TXO142	S	R	MR	S	R
39	TXO148	MR	R	R	MR	R
40	TXO149	S	R	MR	MR	MR
41	TXO151	S	R	MR	MR	MR
42	TXO152	S	R	MR	R	R
43	TXO153	S	R	R	MR	MS
44	TXO154	S	R	MR	MR	R
	R	0	44	14	17	23
	MR	1	0	24	19	15
	MS	3	0	5	3	4
	S	40	0	1	5	2

In this study, we found that some isolates can breakdown the resistance genes in the parental lines. TXO34, TXO104 and TXO133 can overcome resistant genes *Xa21* and *qBB11* in IR1188 while TB0304, TXO54, TXO108, TXO133, TXO134, TXO140 and TXO142 can overcome resistant gene *xa33(t)* in Ba7. Furthermore, TXO7, TXO16, TXO141 and TXO153 can infect PK which carrying *Xa34(t)*. Based on this specificity and our previous experiments, 4 BB isolates TB0304, TXO16, TXO34 and TXO133 were used for evaluation of BB resistance reaction in the pyramid lines.

2.5 Evaluation of resistance in parental lines and pyramiding lines

In order to validate the efficiency of MAS, twenty eight F_4 pyramid lines fixed as homozygous at the target allele of BB resistant genes were evaluated with six *Xoo* isolates TB0304, TXO16, TXO34, TXO37, TXO107 and TXO133. KDML105 showed very susceptible to all *Xoo* isolates while IR62266 harboring *xa5* showed high resistance to all four isolates. IR1188 harboring *Xa21*/*qBB11* exhibited high resistance to five isolates except TXO37 that showed a moderate resistance whereas 104-4-1-19-7 also harboring *Xa21/qBB11* genes showed moderate susceptible and susceptible against *Xoo* isolate TXO34 and TXO37, respectively. This result indicated that *Xa21* and *qBB11* in rice IR1188 genetic background exhibited higher resistance than 104-4-1-19-7 genetic background. Ba7 harboring *xa33(t)* showed high resistance to TXO16 and TXO34, moderate resistance to TXO107, moderate susceptible to TXO133 and susceptible to TB0304. In contrary, PK harboring *Xa34(t)* showed very high resistance to TB0304 and TXO34, moderate resistance to TXO107 and TXO133 and moderate susceptible to TXO16 and TXO37. The phenotypic distribution among parental lines against all six isolates was illustrated in Figure 22.

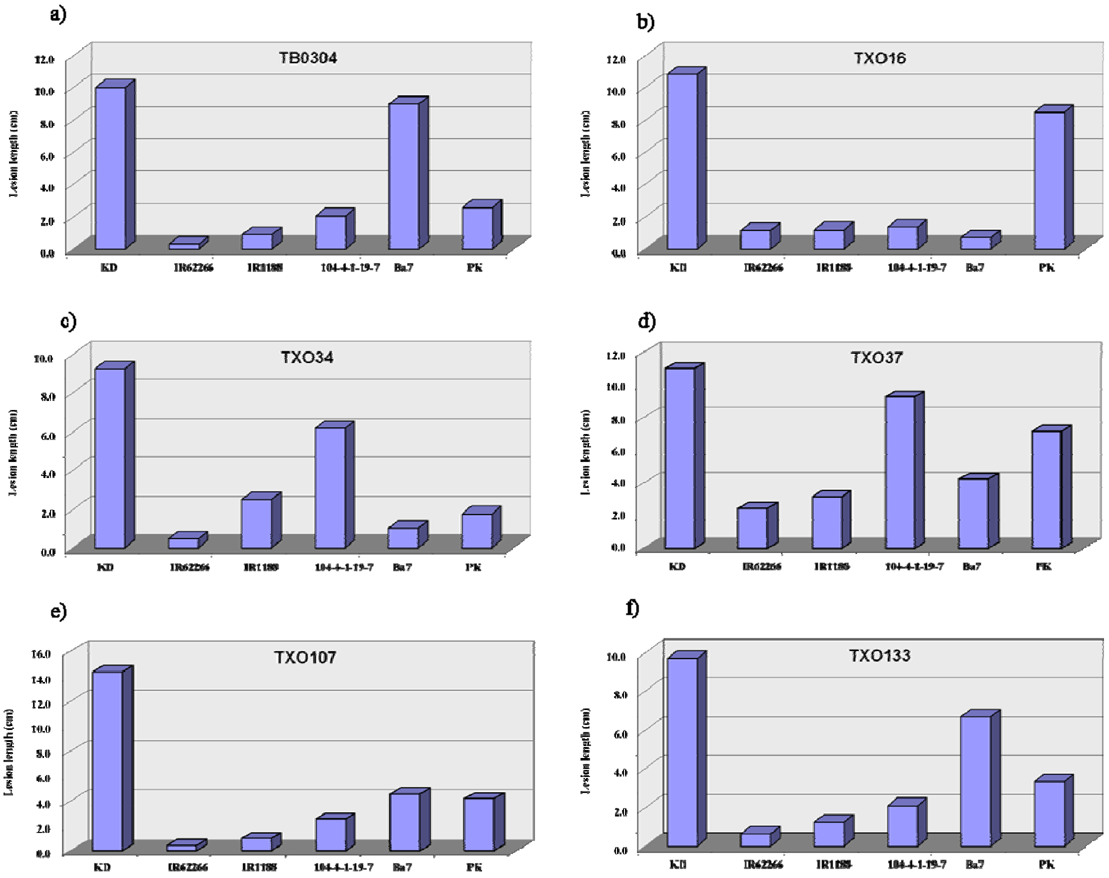


Figure 22 LL of parental lines after inoculated with four *Xoo* isolates a) TB0304, b) TXO16, c) TXO34, d) TXO37, e) TXO107 and f) TXO133.

In BB evaluation experiments, KDML105 showed susceptibility whereas IR62266 showed resistance to all six *Xoo* isolates. LL of KDML105 and IR62266 were ranged from 9.3-14.4 cm and 0.3-2.5 cm, respectively. When inoculated with TB0304, LL of KDML105 and Ba7 were 10.0 ± 3.1 and 9.0 ± 2.0 cm, respectively. Whereas LL of other parents that showed high resistance reaction was ranged from 0.3 - 2.6 cm. All pyramided lines showed high resistance to TB0304. The LL of pyramid lines was ranged from 0.1 - 1.8 cm.

In TXO16 innoculation, LL of KDML105 and PK were 10.9 ± 3.1 and 8.5 ± 1.7, respectively. Whereas LL of other parents that showed high resistance reaction was ranged from 0.7 - 1.3 cm. All pyramid lines showed high resistance reaction. LL of the pyramid lines were ranged from 0.2 - 2.7 cm.

In TXO34 innoculation, LL of KDML105 and 104-4-1-19-7 were 9.3 ± 1.9 and 6.2 ± 2.0 cm, respectively. Whereas LL of other parents that showed high resistance reaction was ranged from 0.5 - 2.5 cm. Most but not all of pyramid lines showed a high resistance reaction. Two pyramid lines carrying *Xa21/qBB11* showed moderate resistance. LL of the pyramid lines were ranged from 0.2 – 3.9 cm.

In TXO37 innoculation, LL of KDML105, 104-4-1-19-7, PK, IR1188 and Ba7 were 11.0 ± 3.3, 9.3 ± 2.6, 7.2 ± 1.5, 3.7 ± 1.4 and 4.2 ± 1.6 cm, respectively. Whereas LL of IR62266 that showed high resistance reaction was 2.5 ± 0.8 cm. Most but not all of pyramid lines showed a high resistance reaction. Four pyramid lines carrying *qBB11*, *Xa21/qBB11* and *xa33(t)/qBB11* showed moderate resistance. LL of the resistant pyramid lines and moderate resistant pyramid lines were rang from 1.1 - 2.8 cm and 3.7 – 4.2 cm, respectively.

In TXO107 innoculation, LL of KDML105, Ba7 and were 14.4 ± 2.8, 4.2 ± 1.6 and 4.2 ± 2.8 cm, respectively. Whereas LL of other parents that showed high resistance reaction was ranged from 0.4 - 2.5 cm. Most but not all of pyramid lines showed a high resistance reaction. One pyramiding line carrying only *qBB11* was moderate resistance. LL of the resistant pyramid lines were ranged from 0.2 – 2.4 cm while moderate resistant pyramid line was 3.6 ± 2.8 cm.

In TXO133 innoculation, LL of KDML105, Ba7 and PK were 9.7 ± 3.1, 6.7 ± 2.6 and 3.3 ± 1.6, respectively. Whereas LL of other parents that showed high resistance reaction was ranged from 0.6 - 2.1 cm. All pyramid lines showed high resistance reaction. LL of the pyramid lines were ranged from 0.3 - 2.0 cm. These results were shown in Table 20. These incidents suggesting that *Xoo* pathogens which virulent to individual *Xa* genes can not overcome these resistance genes when they were combined into the single genotype. Most of pyramid lines carrying *qBB11* gene showed less resistant than lines carrying *Xa34(t)*. Moreover, the pyramid lines with two, three and four genes showed higher resistance than those with single gene as illustrated in Figure 23-25.

Table 20 The resistant reaction in selected F_4 pyramid lines containing various combinations of BB resistance genes evaluated with four *Xoo* isolates. The disease reaction was shown by LL (cm) after inoculation at seedling stage in winter 2008.

Entry	Pedigree	Gene (s)	**Lesion length (mean±*sd* ; cm)**								
			B0304	**		**TXO16**	**		**TXO34**	**	
1	KDML105	Check	10.0 ± 3.1	a	S	10.9 ± 3.1	a	S	9.3 ± 1.9	a	S
2	IR62266	*xa5*	0.3 ± 0.2	lm	R	1.2 ± 0.4	efghij	R	0.5 ± 0.4	ijk	R
3	IR1188	*Xa21/qBB11*	0.9 ± 0.5	ghij	R	1.2 ± 0.6	efghij	R	2.5 ± 1.2	d	R
4	104-4-1-19-7	*Xa21/qBB11*	2.0 ± 1.0	d	R	1.3 ± 0.5	efg	R	**6.2 ± 2.0**	**b**	**MS**
5	Ba7	*xa33(t)*	**9.0 ± 2.0**	**b**	**S**	0.7 ± 0.9	ijklmno	R	1.0 ± 1.2	gh	R
6	PK	*Xa34(t)*	2.6 ± 1.0	c	R	**8.5 ± 1.7**	**b**	**MS**	1.8 ± 0.9	e	R
7	RGDU07099-2-9M-18M	*qBB11*	1.1 ± 0.8	ghi	R	1.5 ± 0.8	e	R	2.5 ± 1.3	d	R
8	RGDU07097-1-1M-5M	*xa5/qBB11*	1.8 ± 0.6	de	R	1.5 ± 0.5	e	R	0.9 ± 0.4	ghi	R
10	RGDU07099-2-9M-8M	*xa5/qBB11*	0.6 ± 0.4	ijkl	R	1.0 ± 0.7	fghijkl	R	1.5 ± 1.2	ef	R
11	RGDU07097-15-26M-8KPS	*xa5/Xa34(t)*	0.3 ± 0.2	lm	R	1.2 ± 0.4	efgh	R	0.2 ± 0.2	k	R
12	RGDU07099-8-21M-5KPS	*xa5/Xa34(t)*	0.4 ± 0.4	klm	R	1.1 ± 0.5	efghijk	R	0.2 ± 0.1	k	R
13	RGDU07097-28-3M-1KPS	*Xa21/qBB11*	1.6 ± 0.9	ef	R	1.3 ± 0.7	efg	R	3.9 ± 1.9	c	MR
14	RGDU07097-28-3M-3KPS	*Xa21/qBB11*	1.3 ± 0.8	fgh	R	1.3 ± 0.6	efg	R	3.7 ± 2.4	c	MR
15	RGDU07097-15-12M-3	*Xa21/Xa34(t)*	0.6 ± 0.4	ijklm	R	1.1 ± 0.5	efghij	R	1.1 ± 0.5	fg	R
16	RGDU07097-15-12M-4	*Xa21/Xa34(t)*	0.8 ± 0.4	ijk	R	1.2 ± 0.5	efghij	R	0.9 ± 0.5	ghi	R
17	RGDU07099-5-51M-23M	*xa33(t)/qBB11*	1.4 ± 0.9	efg	R	2.7 ± 2.0	d	R	0.3 ± 0.4	k	R
18	RGDU07097-28-14M-4KPS	*xa33(t)/Xa34(t)*	0.9 ± 0.5	ij	R	1.4 ± 0.8	ef	R	0.4 ± 0.6	ij	R
19	RGDU07099-6-8M-5KPS	*xa33(t)/Xa34(t)*	0.4 ± 0.3	klm	R	0.5 ± 0.6	lmnop	R	0.2 ± 0.2	k	R
20	RGDU07097-1-17M-1KPS	*xa5/Xa21/qBB11*	0.8 ± 0.3	ijk	R	0.9 ± 0.5	ghijklm	R	0.9 ± 0.3	ghij	R
21	RGDU07097-1-17M-2KPS	*xa5/Xa21/qBB11*	0.9 ± 0.3	ij	R	0.8 ± 0.3	hijklmn	R	1.0 ± 0.2	gh	R

Table 20 (Continued)

Entry	Pedigree	Gene (s)	**Lesion length (mean±*sd* ; cm)**								
			B0304	******		**TXO16**	******		**TXO34**	******	
1	KDML105	Check	10.0 ± 3.1	a	S	10.9 ± 3.1	a	S	9.3 ± 1.9	a	S
2	IR62266	*xa5*	0.3 ± 0.2	lm	R	1.2 ± 0.4	efghij	R	0.5 ± 0.4	ijk	R
3	IR1188	*Xa21/qBB11*	0.9 ± 0.5	ghij	R	1.2 ± 0.6	efghij	R	2.5 ± 1.2	d	R
4	104-4-1-19-7	*Xa21/qBB11*	2.0 ± 1.0	d	R	1.3 ± 0.5	efg	R	**6.2 ± 2.0**	**b**	**MS**
5	Ba7	*xa33(t)*	**9.0 ± 2.0**	**b**	**S**	0.7 ± 0.9	ijklmno	R	1.0 ± 1.2	gh	R
6	PK	*Xa34(t)*	2.6 ± 1.0	c	R	**8.5 ± 1.7**	**b**	**MS**	1.8 ± 0.9	e	R
22	RGDU07097-1-26M-9M	*xa5/Xa21/Xa34(t)*	0.3 ± 0.3	lm	R	0.8 ± 0.4	hijklmn	R	0.3 ± 0.4	k	R
23	RGDU07097-1-26M-6M	*xa5/Xa21/Xa34(t)*	0.3 ± 0.2	lm	R	0.7 ± 0.3	klmnop	R	0.2 ± 0.2	k	R
24	RGDU07099-1-17M-2M	*xa5/xa33(t)/qBB11*	0.7 ± 0.4	ijk	R	0.4 ± 0.4	nop	R	0.2 ± 0.2	k	R
25	RGDU07097-1-26M-10M	*xa5/xa33(t)/qBB11*	0.3 ± 0.2	lm	R	1.1 ± 0.4	efghijk	R	0.3 ± 0.4	k	R
26	RGDU07097-1-27M-1KPS	*xa5/xa33(t)/Xa34(t)*	0.3 ± 0.3	lm	R	0.4 ± 0.3	mnop	R	0.2 ± 0.1	k	R
27	RGDU07097-1-30M-1KPS	*xa5/xa33(t)/Xa34(t)*	0.2 ± 0.4	lm	R	0.4 ± 0.3	mnop	R	0.3 ± 0.3	k	R
28	RGDU07097-26-8M-1KPS	*Xa21/xa33(t)/qBB11*	0.9 ± 0.6	hi	R	0.3 ± 0.2	op	R	0.6 ± 0.5	hijk	R
29	RGDU07099-2-25M-4KPS	*Xa21/xa33(t)/qBB11*	0.5 ± 0.5	jklm	R	0.2 ± 0.2	p	R	0.4 ± 0.4	jk	R
30	RGDU07099-2-12M-5M	*Xa21/xa33(t)/Xa34(t)*	0.2 ± 0.1	m	R	0.3 ± 0.2	op	R	0.3 ± 0.4	k	R
31	RGDU07099-2-12M-9M	*Xa21/xa33(t)/Xa34(t)*	0.2 ± 0.2	lm	R	0.5 ± 0.3	lmnop	R	0.3 ± 0.4	k	R
32	RGDU07099-5-3M-23KPS	*xa5/Xa21/Xa33/qBB11*	0.4 ± 0.4	jklm	R	0.5 ± 0.4	lmnop	R	0.2 ± 0.1	k	R
33	RGDU07097-1-8M-9KPS	*xa5/Xa21/xa33(t)/qBB11*	0.5 ± 0.4	jklm	R	0.3 ± 0.2	op	R	0.4 ± 0.5	k	R
34	RGDU07099-2-12M-10M	*xa5/Xa21/xa33(t)/Xa34(t)*	0.1 ± 0.1	m	R	0.6 ± 0.4	lmnop	R	0.2 ± 0.3	k	R
35	RGDU07099-2-12M-13M	*xa5/Xa21/xa33(t)/Xa34(t)*	0.2 ± 0.2	m	R	0.7 ± 0.5	jklmnop	R	0.3 ± 0.4	k	R

Table 20 (Continued)

Entry	Pedigree	Gene (s)	Lesion length (mean±*sd* ; cm)					
			TXO37 **		**TXO107 ****		**TXO133 ****	
1	KDML105	Check	11.0 ± 3.3 ^{a}	S	14.4 ± 2.8 ^{a}	S	9.7 ± 3.1 ^{a}	S
2	IR62266	*xa5*	2.5 ± 0.8 ^{efghij}	R	0.4 ± 0.3 ^{hijk}	R	0.6 ± 0.4 ^{ijklmn}	R
3	IR1188	*Xa21/qBB11*	3.7 ± 1.4 ^{de}	**MR**	1.0 ± 0.9 ^{fg}	R	1.2 ± 0.6 ^{efgh}	R
4	104-4-1-19-7	*Xa21/qBB11*	9.3 ± 2.6 ^{b}	**S**	2.5 ± 0.9 ^{e}	R	2.1 ± 1.2 ^{d}	R
5	Ba7	*xa33(t)*	4.2 ± 1.6 ^{c}	**MR**	4.5 ± 2.8 ^{c}	**MR**	**6.7 ± 2.6** ^{b}	**MS**
6	PK	*Xa34(t)*	7.2 ± 1.5 ^{b}	**MS**	4.2 ± 1.6 ^{cd}	**MR**	3.3 ± 1.6 ^{c}	MR
7	RGDU07099-2-9M-18M	*qBB11*	4.2 ± 1.7 ^{c}	MR	3.6 ± 2.8 ^{d}	MR	1.1 ± 0.7 ^{efghi}	R
9	RGDU07097-1-1M-5M	*xa5/qBB11*	2.8 ± 1.1 ^{efg}	R	2.2 ± 1.1 ^{e}	R	2.0 ± 0.8 ^{d}	R
10	RGDU07099-2-9M-8M	*xa5/qBB11*	2.8 ± 1.4 ^{efg}	R	2.2 ± 1.5 ^{e}	R	1.0 ± 0.8 ^{fghij}	R
11	RGDU07097-15-26M-8KPS	*xa5/Xa34(t)*	2.3 ± 0.9 ^{efghijkl}	R	0.6 ± 0.4 ^{ghijk}	R	0.3 ± 0.2 ^{n}	R
12	RGDU07099-8-21M-5KPS	*xa5/Xa34(t)*	2.8 ± 1.2 ^{ef}	R	0.9 ± 0.6 ^{fghi}	R	0.7 ± 0.6 ^{ghijklmn}	R
13	RGDU07097-28-3M-1KPS	*Xa21/qBB11*	3.7 ± 1.0 ^{cd}	MR	2.3 ± 1.1 ^{e}	R	1.7 ± 1.0 ^{de}	R
14	RGDU07097-28-3M-3KPS	*Xa21/qBB11*	3.8 ± 1.9 ^{cd}	MR	2.4 ± 1.3 ^{e}	R	1.9 ± 1.2 ^{d}	R
15	RGDU07097-15-12M-3	*Xa21/Xa34(t)*	1.8 ± 1.5 ^{ijklmn}	R	0.6 ± 0.4 ^{ghijk}	R	0.6 ± 0.3 ^{hijklmn}	R
16	RGDU07097-15-12M-4	*Xa21/Xa34(t)*	2.3 ± 1.2 ^{efghijk}	R	0.8 ± 0.4 ^{fghijk}	R	0.6 ± 0.3 ^{ghijklmn}	R
17	RGDU07099-5-51M-23M	*xa33(t)/qBB11*	4.1 ± 1.6 ^{c}	MR	0.8 ± 0.8 ^{fghij}	R	1.6 ± 0.8 ^{de}	R
18	RGDU07097-28-14M-4KPS	*xa33(t)/Xa34(t)*	2.6 ± 1.4 ^{efghi}	R	0.4 ± 0.4 ^{hijk}	R	1.3 ± 0.7 ^{ef}	R
19	RGDU07099-6-8M-5KPS	*xa33(t)/Xa34(t)*	2.7 ± 1.5 ^{efgh}	R	0.3 ± 0.2 ^{k}	R	0.7 ± 0.8 ^{ghijklmn}	R
20	RGDU07097-1-17M-1KPS	*xa5/Xa21/qBB11*	2.1 ± 1.4 ^{fghijklm}	R	1.2 ± 0.4 ^{f}	R	1.0 ± 0.3 ^{fghijk}	R
21	RGDU07097-1-17M-2KPS	*xa5/Xa21/qBB11*	2.2 ± 1.2 ^{fghijkl}	R	1.2 ± 0.3 ^{f}	R	1.1 ± 0.3 ^{efghi}	R

Table 20 (Continued)

Entry	Pedigree	Gene (s)	Lesion length (mean±*sd* ; cm)					
			TXO37 **		**TXO107 ****		**TXO133 ****	
1	KDML105	Check	11.0 ± 3.3 ^{a}	S	14.4 ± 2.8 ^{a}	S	9.7 ± 3.1 ^{a}	S
2	IR62266	*xa5*	2.5 ± 0.8 ^{efghij}	R	0.4 ± 0.3 ^{hijk}	R	0.6 ± 0.4 ^{ijklmn}	R
3	IR1188	*Xa21/qBB11*	3.7 ± 1.4 ^{de}	**MR**	1.0 ± 0.9 ^{fg}	R	1.2 ± 0.6 ^{efgh}	R
4	104-4-1-19-7	*Xa21/qBB11*	9.3 ± 2.6 ^{b}	**S**	2.5 ± 0.9 ^{e}	R	2.1 ± 1.2 ^{d}	R
5	Ba7	*xa33(t)*	4.2 ± 1.6 ^{c}	**MR**	4.5 ± 2.8 ^{c}	**MR**	**6.7 ± 2.6 ^{b}**	**MS**
6	PK	*Xa34(t)*	7.2 ± 1.5 ^{b}	**MS**	4.2 ± 1.6 ^{cd}	**MR**	3.3 ± 1.6 ^{c}	MR
22	RGDU07097-1-26M-9M	*xa5/Xa21/Xa34(t)*	1.4 ± 0.7 ^{mn}	R	0.4 ± 0.3 ^{hijk}	R	0.5 ± 0.4 ^{jklmn}	R
23	RGDU07097-1-26M-6M	*xa5/Xa21/Xa34(t)*	1.5 ± 0.6 ^{lmn}	R	0.3 ± 0.2 ^{ijk}	R	0.4 ± 0.2 ^{jklmn}	R
24	RGDU07099-1-17M-2M	*xa5/xa33(t)/qBB11*	1.5 ± 0.8 ^{klmn}	R	0.9 ± 0.4 ^{fgh}	R	0.7 ± 0.3 ^{ghijklmn}	R
25	RGDU07097-1-26M-10M	*xa5/xa33(t)/qBB11*	1.9 ± 0.6	R	0.3 ± 0.2 ^{hijk}	R	0.5 ± 0.3 ^{jklmn}	R
26	RGDU07097-1-27M-1KPS	*xa5/xa33(t)/Xa34(t)*	1.9 ± 0.7 ^{hijklm}	R	0.3 ± 0.2 ^{k}	R	0.5 ± 0.3 ^{jklmn}	R
27	RGDU07097-1-30M-1KPS	*xa5/xa33(t)/Xa34(t)*	1.5 ± 0.6 ^{lmn}	R	0.2 ± 0.2 ^{k}	R	0.3 ± 0.2 ^{n}	R
28	RGDU07097-26-8M-1KPS	*Xa21/xa33(t)/qBB11*	1.4 ± 1.2 ^{mn}	R	0.3 ± 0.2 ^{jk}	R	1.2 ± 0.6 ^{efg}	R
29	RGDU07099-2-25M-4KPS	*Xa21/xa33(t)/qBB11*	1.1 ± 0.9 ^{n}	R	0.5 ± 0.5 ^{ghijk}	R	0.5 ± 0.4 ^{jklmn}	R
30	RGDU07099-2-12M-5M	*Xa21/xa33(t)/Xa34(t)*	2.0 ± 1.3 ^{fghijklm}	R	0.2 ± 0.2 ^{k}	R	0.3 ± 0.2 ^{n}	R
31	RGDU07099-2-12M-9M	*Xa21/xa33(t)/Xa34(t)*	2.1 ± 1.5 ^{fghijkl}	R	0.4 ± 0.5 ^{hijk}	R	0.4 ± 0.2 ^{klmn}	R
32	RGDU07099-5-3M-23KPS	*xa5/Xa21/Xa33/qBB11*	1.5 ± 0.6 ^{lmn}	R	0.4 ± 0.4 ^{ghijk}	R	0.9 ± 0.5 ^{fghijkl}	R
33	RGDU07097-1-8M-9KPS	*xa5/Xa21/xa33(t)/qBB11*	1.7 ± 0.9 ^{jklmn}	R	0.3 ± 0.1 ^{k}	R	0.9 ± 0.4 ^{fghijklm}	R
34	RGDU07099-2-12M-10M	*xa5/Xa21/xa33(t)/Xa34(t)*	1.5 ± 0.7 ^{klmn}	R	0.3 ± 0.2 ^{ijk}	R	0.3 ± 0.3 ^{lmn}	R
35	RGDU07099-2-12M-13M	*xa5/Xa21/xa33(t)/Xa34(t)*	1.7 ± 0.7 ^{ijklmn}	R	0.3 ± 0.2 ^{hijk}	R	0.4 ± 0.3 ^{mn}	R

** Significant at $P < 0.01$

a, b, …., and p stand for the clustering value on traits which are significant or not significant

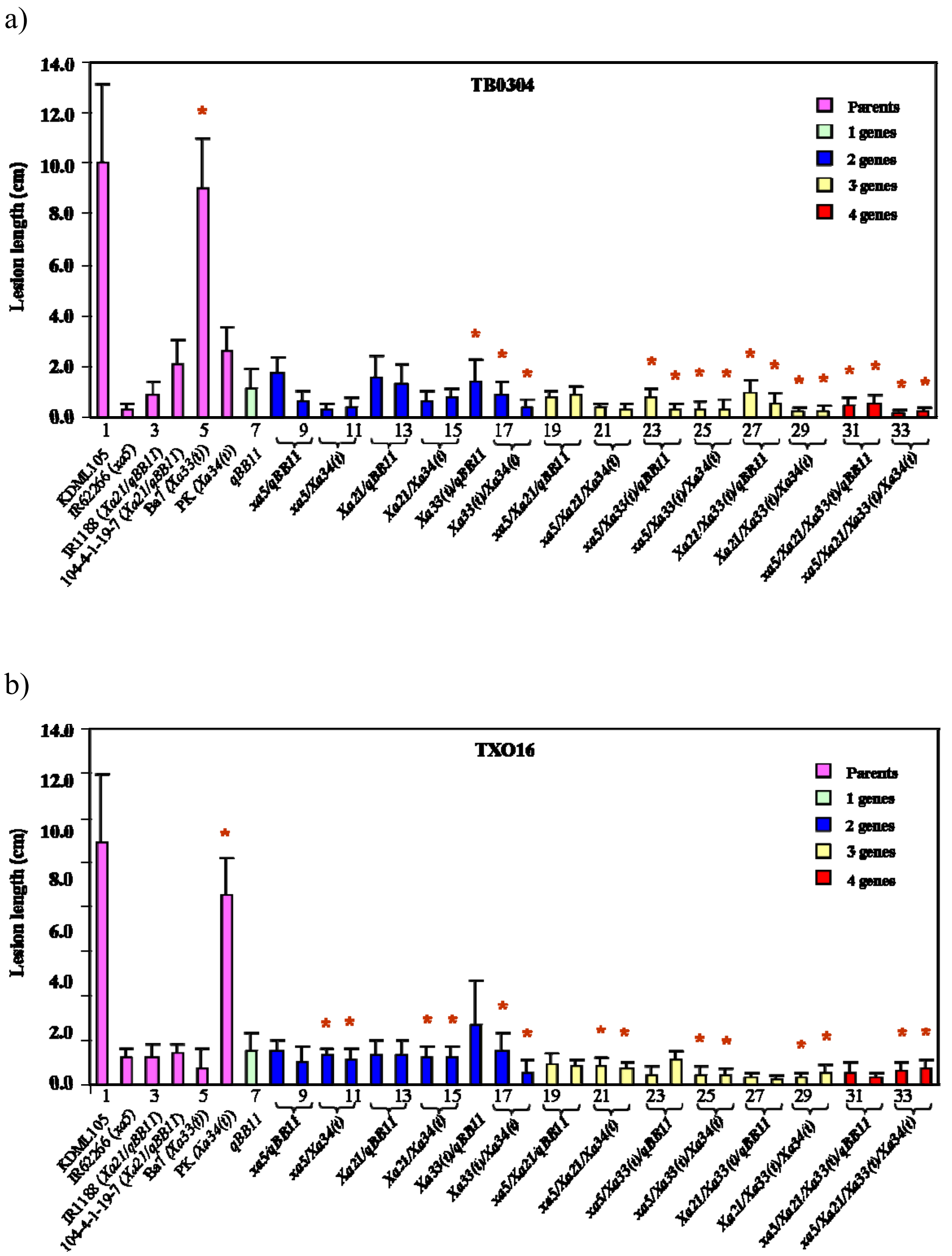


Figure 23 LL of 28 F_4 pyramid lines after inoculation with *Xoo* strains, a) TB0304, KDML105 and Ba7 (*xa33(t)*) showed highly susceptible phenotype. b) TXO16, KDML105 and PK (*Xa34(t)*) showed highly susceptible phenotype. The pyramid lines carried *xa33(t)* (a) and *Xa34(t)* (b) in combination showed higher resistance phenotype than single gene.

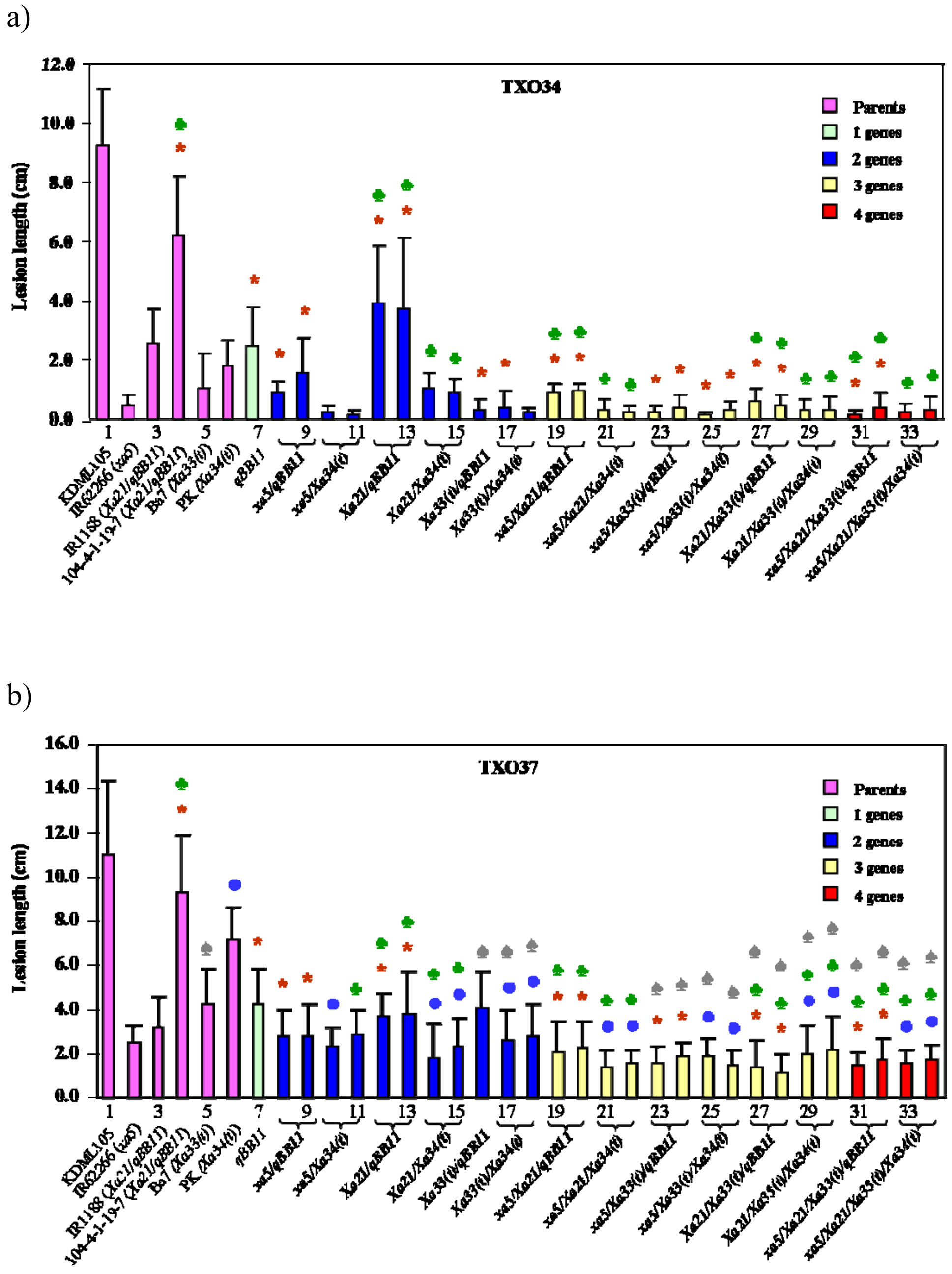


Figure 24 LL of 28 F_4 pyramid lines after inoculation with *Xoo* strain, a) TXO34, KDML105 and 104-4-1-19-7 (*Xa21/qBB11*) showed susceptible. b) TXO37, KDML105, 104-4-1-19-7 (*Xa21/qBB11*) and PK (*Xa34(t)*) showed highly susceptible phenotype. The pyramid lines carried *Xa21/qBB11* (a) and *Xa34(t)* (b) in combination showed highly resistance phenotype.

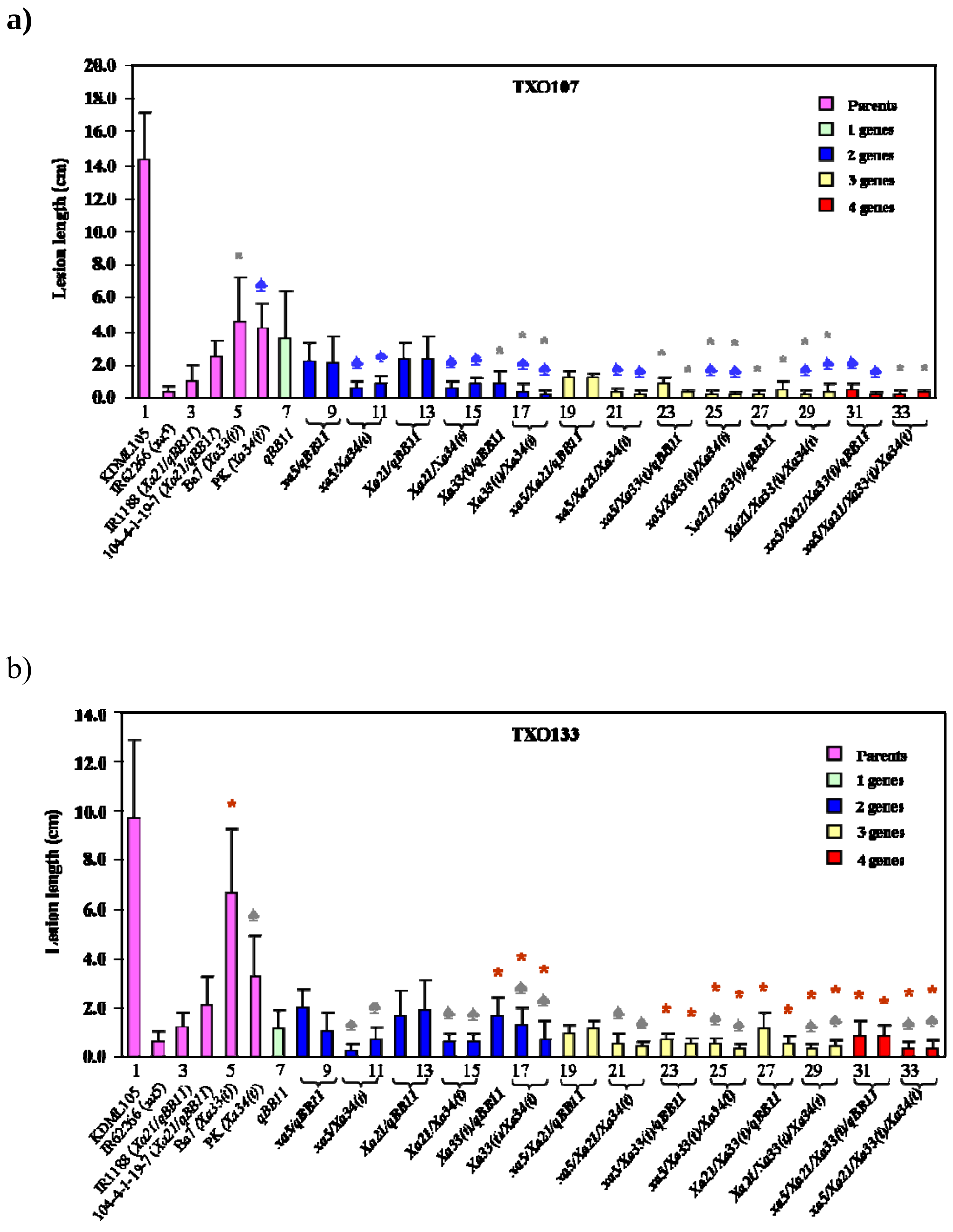


Figure 25 LL of 28 F_4 pyramid lines after inoculation with *Xoo* strain, a) TXO107, KDML105 showed susceptible while Ba7 (*xa33(t)*) and PK (*Xa34(t)*) showed moderate resistance. b) TXO133, KDML105 and Ba7 (*xa33(t)*) showed highly susceptible while PK (*Xa34(t)*) showed moderate resistance. The pyramid lines carried *xa33(t)* and *Xa34(t)* (a) and *Xa21/qBB11* (b) combination showed highly resistance phenotype.

DISCUSSION

BB resistance genes can be identified rapidly by DNA marker tagging approach. In this study, three BB resistance genes including *xa5*, *xa33(t)* and *Xa34(t)* were identified from rice variety IR62266, Ba7 and PK respectively. In IR62266, identified gene was tightly linked to RM122 reported by Pattawatang (2005). This gene was located in the same genomic region of the *xa5*. To identify the relationship between identified gene in IR62266 and the *xa5*, the functional marker PAxa5 (developed by Rice Gene Discovery Unit) which designed at same position as CAPS markers that released by Iyer and McCouch (2007) was used to amplify the *xa5* locus in IR62266 and IRBB5. Our results confirmed that IR62266 carry the *xa5* gene. Furthermore, we checked the pedigree of IRBB5 and IR62266 and found that they had a common ancestor IR1545-339 that was known to develop from a rice cultivar DZ192, an *Aus*-boro variety originating in Bangladesh the *indica* subspecies and belongs to isozyme group II carrying *xa5* gene (Glaszmann, 1987; Ogawa *et al.*, 1998). This result suggests that *xa5* identified from IR62266 was derived form DZ192.

In the Ba7, resistance gene was identified on the long arm of chromosome 6 where two dominant genes (*Xa7* and *Xa27*) were reported (Gu *et al.*, 2004; Sidhu *et al.*, 1978b). *Xa7* was originally identified in rice cultivar ‘DV85’ (Sidhu *et al.*, 1978b). A tightly linked marker of the *Xa7,* RG1091 was mapped to the position 107.5 cM on the Rice Genome Research Program (RGP) map (Kaji and Ogawa, 1995). Additional studies with various molecular markers including AFLP, SSR and STS found that *Xa7* was located at 107.3 cM (Yoshimura et al., 1996; Porter et al., 2003). Later, Chen *et al.* (2008) reported the high-resolution mapping and reported *Xa7* was located at 0.21 cM interval between GDSSR02 and RM20593 markers. RM20589, RM20590, and RM20591 were reportedly located within this interval. In our experiment, RM20590 was identified as the most tightly linked marker to the *xa33(t)*. Even though *Xa7* and *xa33(t)* shared common linked markers, an allelic test needs to be performed to answer whether or not *Xa7* and *xa33(t)* are the same gene. However, *Xa7* and *xa33(t)* had shown different gene actions and specificity in responding to BB isolates. This result indicates that *Xa7* and *xa33(t)* are difference gene or at least difference allele of the same gene.

Xa7 and *xa33(t)* are growth-stage independent. They confer resistance to many Thai *Xoo* isolates at both seedling and booting stages. Sidhu *et al.* (1978) reported that *Xa7* confers resistance only at flowering stage. This is not the case in our experiment using Thai *Xoo* isolates. Seedling resistance is reportedly controlled by a number of known major genes, which confer a high level of resistance throughout crop growth (Ezuka and Horino, 1976). Adult plant resistance is characterized by a high level of resistance at adult stage but the plants are very susceptible in their seedling stage (Zang and Mew, 1985). Zhang, and Mew, (1988) suggested that seedling resistance was more stable than adult plant resistance.

xa33(t) was mapped far away from *Xa27* identified in wild rice *O. minuta* Acc. 101141 (Amante-Bordeos *et al.*, 1992) and *xa32(t)* identified in wild rice *O. barthii* (Singh *et al.*, 2007). *Xa27* was reportedly located between RFLP markers RG424-RG162 (70.4-104.6 cM, Cornell map) on the long arm of chromosome 6, which is about 22.1 cM away from *xa33(t)* and *Xa7*. *xa32(t)* was mapped on the terminal region of chromosome 6 at a distance of 9.3 cM from RM588 (16.1 Mb). Hence, *xa33(t)* in 'Ba7' was certainly different from *Xa27* and *xa32(t)* genes.

xa33(t) confers a semi-dominant gene action. There are few reports on the genetics of semi-BB resistance found in rice. The heterozygous plants of *xa33(t)* exhibited moderate resistance to *Xoo* strains in our experiment. *Xa27* was reportedly conferred semi-dominant gene action to *Xoo* isolates in CO39 genetic background. However, it provides complete resistance at tillering stage in IRBB27 genetic background. The inheritance of *Xa27(t)* as a semi-dominant resistance gene was also observed in the genetic backgrounds of five parental lines of the Chinese hybrid rice (Gu et al., 2004). *Xa21* and *Xa7* showed incomplete dominance in the background of rice hybrids Minghui 63 (Zhang *et al.*, 2006).

Genetic background and growth stage play important roles in determining gene action. In the *xa33(t)*, the segregation ration was 1R:3S in which gene governing the resistance acted as recessive. In the case of *xa9,* which was initially identified as a recessive gene from rice cultivar Sateng (Singh *et al.,* 1983) and found later reinvestigated as dominant in other genetic background at booting and early flowering stages. Ogawa *et al.*, (1986a) reported that rice plants heterozygous for *Xa3* were susceptible when evaluated at maximum tillering. In the *Xa4*, it was reported as a dominant gene against *Xoo* strains CR4 and CXO8 and as a recessive gene against CR6 (Li *et al.*, 1999). These evidences demonstrated that dominant or recessive gene action depended upon the *Xoo* strain and growth stage of the host.

In the PK, resistance gene was identified on the long arm of chromosome 11 where ten resistance genes have been reported including *Xa3*, *Xa4*, *Xa6*, *xa9*, *Xa10*, *Xa21*, *Xa22*, *Xa23*, *Xa26* and *Xa30*. *Xa3*, *Xa4*, *Xa6*, *xa9*, *Xa22* and *Xa26* were reported as the same gene or a multi-gene family (Ogawa *et al.*, 1986b; Sun *et al.*, 2004; Xiang *et al.*, 2006). In the present experiment, the identified gene was different from the positive allele of the *Xa21* in IRBB21. When PB7-8 (Chunwongse *et al.*, 1993) was used to amply PK and IRBB21 genomic DNA, it gave a different banding pattern. This result indicated that resistance gene possessing by PK and IRBB21 was difference. The resistance gene in PK might be different from *Xa23*, *Xa30* and *Xa10* genes. *Xa10* was identified from rice cultivar, Cas 209 (Mew *et al.*, 1982; Yoshimura *et al.*, 1983) while *Xa30* and *Xa23* were identified from *O. rufipogon* (Jin *et al.*, 2007; Zhang *et al.*, 1998). The *Xa10* locus was initially mapped between the RAPD marker O072000 and RFLP marker CDO365 (Yoshimura *et al.*, 1995). According to the genome position, *Xa30*, *Xa23* and *Xa10* were located at approximately 19.6, 21.40 and 21.66 Mb, respectively while the resistance gene in PK was located at around 29.49 Mb on the rice chromosome 11. *Xa3* and *Xa26* were concluded as the same gene (Sun *et al.*, 2004; Xiang *et al.*, 2006). Its locus was mapped between flanking markers RM224 and Y6855RA (Yang *et al.*, 2003). Although, *Xa3/Xa26* and the resistance gene in PK shared common linked markers but no evidence has obtained yet whether they share the same genomic sequence or they are different loci and tightly linked to each other. The answers of these questions could be provided in the near future when the BB resistance genes have been cloned. Consequently, we tentatively designated the resistance gene in PK as *Xa34(t)*. Although, *qBB11* carried by rice variety IR1188 was mapped at the same region but they were responded differently to the *Xoo* strain.

BB resistance can rapidly be identified using near isogenic lines (Martin *et al.*, 1991) and marker-trait association approaches (Michelmore *et al.*, 1991). The success of these approaches requires an accuracy of phenotype validation (Wang *et al.*, 2001). In our study, we modified the BSA approaches by genotyping individual plants of extremely resistant and susceptible groups. The advantage is that it provides higher resolution and tendency of linked markers to the resistance gene. The identified linked markers can be directly used for MAS.

Combining genes/QTL for BB resistance in a single genotype is difficult task and can not be easily achieved using conventional breeding. Yoshimura *et al.*, (1995) reported that action of one major gene may mask the action of another in conventional phenotypic selection. Accumulation of major genes for BB resistance in an elite genotype by conventional breeding is laborious and time-consuming when one or more genes are effective against all known isolates of the pathogen. Nowadays, advanced in molecular biology makes it possible and convenient to improve the BB resistance by transformation and MAS, However, transgenic technique is not only time-consuming and costly but it also limit by technical problems such as gene silence, unstable inheritance and security (Deng *et al.*, 2006). In this study, none of Thai *Xoo* isolates in the collection are compatible with *xa5*. Therefore, only phenotypic screening could not be able to distinguish the rice lines that have *xa5* in combinations from others BB resistance genes *Xa21*, *xa33(t)*, *Xa34(t)* and *qBB11*. Because of these reasons, MAS was considered to be necessary for introgression of these resistance genes into Thai rice cultivars.

MAS have distinctive priority in multigene pyramiding. The advantages of MAS include precise, speediness, and independency for genotyping (Deng *et al.*, 2006). According to our results, molecular markers linked to BB resistance genes could identify resistant plants associated with theoretic lines. So, we can know amount of lines that need to generate in each generation. Moreover, the closely linked DNA markers can be used to accelerate the fixation of favorable alleles and increasing the efficiency of plant breeding with the maximum percentage of recurrent parent genome (Babu *et al.*, 2004). MAS in the large populations were laborious, costly and time-consuming. To reduce these obstacles, we applied MAS with stepwise selection approach. It can reduce number of samples that have to be identified with many linked markers. For example, seventy BC_1F_1 of pyramid *xa5/Xa21/qBB11* was selected at *xa5* locus in the first step. It was reduced to 33 lines for *Xa21/qBB11* selection and then reduced to 18 lines in the final selection.

All markers showed highly effective for identification of resistant alleles of *Xa* genes in our study. Two functional markers (FM) PB7-8 and PAxa5 showed highly effective for identification of resistant *Xa21* and *xa5* alleles. These markers are completely predictive of the functional nucleotide polymorphism that differentiates resistant and susceptible alleles. FM was superior than random DNA markers such as RFLP, SSR and AFLP because it completely linkage with the trait. The primers of FM were normally assigned from the genomic region within the gene where it causes the phenotypic trait variation. FM can be used to fix gene alleles in several genetic backgrounds without additional calibration. This would be a major advance in marker applications, particularly in plant breeding. More generally, FM can be used to avoid genetic drift at characterized loci (Andersen and Lübberstedt, 2003). Therefore, FM is becoming importance because of their accuracy. Although other three target genes, *xa33(t)*, *Xa34(t)* and *qBB11* did not selected by FM because of they are not yet cloned now but tightly linked markers could be perform to select them in this study with the high accuracy. The performance of linked marker depend on the accuracy of genetic map and distant between gene/QTL and markers ((Dubcovsky, 2004).

Resistant gene *xa5* showed the broadest resistance spectrum against Thai *Xoo* isolates and conferred high resistance at all growth stage. This result was supported by Jeung *et al.*, (2006) that *xa5* conferred resistance to all Korea *Xoo* isolates. The recessive gene mediated resistance was more complex and might not be governed by a single gene. *xa5* region was reported to carry five know defense-related genes by in *silico* analysis of entire region between the STS marker RG556 linked to this gene (Kottapalli *et al.*, 2007).

Xa34(t), *xa33(t)* and *Xa21/qBB11* conferred race specificity against Thai *Xoo* isolates. *Xa21* which reported to confer board resistance to many *Xoo* strain in China and India was not resistance against many isolates in our experiment. Resistance to specific *Xoo* strains is governed by both major resistance genes with a qualitative effect that condition complete resistance and polygenes with a quantitative effect (QTL) that condition partial resistance (Li *et al.*, 2006). A complex genetic network of epistatic effects between resistance genes and QTL for resistance in rice was revealed by Li *et al.* (2006). The interactions between alleles at the rice resistance loci and alleles at the corresponding avirulence loci in *Xoo* lead to complete resistance. Whereas interactions between rice QTL for resistance and corresponding aggressiveness loci in *Xoo* lead to partial resistance (Niño-Lui et al., 2006). For example, a single dominant gene *Xa4* which wildly used in Asian rice breeding programs conferred durable resistance in cultivar IR20 and IR64 but act as recessive QTL and show quantitative complementation when pyramided with other resistance genes in elite cultivars (Niño-Lui *et al.*, 2006). The breakdown of *Xa4*-mediated resistance was manifested by significant changes in the qualitative action of the *Xa4* and by a quantitative reduction of 50% in magnitude of effect of *Xa4* gene (Li *et al.*, 1999).Now a day, *Xa4* and *Xa21* become susceptible to BB in Philippines, India, Indonesia, and China (Davierwala *et al.*, 2001; IRRI, 1973; Huang *et al.*, 1997; Mew and Vera-Cruz, 1979; Zhang *et al.*, 1988; Zhang *et al.*, 1995).

The pyramid lines had a higher level of resistance and broader spectrum of resistance than parental lines or lines with a single gene. These broader spectrum and higher levels of resistance in the pyramids might be due to interaction and/or complementation between the resistance genes (Haung *et al.*, 1997). Li *et al.*, (1999) reported that a high level of durable resistance to *Xoo* can be achieved by the cumulative effects of multiple QTLs, including the residual effects of defeated major resistance genes. Lesion lengths of pyramided lines were significantly shorter than single gene parental lines even though the pyramided lines were inoculated with virulent isolates to individual *Xa* genes.

More resistance genes need to be identify and pyramiding together into the elite cultivars to ensure the lifelong of BB resistance. Most of major genes have been overcome by new or unrecognized pathogen races. We realized that *xa5* will almost certainly be one day overcome by new virulent *Xoo* races in the future whenever it widely used in breeding programs. Fortunately, this can be prevented by combining with other resistance genes. Pyramiding of two or more resistance genes should lead to more durable resistance in rice. In this study, pyramiding genes conferring board-spectrum and race specific resistance through MAS were successfully conducted. The pyramiding lines obtained in our study can be used as genetic resources for BB resistance in breeding programs that will be paving way for an environmental-friendly means to achieve a better disease management. Moreover, the success will facilitate future efforts to transfer combinations of BB resistance genes into other preferred rice cultivars.

CONCLUSION AND RECOMMENDATION

In this study, we identified the three genes for BB resistance, *xa5*, *xa33(t)* and *Xa34(t)* and their linked markers in rice cultivars IR62266, Ba7 and PK. These genes can improve BB resistance in the rice breeding program by MAS. *xa5* was located on chromosome 5 and had a recessive gene action. This gene was already cloned in which PAxa5 was developed as gene specific marker in this study. *xa33(t)* was recessive gene located on the long arm of rice chromosome 6. RM30, RM7243, RM5509 and RM400 were identified as tightly linked markers that can clearly discriminate between resistant and susceptible phenotypes. However, heterozygote of *xa33(t)* showed intermediate resistance. *Xa34(t)* is a dominant gene located on rice chromosome 11 where many BB resistant genes were reported. RM224 was identified as the tightly linked marker that clearly discriminate banding pattern between resistant and susceptible phenotypes. Although *Xa34(t)* and other BB resistance genes were located in the same region and shared common linked markers but no evidence has yet been obtained whether they share the same genomic sequence or whether they are tightly linked to each other.

The pyramided lines carrying more than two genes showed higher and broader resistance spectrum than lines carrying a single gene. *xa5* was the most effective, follow by *Xa34(t)*, *xa33(t)* and *Xa21/qBB11* against six *Xoo* isolates TB0304, TXO16, TXO34, TXO37, TXO107 and TXO133. So far, the pyramid lines obtained in this study can be used as genetic resources for improvement of BB resistance in breeding programs.

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APPENDIX

Appendix Table 1 List of 34 SSR markers obtained from the public database released by Gramene (www.gramene.org). These markers were used to survey in parental lines, KDML105 and IR62266. Nineteen polymorphic markers were specified by *.

Entry	Chr.	Marker	
1	1	RM104	
2	2	RM27	
3	2	RM263	*
4	2	RM29	
5	2	RM174	
6	2	RM145	
7	4	RM261	*
8	4	RM273	*
9	4	RM255	
10	4	RM317	*
11	4	RM280	*
12	4	RM127	
13	5	RM507	*
14	5	RM153	*
15	5	RM122	*
16	5	RM13	*
17	5	RM39	
18	5	RM161	
19	5	RM26	*
20	8	RM256	
21	8	RM210	*
22	8	RM80	
23	9	RM242	*
24	9	RM201	*
25	9	RM215	*
26	9	RM205	*
27	11	RM209	
28	11	RM229	
29	11	RM21	*
30	11	RM206	*
31	11	RM254	*
32	11	RM224	*
33	11	RM144	
34	11	RM139	

* = Polymorphic marker

Appendix Table 2 List of 114 SSR markers obtained from the public database (www.gramene.org) that were used to survey in parental lines, PK and Ba7. 62 polymorphic markers were specified as *.

Entry	Chr.	Marker		Entry	Chr.	Marker		Entry	Chr.	Marker	
1	1	RM495	*	39	5	RM289		77	8	RM337	*
2	1	RM1		40	5	RM164	*	78	8	RM38	
3	1	RM243		41	5	RM39		79	8	RM25	*
4	1	RM312		42	5	RM161	*	80	8	RM339	
5	1	RM5		43	5	RM26		81	8	RM210	*
6	1	RM212	*	44	5	RM31		82	8	RM230	
7	1	RM472		45	5	RM334	*	83	8	RM264	
8	1	RM14		46	6	RM170	*	84	9	RM316	
9	2	RM154	*	47	6	RM225	*	85	9	RM219	*
10	2	RM279	*	48	6	RM50		86	9	RM105	*
11	2	RM174		49	6	RM136	*	87	9	RM257	*
12	2	RM27		50	6	RM3		88	9	RM278	*
13	2	RM341	*	51	6	RM8239		89	9	RM215	
14	2	RM263		52	6	RM162	*	90	9	RM245	*
15	2	RM6		53	6	RM343		91	10	RM222	
16	2	RM213		54	6	RM7638		92	10	RM311	*
17	3	RM60		55	6	RM7309		93	10	RM184	*
18	3	RM231	*	56	6	RM528		94	10	RM171	*
19	3	RM7		57	6	RM30		95	10	RM147	*
20	3	RM282	*	58	6	RM1130		96	10	RM496	*
21	3	RM16	*	59	6	RM5988	*	97	11	RM286	*
22	3	RM55		60	6	RM7641		98	11	RM332	*
23	3	RM416	*	61	6	RM6458		99	11	RM287	*
24	3	RM227	*	62	6	RM7243	*	100	11	RM209	*
25	4	RM307	*	63	6	RM3430		101	11	RM229	*
26	4	RM335	*	64	6	RM5509	*	102	11	RM21	*
27	4	RM261	*	65	6	RM400	*	103	11	RM206	*
28	4	RM185	*	66	6	RM340	*	104	11	RM254	
29	4	RM142		67	6	RM461	*	105	11	RM224	
30	4	RM273	*	68	6	RM103	*	106	11	RM139	
31	4	RM255	*	69	7	RM436		107	11	RM144	*
32	4	RM127	*	70	7	RM125	*	108	12	RM415	
33	4	RM124	*	71	7	RM2		109	12	RM19	
34	4	RM280	*	72	7	RM11		110	12	RM83	
35	5	RM507		73	7	RM10	*	111	12	RM277	
36	5	RM153	*	74	7	RM234	*	112	12	RM309	*
37	5	RM122	*	75	7	RM18	*	113	12	RM270	
38	5	RM13		76	7	RM172	*	114	12	RM12	

* = Polymorphic marker

Appendix Table 3 Genotype and LL of 190 F$_3$ individuals from the cross between KD and IR62266. LL was calculated as mean in responding to each *Xoo* isolate. KD = homozygous KDML105, IR = homozygous IR62266 and H = heterozygous.

Entry	Genotype			LL (mean ± *sd*, cm)		
	RM122	RM153	RM507	TXO1	TXO2	TXO5
1	KD	KD	KD	8.5 ± 2.6	7.4 ± 3.7	12.9 ± 3.3
2	H	H	H	5.6 ± 5.0	3.9 ± 3.3	10.7 ± 6.4
3	KD	KD	KD	8.9 ± 1.5	8.2 ± 3.0	11.4 ± 2.9
4	IR	H	IR	1.9 ± 0.5	1.0 ± 0.5	2.0 ± 0.6
5	H	H	H	8.5 ± 1.5		6.7 ± 6.3
6	IR	IR	IR	2.6 ± 0.8	0.7 ± 0.4	2.9 ± 1.0
7	H	H	H	7.3 ± 3.3	3.0 ± 1.8	9.8 ± 5.5
8	H	H	H	6.0 ± 2.9	5.8 ± 3.2	10.5 ± 1.7
9	IR	IR	IR	1.9 ± 0.7	1.1 ± 0.3	3.3 ± 1.0
10	H	H	H	7.9 ± 1.1	3.9 ± 3.0	6.3 ± 4.6
11	H	H	H	6.0 ± 2.4	5.2 ± 0.9	8.5 ± 4.6
12	KD	KD	KD	8.1 ± 2.9	3.5 ± 1.3	11.5 ± 2.6
13	H	H	H	5.7 ± 2.7	3.3 ± 0.2	8.8 ± 3.8
14	H	H	H	7.2 ± 4.2	4.1 ± 2.9	9.6 ± 4.9
15	IR	IR	IR	2.3 ± 0.7	2.2 ± 0.9	2.8 ± 0.7
16	KD	H	KD	8.8 ± 3.4	4.4 ± 3.1	8.9 ± 6.4
17	H	H	H	6.1 ± 3.3	4.4 ± 2.7	6.5 ± 4.8
18	KD	KD	KD	6.4 ± 1.6	3.2 ± 0.6	11.3 ± 1.7
19	H	H	H	4.8 ± 3.6	4.2 ± 2.0	9.1 ± 4.5
20	H	H	H	2.7 ± 1.5	3.1 ± 1.5	7.8 ± 5.6
21	H	H	H	9.1 ± 1.1	4.6 ± 2.1	12.6 ± 4.9
22	H	H	H	8.7 ± 1.2	5.0 ± 2.0	8.4 ± 5.6
23	H	H	H	8.2 ± 2.4	2.7 ± 1.2	7.4 ± 3.8
24	KD	KD	KD	9.5 ± 2.6	4.4 ± 2.6	12.2 ± 2.6
25	IR	IR	IR	1.9 ± 0.2	0.7 ± 0.1	2.0 ± 0.5
26	H	H	H	9.3 ± 0.9		9.4 ± 5.1
27	IR	IR	IR	2.7 ± 1.0	0.3 ± 0.4	3.1 ± 2.7
28	H	H	H	7.8 ± 4.1	3.6 ± 1.8	11.3 ± 5.5
29	H	H	H	7.2 ± 2.9	2.5 ± 2.2	9.8 ± 6.1
30	H	H	H	9.0 ± 2.3	3.9 ± 2.4	8.1 ± 7.0
31	KD	KD	KD	8.9 ± 4.4	5.0 ± 3.1	10.1 ± 2.0
32	IR	IR	IR	2.5 ± 1.2	1.0 ± 0.3	3.4 ± 0.9
33	IR	IR	IR	1.7 ± 0.5	0.6 ± 0.2	2.9 ± 1.5
34	H	H	H	5.3 ± 3.7	2.7 ± 1.3	4.8 ± 3.3
35	IR	IR	IR	2.1 ± 0.7	0.6 ± 0.3	2.5 ± 1.6
36	KD	KD	KD	10.6 ± 1.9	6.7 ± 2.9	11.6 ± 3.2
37	IR	IR	IR	2.6 ± 0.5	1.3 ± 0.7	3.1 ± 1.0
38	H	H	H	7.1 ± 3.7	4.9 ± 1.9	4.4 ± 2.8
39	H	H	H	7.4 ± 3.6	4.9 ± 4.7	13.4 ± 4.9
40	H	KD	KD	11.7 ± 7.5		9.5 ± 3.5
41	KD	KD	KD	9.0 ± 3.4	6.6 ± 3.0	11.3 ± 2.1

Appendix Table 3 (Continued)

Entry	**Genotype**			**LL (mean ± *sd*, cm)**		
	RM122	**RM153**	**RM507**	**TXO1**	**TXO2**	**TXO5**
42	H	H	H		4.2 ± 2.5	
43	IR	IR	IR	2.4 ± 0.5	2.5 ± 3.0	3.7 ± 2.5
44	KD	KD	KD	8.7 ± 2.1	6.0 ± 3.0	13.4 ± 3.4
45	KD	KD	KD	8.4 ± 2.0	7.7 ± 4.7	13.0 ± 5.6
46	H	H	H	7.1 ± 3.9	5.5 ± 2.9	8.4 ± 3.9
47	H	H	H	7.6 ± 3.6	1.6 ± 0.8	7.5 ± 4.6
48	H	H	H	7.2 ± 3.5	4.5 ± 1.3	8.4 ± 5.5
49	IR	IR	IR	2.3 ± 1.1	1.2 ± 0.4	2.1 ± 1.0
50	KD	KD	KD			6.8 ± 3.7
51	H	H	H	7.6 ± 3.2	3.5 ± 2.5	7.2 ± 3.6
52	H	H	H	7.4 ± 2.7	4.9 ± 1.4	
53	H	H	H			4.8 ± 4.3
54	H	H	H	7.2 ± 5.1	3.0 ± 2.7	
55	KD	KD	H	9.7 ± 2.1	6.5 ± 1.2	9.3 ± 2.2
56	KD	KD	KD	10.1 ± 2.0	5.3 ± 3.6	7.1 ± 4.0
57	H	H	H	4.8 ± 3.5	3.5 ± 4.8	8.2 ± 3.3
58	H	H	H	9.5 ± 2.9	5.8 ± 3.5	5.6 ± 3.3
59	H	H	H	8.0 ± 2.8	3.6 ± 2.2	
60	H	KD	KD	8.8 ± 2.1	6.5 ± 2.9	7.6 ± 3.5
61	H	H	H	6.8 ± 3.1	4.2 ± 3.5	9.9 ± 1.5
62	IR	IR	IR	2.3 ± 0.6	1.5 ± 0.8	7.1 ± 3.5
63	IR	IR	IR	2.6 ± 0.6	1.5 ± 0.6	2.3 ± 0.7
64	H	H	H			2.5 ± 1.2
65	H	H	H	6.6 ± 3.3	5.5 ± 2.4	
66	H	H	H	7.0 ± 4.2	4.7 ± 2.9	10.3 ± 3.7
67	H	H	H	9.7 ± 4.3	3.8 ± 3.5	8.7 ± 4.0
68	KD	KD	KD			7.7 ± 4.4
69	KD	KD	KD	9.2 ± 2.0	4.9 ± 1.8	9.8 ± 2.8
70	H	H	H	7.5 ± 4.4	4.7 ± 3.9	7.0 ± 5.1
71	H	H	H	8.4 ± 2.9	±	7.2 ± 4.0
72	H	H	H	5.8 ± 3.4	5.9 ± 4.9	8.0 ± 3.8
73	KD	KD	KD	8.4 ± 2.0	6.8 ± 2.7	13.7 ± 4.2
74	KD	KD	KD		6.6 ± 1.5	
75	H	H	H	6.5 ± 3.1	5.9 ± 2.1	7.7 ± 5.7
76	KD	KD	KD	8.2 ± 1.7	6.4 ± 2.6	10.8 ± 4.4
77	IR	IR	IR	2.1 ± 2.0	0.8 ± 0.5	2.2 ± 0.8
78	KD	KD	KD	9.8 ± 2.4	5.8 ± 3.2	13.6 ± 4.9
79	IR	IR	IR	2.6 ± 1.4	1.0 ± 0.5	2.2 ± 0.9
80	KD	KD	KD	6.3 ± 1.5	3.3 ± 1.4	8.1 ± 2.3
81	KD	KD	KD	8.1 ± 2.2	5.7 ± 2.5	10.9 ± 1.6
82	H	H	H	7.2 ± 3.3	5.9 ± 5.1	8.7 ± 6.4
83	H	H	0	8.2 ± 3.4	7.2 ± 5.2	8.7 ± 6.2
84	IR	IR	IR	2.3 ± 0.6	1.3 ± 0.6	3.4 ± 2.6
85	KD	KD	KD	10.8 ± 1.9	4.2 ± 1.0	13.5 ± 4.8
86	H	H	H			
87	H	H	H	10.7 ± 1.9	2.8 ± 1.8	14.9 ± 3.8

Appendix Table 3 (Continued)

Entry	**Genotype**			**LL (mean ± *sd*, cm)**		
	RM122	**RM153**	**RM507**	**TXO1**	**TXO2**	**TXO5**
88	H	H	H	9.6 ± 4.3	3.0 ± 1.4	7.9 ± 4.3
89	IR	IR	IR	2.3 ± 0.6	1.6 ± 0.9	4.6 ± 3.2
90	H	H	H	10.0 ± 4.8	4.3 ± 2.1	7.4 ± 5.7
91	KD	KD	KD	11.6 ± 2.1	4.5 ± 2.5	12.0 ± 3.3
92	IR	IR	IR	3.6 ± 2.4	3.1 ± 3.6	3.4 ± 1.4
93	H	H	H	8.8 ± 3.5	2.9 ± 1.1	11.3 ± 5.9
94	KD	H	H	11.3 ± 1.9	4.2 ± 1.0	15.4 ± 4.2
95	IR	IR	IR	2.9 ± 0.7	2.2 ± 1.1	3.9 ± 4.3
96	IR	IR	IR	2.1 ± 2.0	0.6 ± 0.2	1.8 ± 0.8
97	H	H	H	6.4 ± 4.4	3.0 ± 3.1	16.0 ± 5.0
98	H	H	H	7.8 ± 9.4	3.2 ± 1.6	8.2 ± 4.9
99	H	H	H	10.7 ± 11.6	3.6 ± 3.4	11.3 ± 5.4
100	IR	IR	IR	2.1 ± 0.8	1.9 ± 1.4	4.1 ± 2.1
101	H	IR	IR	4.6 ± 2.6		6.5 ± 3.4
102	H	H	H	6.7 ± 3.2	4.8 ± 2.8	9.3 ± 3.4
103	H	H	H	5.9 ± 1.9		
104	H	H	H	7.6 ± 1.9	3.3 ± 3.3	6.4 ± 4.2
105	H	H	H	7.3 ± 3.3	3.0 ± 1.2	11.3 ± 5.0
106	H	H	H	5.1 ± 2.6	2.9 ± 1.2	7.8 ± 5.3
107	IR	IR	IR	2.1 ± 0.6	2.3 ± 3.4	3.0 ± 1.5
108	KD	KD	KD	10.0 ± 4.8	5.0 ± 2.0	8.8 ± 4.8
109	KD	KD	KD	8.1 ± 2.2	4.6 ± 3.6	4.7 ± 2.2
110	H	H	H	6.3 ± 2.9	3.5 ± 2.1	10.0 ± 6.3
111	H	H	H	6.0 ± 3.6	2.0 ± 2.1	5.4 ± 4.4
112	H	H	H	9.2 ± 3.0	3.1 ± 1.8	7.2 ± 4.4
113	KD	KD	KD	7.8 ± 2.3	3.6 ± 1.8	4.7 ± 2.9
114	KD	KD	KD	11.9 ± 2.6	4.7 ± 2.1	8.1 ± 3.9
115	H	H	H	5.1 ± 2.9	3.5 ± 2.2	4.0 ± 3.1
116	KD	KD	0	10.3 ± 10.5	4.2 ± 1.4	5.7 ± 2.7
117	H	H	H	8.6 ± 4.0	4.9 ± 1.5	8.9 ± 8.1
118	H	H	H	7.1 ± 3.0	3.7 ± 2.6	4.6 ± 2.5
119	H	H	H	7.8 ± 2.9	6.1 ± 1.6	7.0 ± 5.5
120	KD	KD	KD	8.9 ± 2.9	5.9 ± 2.6	8.8 ± 5.6
121	H	H	H	6.7 ± 3.7	2.1 ± 2.0	8.8 ± 5.3
122	H	H	H	9.9 ± 3.8	2.7 ± 1.4	11.6 ± 6.5
123	H	H	H		2.6 ± 1.2	
124	H	H	H	8.9 ± 4.3		15.7 ± 8.1
125	H	H	H	11.3 ± 1.6	2.7 ± 2.5	15.6 ± 6.9
126	IR	IR	IR	1.7 ± 0.6	1.9 ± 1.7	1.5 ± 0.5
127	H	H	H	7.1 ± 5.1	3.9 ± 4.3	11.1 ± 5.8
128	H	H	H	7.0 ± 3.7	2.8 ± 1.6	8.7 ± 5.3
129	H	H	H	6.1 ± 3.7	2.8 ± 0.9	10.8 ± 6.6
130	H	H	H	8.0 ± 1.7	2.8 ± 2.2	7.3 ± 5.1
131	KD	KD	KD	8.4 ± 2.2	7.3 ± 4.3	
132	KD	KD	KD	8.2 ± 2.1	5.4 ± 2.4	
133	KD	KD	KD	7.6 ± 2.2	2.1 ± 2.1	3.5 ± 0.9

Appendix Table 3 (Continued)

Entry	Genotype			LL (mean ± *sd*, cm)		
	RM122	RM153	RM507	TXO1	TXO2	TXO5
134	KD	KD	KD	8.5 ± 3.1	5.2 ± 1.2	8.2 ± 4.3
135	IR	IR	IR	2.1 ± 0.7	3.2 ± 3.1	
136	H	H	H	5.9 ± 2.9	4.2 ± 2.2	7.5 ± 3.5
137	H	H	H	7.7 ± 4.4	5.8 ± 1.8	9.3 ± 3.8
138	H	H	H	7.1 ± 3.8	4.3 ± 2.6	7.4 ± 5.3
139	H	KD	KD	9.6 ± 3.4	6.0 ± 3.0	8.7 ± 7.0
140	IR	IR	IR	2.5 ± 0.6	1.6 ± 0.5	2.0 ± 2.0
141	KD	KD	KD	7.6 ± 2.1	6.3 ± 3.7	3.7 ± 0.1
142	H	H	H	8.2 ± 4.9	5.3 ± 2.5	2.1 ± 1.2
143	KD	KD	KD	12.7 ± 3.9	5.6 ± 3.1	5.2 ± 2.0
144	IR	IR	IR	4.2 ± 1.6	1.4 ± 0.7	1.8 ± 0.7
145	H	H	H	8.9 ± 4.2	3.4 ± 2.2	6.2 ± 4.9
146	KD	KD	KD	10.1 ± 2.8	7.7 ± 2.9	4.3 ± 2.3
147	KD	KD	KD	9.0 ± 4.3	4.6 ± 2.8	4.4 ± 2.5
148	H	H	H	10.6 ± 4.8	6.7 ± 3.9	6.0 ± 4.4
149	H	H	H	9.6 ± 3.9	6.2 ± 3.3	4.6 ± 1.6
150	H	H	H	6.9 ± 4.0	6.6 ± 4.0	10.4 ± 5.9
151	H	H	H	8.4 ± 3.0	4.1 ± 2.4	12.3 ± 5.2
152	H	H	H	6.7 ± 3.3	5.2 ± 2.0	10.9 ± 4.5
153	KD	KD	0	8.4 ± 2.7	7.3 ± 3.7	15.1 ± 6.8
154	KD	KD	KD	9.6 ± 2.3	5.4 ± 2.7	17.6 ± 5.7
155	H	IR	IR	5.1 ± 3.5	4.6 ± 2.0	9.2 ± 4.3
156	IR	IR	IR	2.0 ± 0.7	1.8 ± 1.2	3.7 ± 2.9
157	H	H	H	7.2 ± 4.2	2.4 ± 1.0	7.4 ± 5.4
158	H	H	H	7.5 ± 3.6	4.7 ± 2.1	9.3 ± 6.7
159	IR	IR	IR	2.5 ± 0.8	1.5 ± 0.4	3.0 ± 1.5
160	H	H	H	9.4 ± 3.1	5.7 ± 2.0	11.1 ± 5.0
161	KD	KD	KD	11.1 ± 2.3	5.8 ± 3.5	8.9 ± 3.5
162	KD	KD	KD	11.8 ± 3.9	7.2 ± 2.3	11.4 ± 3.8
163	H	H	H	8.7 ± 5.0	2.7 ± 2.5	8.6 ± 5.5
164	KD	KD	KD	10.6 ± 1.9	6.2 ± 3.1	7.0 ± 3.0
165	KD	KD	KD	9.8 ± 2.5	4.5 ± 2.3	6.8 ± 1.7
166	H	H	H	8.5 ± 4.8	5.4 ± 2.6	6.8 ± 4.1
167	H	H	H	9.1 ± 3.9	4.8 ± 3.7	9.0 ± 3.5
168	KD	KD	KD	9.8 ± 2.6	5.5 ± 0.9	9.3 ± 3.6
169	IR	IR	IR	3.3 ± 0.9	1.8 ± 2.3	2.8 ± 1.8
170	IR	IR	IR	2.3 ± 0.7	1.7 ± 2.0	2.2 ± 0.9
171	IR	IR	IR	2.4 ± 0.7	1.1 ± 0.4	3.3 ± 1.5
172	IR	IR	IR	2.9 ± 0.7	0.8 ± 0.5	2.8 ± 1.2
173	IR	IR	IR	2.2 ± 0.4	1.1 ± 0.5	2.4 ± 0.7
174	IR	IR	IR		2.2 ± 1.6	
175	IR	IR	IR	2.2 ± 0.6	1.4 ± 1.1	3.1 ± 1.1
176	H	H	H	7.0 ± 3.3	2.3 ± 0.7	10.5 ± 5.3
177	IR	IR	IR	2.2 ± 0.9	1.5 ± 0.4	2.8 ± 0.9
178	IR	IR	IR	2.4 ± 0.9	1.0 ± 0.4	2.7 ± 0.9
179	H	H	H	7.6 ± 3.7	4.9 ± 2.9	9.2 ± 5.5

Appendix Table 3 (Continued)

Entry	**Genotype**			**LL (mean ± *sd*, cm)**		
	RM122	**RM153**	**RM507**	**TXO1**	**TXO2**	**TXO5**
180	H	H	H	7.8 ± 4.5	8.5 ± 3.4	12.1 ± 4.4
181	KD	KD	KD		5.7 ± 2.4	16.6 ± 3.9
182	H	H	H	7.6 ± 4.5		10.2 ± 7.5
183	KD	KD	KD	12.4 ± 2.5	7.4 ± 3.0	16.0 ± 4.8
184	H	H	H		6.2 ± 2.3	
185	KD	KD	KD	11.6 ± 1.9	7.8 ± 2.8	16.0 ± 3.4
186	H	H	H	12.1 ± 3.7	4.2 ± 4.0	15.8 ± 6.1
187	H	H	H	7.7 ± 2.8	4.1 ± 3.5	10.2 ± 4.2
188	IR	IR	IR	1.9 ± 0.3	1.2 ± 0.4	2.4 ± 0.6
189	KD	KD	KD	11.0 ± 2.8	3.8 ± 1.1	13.4 ± 4.8
190	H	H	H	8.3 ± 4.5	4.6 ± 2.1	14.2 ± 3.6
	KD	KD	KD	12.5 ± 3.4	7.3 ± 3.0	14.3 ± 3.5
	IR	IR	IR	2.0 ± 1.0	1.6 ± 1.3	2.3 ± 0.5

Appendix Table 4 Genotypes and LL of 161 BC_2F_3 individuals from the cross between PK and Ba7 for BB resistance. LL was measured in responding to *Xoo* isolate TXO16. Ba = homozygous Ba7, PK = homozygous Pin Kaset and H = heterozygous.

Entry	**Pedigree**	**TXO16**	**Genome position (Mb)**								
			27.15	**27.16**	**27.25**	**27.43**	**27.56**	**28.01**	**27.82**	**28.43**	**28.59**
		LL (mean±*sd* ; cm)	**RM20523**	**RM20536**	**RM30**	**RM3430**	**RM7243**	**RM20590**	**RM5509**	**RM400**	**RM340**
1	RGDU05228-3-570-1	4.2 ± 2.2	H	H	H	H	H	H	H	Ba	PK
2	RGDU05228-3-570-2	5.8 ± 2.9	H	H	H	H	H	H	H	H	H
3	RGDU05228-3-570-3	0.9 ± 0.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	PK
4	RGDU05228-3-570-4	4.2 ± 2.9	H	H	H	H	H	H	H	H	PK
5	RGDU05228-3-570-5	9.2 ± 3.2	PK	PK	PK	PK	PK	PK	PK	PK	H
6	RGDU05228-3-570-6	4.0 ± 3.1	H	H	H	H	H	H	H	H	H
7	RGDU05228-3-570-7	5.7 ± 2.1	PK	PK	PK	PK	PK	PK	PK	PK	Ba
8	RGDU05228-3-570-8	2.9 ± 3.5	H	H	H	H	H	Ba	Ba	Ba	H
9	RGDU05228-3-570-9	3.9 ± 1.8	H	H	H	H	H	H	H	H	H
10	RGDU05228-3-570-10	4.8 ± 3.0	H	H	H	H	H	H	H	H	H
11	RGDU05228-3-570-11	6.2 ± 2.5	PK	PK	PK	PK	PK	PK	PK	PK	H
12	RGDU05228-3-570-12	4.7 ± 3.0	H	H	H	H	H	H	H	H	Ba
13	RGDU05228-3-570-13	1.3 ± 1.2	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
14	RGDU05228-3-570-14	3.8 ± 2.0	H	H	H	H	H	H	H	H	H
15	RGDU05228-3-570-15	6.9 ± 3.4	H	PK	H	H	H	H	H	H	Ba
16	RGDU05228-3-570-16	4.6 ± 2.0	H	H	H	H	H	H	H	H	PK
17	RGDU05228-3-570-17	9.2 ± 3.6	PK	PK	PK	PK	PK	PK	PK	PK	PK
18	RGDU05228-3-570-18	5.1 ± 4.5	H	H	H	H	H	H	H	H	H
19	RGDU05228-3-570-19	1.2 ± 0.8	Ba	H	Ba	Ba	Ba	Ba	Ba	Ba	H
20	RGDU05228-3-570-20	2.8 ± 0.9	H	H	H	H	H	H	H	H	H
21	RGDU05228-3-570-21	4.7 ± 3.7	H	H	H	H	H	H	H	H	H
22	RGDU05228-3-570-22	0.3 ± 0.4	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
23	RGDU05228-3-570-23	4.9 ± 2.5	H	H	H	H	H	H	H	H	PK
24	RGDU05228-3-570-24	2.4 ± 1.2	Ba	Ba	Ba	H	Ba	H	Ba	H	H
25	RGDU05228-3-570-25	7.8 ± 1.7	H	H	H	H	H	H	H	H	Ba

Appendix Table 4 (Continued)

Entry	**Pedigree**	**TXO16**	**Genome position (Mb)**								
			27.15	**27.16**	**27.25**	**27.43**	**27.56**	**28.01**	**27.82**	**28.43**	**28.59**
		LL (mean±*sd* ; cm)	**RM20523**	**RM20536**	**RM30**	**RM3430**	**RM7243**	**RM20590**	**RM5509**	**RM400**	**RM340**
26	RGDU05228-3-570-26	1.0 ± 0.7	H	H	H	H	H	Ba	H	Ba	Ba
27	RGDU05228-3-570-27	1.6 ± 1.5	Ba	Ba	Ba	H	Ba	Ba	Ba	Ba	H
28	RGDU05228-3-570-28	2.7 ± 1.9	H	H	H	H	H	H	H	H	PK
29	RGDU05228-3-570-29	12.7 ± 9.8	PK	PK	PK	PK	PK	PK	PK	PK	H
30	RGDU05228-3-570-30	4.4 ± 2.0	H	H	H	Ba	H	H	H	H	H
31	RGDU05228-3-570-31	1.4 ± 0.8	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
32	RGDU05228-3-570-32	11.2 ± 8.8	H	H	H	H	H	H	H	H	H
33	RGDU05228-3-570-33	5.6 ± 3.0	H	H	H	H	H	H	H	H	H
34	RGDU05228-3-570-34	6.2 ± 3.0	H	H	H	H	H	H	H	H	Ba
35	RGDU05228-3-570-35	4.6 ± 1.7	H	H	H	H	H	H	H	H	PK
36	RGDU05228-3-570-36	3.2 ± 1.8	H	H	H	H	H	H	H	H	H
37	RGDU05228-3-570-37	4.7 ± 1.9	H	H	H	H	H	H	H	H	H
38	RGDU05228-3-570-38	10.4 ± 4.3	PK	PK	PK	PK	PK	PK	PK	PK	H
39	RGDU05228-3-570-39	7.8 ± 2.4	H	H	H	Ba	H	H	H	H	H
40	RGDU05228-3-570-40	1.3 ± 1.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
41	RGDU05228-3-570-41	4.8 ± 2.6	PK	PK	PK	H	PK	H	PK	H	Ba
42	RGDU05228-3-570-42	3.6 ± 2.3	H	H	H	PK	H	H	H	H	H
43	RGDU05228-3-570-43	8.6 ± 2.5	PK	PK	PK	PK	PK	PK	PK	PK	H
44	RGDU05228-3-570-44	13.5 ± 10.6	H	H	H	H	H	H	H	H	H
45	RGDU05228-3-570-45	6.8 ± 2.1	PK	PK	PK	PK	PK	PK	PK	PK	H
46	RGDU05228-3-570-46	9.2 ± 3.6	PK	PK	PK	PK	PK	PK	PK	PK	PK
47	RGDU05228-3-570-47	9.5 ± 2.9	PK	PK	PK	PK	PK	PK	PK	PK	H
48	RGDU05228-3-571-1	1.2 ± 1.1	Ba	H	Ba	Ba	Ba	H	Ba	Ba	H
49	RGDU05228-3-571-2	6.0 ± 2.5	H	H	H	H	H	H	H	H	PK
50	RGDU05228-3-571-3	4.8 ± 1.8	H	H	H	H	H	H	H	H	H
51	RGDU05228-3-571-4	3.5 ± 0.1	H	H	H	H	H	H	H	H	PK
52	RGDU05228-3-571-5	2.2 ± 3.5	Ba	PK	Ba	Ba	Ba	Ba	Ba	Ba	PK
53	RGDU05228-3-571-6	9.6 ± 5.1	PK	PK	PK	PK	PK	PK	PK	H	H
54	RGDU05228-3-571-7	2.9 ± 1.0	H	H	H	H	H	H	H	H	H
55	RGDU05228-3-571-8	2.6 ± 1.5	H	H	H	H	H	H	H	H	PK

Appendix Table 4 (Continued)

Entry	**Pedigree**	**TXO16**	**Genome position (Mb)**								
			27.15	**27.16**	**27.25**	**27.43**	**27.56**	**28.01**	**27.82**	**28.43**	**28.59**
		LL (mean±*sd* ; cm)	**RM20523**	**RM20536**	**RM30**	**RM3430**	**RM7243**	**RM20590**	**RM5509**	**RM400**	**RM340**
56	RGDU05228-3-571-9	10.1 ± 1.7	PK	PK	PK	PK	PK	PK	PK	PK	H
57	RGDU05228-3-571-10	7.3 ± 1.0	PK	PK	PK	PK	PK	PK	PK	PK	H
58	RGDU05228-3-571-11	4.0 ± 2.1	H	H	H	H	H	H	H	H	H
59	RGDU05228-3-571-12	8.3 ± 3.4	PK	PK	PK	PK	PK	PK	PK	PK	H
60	RGDU05228-3-571-13	3.7 ± 2.0	H	H	H	H	H	H	H	H	Ba
61	RGDU05228-3-571-14	2.7 ± 1.5	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
62	RGDU05228-3-571-15	8.6 ± 2.5	PK	PK	PK	PK	PK	PK	PK	PK	H
63	RGDU05228-3-571-16	5.7 ± 3.2	H	H	H	H	H	H	H	H	PK
64	RGDU05228-3-571-17	9.0 ± 2.9	PK	PK	PK	PK	PK	PK	PK	PK	H
65	RGDU05228-3-571-18	3.8 ± 1.8	H	H	H	H	H	H	H	H	H
66	RGDU05228-3-571-19	0.5 ± 0.4	Ba	PK	Ba	Ba	Ba	Ba	Ba	Ba	Ba
67	RGDU05228-3-571-20	7.0 ± 3.2	PK	PK	PK	PK	PK	PK	PK	PK	H
68	RGDU05228-3-571-21	4.8 ± 1.9	H	H	H	H	H	H	H	H	H
69	RGDU05228-3-571-22	6.5 ± 2.2	PK	PK	PK	PK	PK	PK	PK	PK	PK
70	RGDU05228-3-571-23	3.6 1.6	H	H	H	H	H	H	H	H	H
71	RGDU05228-3-571-24	5.1 2.2	PK	PK	PK	PK	PK	PK	PK	PK	PK
72	RGDU05228-3-571-25	6.0 1.6	H	H	H	H	H	H	H	H	PK
73	RGDU05228-3-571-26	3.1 1.6	H	H	H	H	H	H	H	H	H
74	RGDU05228-3-571-27	4.6 2.7	H	H	H	H	H	H	H	H	H
75	RGDU05228-3-571-28	3.7 1.2	H	H	H	H	H	H	H	H	H
76	RGDU05228-3-571-29	5.3 1.5	H	H	H	H	H	H	H	PK	PK
77	RGDU05228-3-571-30	4.8 1.8	H	H	H	H	H	H	H	H	H
78	RGDU05228-3-571-31	5.1 3.2	H	H	H	H	H	H	H	H	H
79	RGDU05228-3-571-32	3.4 1.4	H	H	H	H	H	H	H	H	H
80	RGDU05228-3-571-33	2.9 2.1	H	H	H	H	H	H	H	H	PK
81	RGDU05228-3-571-34	2.8 1.1	H	H	H	H	H	H	H	H	PK
82	RGDU05228-3-571-35	4.2 1.7	H	H	H	H	H	H	H	H	H
83	RGDU05228-3-571-36	0.6 0.4	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
84	RGDU05228-3-571-37	7.7 2.7	PK	PK	PK	PK	PK	PK	PK	PK	Ba
85	RGDU05228-3-571-38	11.1 1.1	PK	PK	PK	PK	PK	PK	PK	PK	PK

Appendix Table 4 (Continued)

Entry	Pedigree	TXO16		Genome position (Mb)								
				27.15	27.16	27.25	27.43	27.56	28.01	27.82	28.43	28.59
		LL (mean±*sd* ; cm)		RM20523	RM20536	RM30	RM3430	RM7243	RM20590	RM5509	RM400	RM340
86	RGDU05228-3-571-39	6.8	1.9	H	H	H	H	H	H	H	H	H
87	RGDU05228-3-571-40	2.0	0.6	H	H	H	H	H	H	H	H	H
88	RGDU05228-3-665-1	5.8	3.7	H	H	H	H	H	H	H	H	
89	RGDU05228-3-665-2	6.1	4.1	H	H	H	H	H	H	H	H	H
90	RGDU05228-3-665-3	3.6	1.7	H	H	H	H	H	H	H	H	H
91	RGDU05228-3-665-4	8.7	2.5	PK	PK	PK	PK	PK	PK	PK	H	H
92	RGDU05228-3-665-5	2.1	0.8	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
93	RGDU05228-3-665-6	5.7	0.3	H	H	H	H	H	H	H	H	Ba
94	RGDU05228-3-665-7	5.6	2.5	H	H	H	H	H	H	H	H	H
95	RGDU05228-3-665-8	6.7	2.1	PK	PK	PK	PK	PK	PK	PK	PK	Ba
96	RGDU05228-3-665-9	5.3	2.8	H	H	H	H	H	H	H	H	H
97	RGDU05228-3-665-10	8.3	2.8	PK	PK	PK	PK	PK	PK	PK	PK	Ba
98	RGDU05228-3-665-11	10.6	1.9	PK	PK	PK	PK	PK	PK	PK	PK	H
99	RGDU05228-3-665-12	7.3	2.4	PK	PK	PK	PK	PK	H	PK	H	PK
100	RGDU05228-3-665-13	6.9	3.0	H	H	H	H	H	H	H	H	PK
101	RGDU05228-3-665-14	1.6	0.9	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	PK
102	RGDU05228-3-665-15	8.2	1.9	H	H	H	H	H	H	H	H	Ba
103	RGDU05228-3-665-16	5.1	1.8	H	H	H	H	H	H	H	H	H
104	RGDU05228-3-665-17	5.1	1.2	H	H	H	H	H	H	H	H	H
105	RGDU05228-3-665-18	3.3	1.7	H	H	H	H	H	H	H	H	PK
106	RGDU05228-3-665-19	1.8	1.9	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
107	RGDU05228-3-665-20	5.7	1.9	PK	PK	PK	PK	PK	PK	PK	H	Ba
108	RGDU05228-3-665-21	3.7	2.0	H	H	H	H	H	H	H	H	H
109	RGDU05228-3-665-22	1.0	0.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
110	RGDU05228-3-665-23	7.6	3.0	H	H	H	H	H	PK	H	PK	H
111	RGDU05228-3-665-24	7.0	1.9	PK	PK	PK	PK	PK	PK	PK	PK	PK
112	RGDU05228-3-665-25	1.4	0.5	H	H	H	H	H	H	H	H	H
113	RGDU05228-3-665-26	5.5	3.0	H	H	H	H	H	H	H	H	Ba
114	RGDU05228-3-665-27	2.5	1.0	H	H	H	H	PK	H	H	H	H
115	RGDU05228-3-665-28	6.7	1.9	H	H	H	H	H	H	H	H	H

Appendix Table 4 (Continued)

Entry	**Pedigree**	**TXO16**		**Genome position (Mb)**								
				27.15	**27.16**	**27.25**	**27.43**	**27.56**	**28.01**	**27.82**	**28.43**	**28.59**
		LL (mean±*sd* ; cm)		**RM20523**	**RM20536**	**RM30**	**RM3430**	**RM7243**	**RM20590**	**RM5509**	**RM400**	**RM340**
116	RGDU05228-3-665-29	1.6	1.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
117	RGDU05228-3-665-30	13.1	3.0	PK	PK	PK	PK	PK	PK	PK	PK	H
118	RGDU05228-3-665-31	6.4	2.0	H	H	H	H	H	H	H	H	H
119	RGDU05228-3-665-32	0.8	0.2	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
120	RGDU05228-3-665-33	0.4	0.3	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
121	RGDU05228-3-665-34	3.4	1.6	H	H	H	H	H	H	H	H	Ba
122	RGDU05228-3-665-35	8.2	2.5	PK	PK	PK	PK	PK	PK	PK	PK	H
123	RGDU05228-3-665-36	5.2	3.3	H	H	H	H	H	H	H	H	PK
124	RGDU05228-3-665-37	7.8	4.6	H	H	H	H	H	H	H	H	H
125	RGDU05228-3-665-38	9.9	2.1	PK	PK	PK	PK	PK	PK	PK	H	Ba
126	RGDU05228-3-665-39	6.8	1.8	PK	PK	PK	PK	PK	H	H	H	H
127	RGDU05228-3-169-1	5.6	3.0	H	H	H	H	H	H	H	H	H
128	RGDU05228-3-169-2	5.8	0.4	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
129	RGDU05228-3-169-3	9.2	2.9	PK	PK	PK	PK	PK	PK	PK	PK	H
130	RGDU05228-3-169-4	7.1	3.8	H	H	H	H	H	H	H	H	H
131	RGDU05228-3-169-5	6.1	2.7	Ba	Ba	Ba	Ba	H	H	H	H	H
132	RGDU05228-3-169-6	6.0	2.7	H	H	H	H	H	H	H	H	PK
133	RGDU05228-3-169-7	8.9	3.2	PK	PK	PK	PK	PK	PK	PK	H	H
134	RGDU05228-3-169-8	1.2	0.8	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
135	RGDU05228-3-169-9	0.6	0.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
136	RGDU05228-3-169-10	6.6	0.3	H	H	H	H	H	H	H	H	H
137	RGDU05228-3-169-11	6.4	2.5	H	H	H	H	H	H	H	H	PK
138	RGDU05228-3-169-12	9.0	5.4	PK	PK	PK	H	PK	H	H	H	H
139	RGDU05228-3-169-13	5.2	2.3	H	H	H	H	H	H	H	H	PK
140	RGDU05228-3-169-14	9.0	3.6	PK	PK	PK	PK	PK	PK	PK	PK	PK
141	RGDU05228-3-169-15	5.3	2.9	H	H	H	H	H	H	H	H	PK
142	RGDU05228-3-169-16	6.9	4.4	H	H	H	H	H	H	H	H	Ba
143	RGDU05228-3-169-17	6.1	2.6	H	H	H	PK	PK	PK	PK	PK	H
144	RGDU05228-3-169-18	5.3	2.4	H	H	H	H	H	H	H	H	H
145	RGDU05228-3-169-19	7.2	2.8	PK	PK	PK	PK	PK	PK	PK	PK	H

Appendix Table 4 (Continued)

Entry	Pedigree	TXO16		Genome position (Mb)								
				27.15	27.16	27.25	27.43	27.56	28.01	27.82	28.43	28.59
		LL (mean±*sd* ; cm)		RM20523	RM20536	RM30	RM3430	RM7243	RM20590	RM5509	RM400	RM340
146	RGDU05228-3-169-20	7.4	1.9	PK	PK	PK	PK	PK	PK	PK	PK	Ba
147	RGDU05228-3-169-21	5.3	3.4	H	H	H	H	H	H	H	H	PK
148	RGDU05228-3-169-22	8.2	3.1	H	H	H	H	H	H	H	H	H
149	RGDU05228-3-169-23	10.0	2.0	PK	PK	PK	PK	PK	PK	PK	PK	H
150	RGDU05228-3-169-24	8.7	3.2	H	H	H	H	H	H	H	H	PK
151	RGDU05228-3-169-25	4.1	2.1	H	H	H	H	H	H	H	H	PK
152	RGDU05228-3-169-26	1.5	0.5	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H	H
153	RGDU05228-3-169-27	7.0	3.0	H	H	H	H	H	H	H	H	PK
154	RGDU05228-3-169-28	1.6	1.6	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H
155	RGDU05228-3-169-29	6.6	2.5	H	H	H	H	H	H	H	H	H
156	RGDU05228-3-169-30	3.3	2.2	H	H	H	H	H	H	H	H	PK
157	RGDU05228-3-169-31	6.5	0.8	PK	PK	PK	PK	PK	PK	PK	PK	H
158	RGDU05228-3-169-32	2.5	0.8	H	H	H	H	H	H	H	H	PK
159	RGDU05228-3-169-33	1.1	1.1	Ba	Ba	Ba	Ba	Ba	Ba	Ba	H	Ba
160	RGDU05228-3-169-34	1.3	0.8	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba	Ba
161	RGDU05228-3-169-35	7.1	2.5	H	H	H	H	H	H	H	H	PK

Appendix Table 5 Genotypes of 104 F_1 progenies from the cross between Py-*xa5/Xa21/qBB11* and Py-*xa33(t)/Xa34(t)* used for development of F_2.

Entry	**Gene**	***xa5***		***xa33(t)***	
	Pedigree	**PAxa5**	**RM7243**	**RM5509**	**RM400**
	KDML105	3	3	3	3
	IR62266	**1**	3	7	7
	Ba7	3	**1**	**1**	**1**
	PK	3	3	3	3
	IR1188	3	3	5	1
1	RGDU07095-1	13	13	15	13
2	RGDU07095-2	13	3	3	13
3	RGDU07095-3	13	13	15	13
4	RGDU07095-4	13	13	15	3
5	RGDU07095-5	13	3	3	3
6	RGDU07095-6	13	13	15	13
7	RGDU07095-7	13	13	15	13
8	RGDU07095-8	13	3	3	3
9	RGDU07095-9	13	13	15	13
10	RGDU07095-10	13	3	3	3
11	RGDU07095-11	13	3	3	3
12	RGDU07095-12	13	3	3	3
13	RGDU07095-13	13	3	3	3
14	RGDU07095-14	13	3	3	3
15	RGDU07095-15	13	13	15	13
16	RGDU07095-16	13	13	15	13
17	RGDU07095-17	13	3	3	3
18	RGDU07095-18	13	13	15	13
19	RGDU07095-19	13	3	3	3
20	RGDU07095-20	13	3	3	3
21	RGDU07095-21	13	13	13	13
22	RGDU07095-22	13	13	13	13
23	RGDU07095-23	13	3	3	3
24	RGDU07095-24	13	13	15	13
25	RGDU07095-25	13	3	3	3
26	RGDU07095-27	13	13	-	3
27	RGDU07095-28	13	13	15	13
28	RGDU07095-29	13	3	3	3
29	RGDU07096-2	**13**	**13**	**13**	**13**
30	RGDU07096-3	13	3	3	3
31	RGDU07096-4	13	13	13	13
32	RGDU07096-5	13	13	0	13
33	RGDU07096-6	13	3	3	3
34	RGDU07096-7	13	3	3	3
35	RGDU07097-1	**13**	**13**	**13**	**13**
36	RGDU07097-2	13	3	3	3
37	RGDU07097-3	13	3	3	3
38	RGDU07097-4	13	3	3	3

Appendix Table 5 (Continued)

Entry	Gene	*xa5*	*xa33(t)*		
	Pedigree	**PAxa5**	**RM7243**	**RM5509**	**RM400**
39	RGDU07097-5	13	13	15	13
40	RGDU07097-6	13	13	15	13
41	RGDU07097-7	13	13	15	13
42	RGDU07097-8	13	3	3	3
43	RGDU07097-9	13	3	3	3
44	RGDU07097-10	13	3	3	3
45	RGDU07097-11	13	13	15	13
46	RGDU07097-12	**13**	**13**	**13**	**13**
47	RGDU07097-13	13	3	3	3
48	RGDU07097-14	**13**	**13**	**13**	**13**
49	RGDU07097-15	**13**	**13**	**13**	**3**
50	RGDU07097-16	**13**	**13**	**13**	**13**
51	RGDU07097-17	13	13	15	13
52	RGDU07097-18	13	3	3	3
53	RGDU07097-19	13	3	3	3
54	RGDU07097-20	**13**	**13**	**13**	**13**
55	RGDU07097-21	13	13	15	13
56	RGDU07097-22	13	3	3	3
57	RGDU07097-23	13	3	3	3
58	RGDU07097-24	13	3	3	3
59	RGDU07097-25	13	3	3	3
60	RGDU07097-26	**13**	**13**	**13**	**13**
61	RGDU07097-27	**13**	**13**	**13**	**13**
62	RGDU07097-28	**13**	**13**	**13**	**13**
63	RGDU07097-29	13	13	15	13
64	RGDU07097-30	13	3	-	3
65	RGDU07099-1	**13**	**13**	**13**	**13**
66	RGDU07099-2	**13**	**13**	**13**	**13**
67	RGDU07099-3	**13**	**13**	**13**	**13**
68	RGDU07099-4	13	13	13	13
69	RGDU07099-5	**13**	**13**	**13**	**13**
70	RGDU07099-6	**13**	**13**	**13**	**13**
71	RGDU07099-7	13	3	3	3
72	RGDU07099-8	**13**	**13**	**13**	**13**
73	RGDU07099-9	13	3	3	3
74	RGDU07099-10	13	3	3	3
75	RGDU07099-11	13	3	3	3
76	RGDU07094-1	13	13	15	13
77	RGDU07094-2	13	13	15	13
78	RGDU07094-3	13	13	15	13
79	RGDU07094-4	13	3	35	3
80	RGDU07094-5	13	3	35	3
81	RGDU07094-6	13	13	15	13
82	RGDU07094-7	13	13	15	13
83	RGDU07094-8	13	13	15	13
84	RGDU07094-9	13	3	35	3

Appendix Table 5 (Continued)

Entry	**Gene**	***xa5***	***xa33(t)***		
	Pedigree	**PAxa5**	**RM7243**	**RM5509**	**RM400**
85	RGDU07094-10	13	3	35	3
86	RGDU07094-11	13	3	35	3
87	RGDU07094-12	13	3	35	3
88	RGDU07094-13	13	13	15	13
89	RGDU07094-14	13	3	35	3
90	RGDU07094-15	13	13	15	13
91	RGDU07094-16	13	3	35	3
92	RGDU07094-17	13	13	15	13
93	RGDU07094-18	13	13	15	13
94	RGDU07094-19	13	13	15	13
95	RGDU07094-20	13	13	15	13
96	RGDU07094-21	13	3	35	3
97	RGDU07094-22	13	13	15	13
98	RGDU07094-23	13	3	35	3
99	RGDU07094-24	13	13	35	13
100	RGDU07094-25	13	13	15	13
101	RGDU07094-26	13	3	35	3
102	RGDU07094-27	13	3	35	3
103	RGDU07094-28	13	13	15	13
104	RGDU07094-29	13	3	35	3

Appendix Table 6 Genotypes of 500 F_2 individuals from the cross between Py-*xa5/Xa21/qBB11* and Py-*xa33(t)/Xa34(t)*.

Entry	Pedigree	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
	KDML105	3	3	5	3	3	3
	IR1188	3	**1**	**1**	3	5	1
	Ba7	3	4	7	**1**	**1**	**1**
	IR62266	**1**	3	9	3	7	5
	PK	3	3	**3**	3	3	3
	104-4-1-19-7	3	**1**	**1**	3	3	3
1	RGDU07096-2-1M	1/3	1/3	1/3	3	3	1/3
2	RGDU07096-2-2M	1/3	1/3	1/3	1/3	1/3	1/3
3	RGDU07096-2-3M	1	1/3	1/3	1/3	1/3	1/3
4	RGDU07096-2-4M	1/3	1	1	1/3	1/3	1/3
5	RGDU07096-2-5M	1/3	1	1	1/3	1/3	1/3
6	RGDU07096-2-6M	1	1/3	1/3	1/3	1/3	1/3
7	RGDU07096-2-7M	1/3	1	1	3	3	1/3
8	RGDU07096-2-8M	1/3	3	3	1/3	1/3	1/3
9	RGDU07096-2-9M	1/3	1	1/3	3	3	3
10	RGDU07096-2-10M	1	1/3	1/3	1	1	1
11	RGDU07096-2-11M	1/3	3	3	3	3	3
12	RGDU07096-2-12M	1	3	1/3	3	3	3
13	RGDU07096-2-13M	1	3	3	3	3	3
14	RGDU07096-2-14M	1/3	3	3	3	3	3
15	RGDU07096-2-15M	1/3	1/3	1/3	1/3	1/3	1/3
16	RGDU07097-1-1M	1	3	1/3	3	3	3
17	RGDU07097-1-2M	3	1	1/3	3	3	3
18	RGDU07097-1-3M	13	1/3	1	1/3	1/3	1/3
19	RGDU07097-1-4M	3	1/3	1/3	1	1	1
20	RGDU07097-1-5M	13	1	1	1/3	1/3	1/3
21	RGDU07097-1-6M	13	3	3	1/3	1/3	1/3
22	RGDU07097-1-7M	13	1	1/3	1/3	1/3	1/3
23	RGDU07097-1-8M	1	1	1	1	1	1
24	RGDU07097-1-9M	3	1/3	1/3	1/3	1/3	1/3
25	RGDU07097-1-10M	1/3	1/3	1	1/3	1/3	1/3
26	RGDU07097-1-11M	1/3	3	1/3	3	3	3
27	RGDU07097-1-12M	1/3	1/3	1/3	1/3	1/3	1/3
28	RGDU07097-1-13M	1	1/3	1/3	1/3	1/3	1/3
29	RGDU07097-1-14M	13	3	3	1	1	1
30	RGDU07097-1-15M	13	13	1/3	1/3	1/3	1/3
31	RGDU07097-1-16M	1	1	1	1/3	1/3	1/3
32	RGDU07097-1-17M	1	1	1	3	3	3
33	RGDU07097-1-18M	1	1	1	1/3	1/3	1/3
34	RGDU07097-1-19M	1/3	1	1	1/3	1/3	1/3
35	RGDU07097-1-20M	1/3	1	1	1	1	1
36	RGDU07097-1-21M	1/3	1/3	1/3	1/3	1/3	1
37	RGDU07097-1-22M	1	1/3	1	1	1	1
38	RGDU07097-1-23M	1/3	1/3	1/3	1	1	1
39	RGDU07097-1-24M	3	3	1/3	1/3	1/3	1/3
40	RGDU07097-1-25M	1/3	1	1	3	3	3

Appendix Table 6 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
41	RGDU07097-1-26M	1	1/3	3	3	3	3
42	RGDU07097-1-27M	1	3	3	1	1	1
43	RGDU07097-1-28M	1/3	1/3	1/3	1/3	1/3	1/3
44	RGDU07097-1-29M	1/3	1/3	3	3	3	3
45	RGDU07097-1-30M	1	3	3	1	1	1
46	RGDU07097-1-31M	1/3	1	1	1	1	1
47	RGDU07097-1-32MKPS	3	1/3	1/3	3	3	1/3
48	RGDU07097-1-33M	1/3	3	3	1/3	3	3
49	RGDU07097-1-34MKPS	1/3	1/3	1/3	1/3	1/3	1
50	RGDU07097-1-35M	1/3	1	1	1	1	1
51	RGDU07097-1-36M	1/3	1/3	1/3	1/3	1/3	1/3
52	RGDU07097-1-37M	3	1	1/3	3	3	1/3
53	RGDU07097-1-38MKPS	1/3	1/3	1/3	1/3	1/3	1/3
54	RGDU07097-1-39M	1/3	1/3	1/3	1/3	1/5	3
55	RGDU07097-1-40M	1/3	1/3	1/3	1/3	1/3	1/3
56	RGDU07097-1-41MKPS	3	1/3	1/3	3	3	3
57	RGDU07097-1-42M	1	3	3	1	1	1
58	RGDU07097-1-43M	1	1/3	1/3	3	3	3
59	RGDU07097-1-44M	3	1	1	1/3	1/3	1/3
60	RGDU07097-1-45M	1/3	1/3	1/3	3	3	3
61	RGDU07097-1-46M	1/3	3	3	1/3	1/3	1/3
62	RGDU07097-1-47M	1	3	1/3	3	3	3
63	RGDU07097-1-48M	1	3	3	1/3	1/3	1/3
64	RGDU07097-1-49MKPS	1/3	1	1	1/3	1/3	1/3
65	RGDU07097-1-50M	1/3	1	1	1	1	1
66	RGDU07097-1-51M	3	1/3	1/3	1/3	1/3	1/3
67	RGDU07097-12-1MKPS	3	3	3	1	1	1
68	RGDU07097-14-1M	1/3	1/3	3	3	3	3
69	RGDU07097-14-2M	1/3	1/3	1/3	1	1	1
70	RGDU07097-14-3M	1/3	3	3	3	3	3
71	RGDU07097-15-1M	1/3	3	1/3	1/3	1/3	3
72	RGDU07097-15-2M	1	1	1	1	1	3
73	RGDU07097-15-3M	1	1/3	1/3	1	1	3
74	RGDU07097-15-4M	3	1/3	1/3	1/3	1/3	3
75	RGDU07097-15-5M	1/3	1/3	1/3	3	3	3
76	RGDU07097-15-6M	1	1	1/3	1/3	1/3	3
77	RGDU07097-15-7M	3	1/3	1/3	1	1	3
78	RGDU07097-15-8MKPS	1/3	1/3	3	3	3	3
79	RGDU07097-15-9M	1/3	1/3	1	1	1	3
80	RGDU07097-15-10M	1	1/3	1/3	1/3	1/3	3
81	RGDU07097-15-11M	1/3	3	3	3	3	3
82	RGDU07097-15-12M	3	1/3	3	3	3	3
83	RGDU07097-15-13MKPS	1/3	1/3	1/3	1/3	1/3	3
84	RGDU07097-15-14M	3	1/3	1/3	3	3	3
85	RGDU07097-15-15M	1	1	1	1/3	1/3	3
86	RGDU07097-15-16M	1/3	1/3	1/3	1	1	3
87	RGDU07097-15-17M	1	1/3	1/3	3	3	3
88	RGDU07097-15-18M	1	1/3	1/3	1	1	3
89	RGDU07097-15-19M	3	3	3	3	3	3
90	RGDU07097-15-20M	1/3	1/3	1/3	1/3	1/3	3

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
91	RGDU07097-15-21M	1	1/3	1	1	1	3
92	RGDU07097-15-22M	1	1	1	1/3	1/3	3
93	RGDU07097-15-23M	1/3	1	1	1/3	1/3	3
94	RGDU07097-15-24M	1	1/3	1/3	1	1	3
95	RGDU07097-15-25M	3	3	3	1/3	1/3	3
96	RGDU07097-15-26M	1	3	3	3	3	3
97	RGDU07097-15-27M	3	3	3	3	3	3
98	RGDU07097-15-28M	3	1/3	1/3	1/3	1/3	3
99	RGDU07097-15-29M	3	1/3	1/3	1/3	1/3	3
100	RGDU07097-15-30M	1	1/3	1/3	3	3	3
101	RGDU07097-15-31M	1/3	3	1/3	3	3	3
102	RGDU07097-15-32M	3	3	1/3	1	1	3
103	RGDU07097-15-33M	1/3	3	3	1	1	3
104	RGDU07097-15-34M	3	1/3	3	1	1	3
105	RGDU07097-15-35M	3	3	3	3	3	3
106	RGDU07097-16-1M	13	3	3	1	1	1
107	RGDU07097-16-2M	1	3	3	1	1	1/3
108	RGDU07097-16-3MKPS	3	1	1	1/3	1/3	1/3
109	RGDU07097-16-4M	1/3	1/3	1/3	1/3	1/3	1/3
110	RGDU07097-20-1M	1/3	1/3	1/3	1/3	1/3	1/3
111	RGDU07097-20-2M	1/3	1/3	3	1	1/3	1/3
112	RGDU07097-20-3M	1	1	1	1	1	1
113	RGDU07097-20-4M	1	1/3	3	1/3	1/3	1/3
114	RGDU07097-20-5M	1/3	1	1/3	1/3	1/3	1/3
115	RGDU07097-20-6MKPS	3	1/3	3	1/3	1/3	1/3
116	RGDU07097-20-7M	1/3	1/3	1/3	1	1	3
117	RGDU07097-20-8M	1/3	1	1	3	3	3
118	RGDU07097-20-9MKPS	3	1	1	3	3	3
119	RGDU07097-26-1M	1/3	1/3	1/3	1/3	1/3	1/3
120	RGDU07097-26-2M	3	1	1	3	3	3
121	RGDU07097-26-3M	1/3	3	3	1/3	1/3	1/3
122	RGDU07097-26-4M	1/3	1	1/3	1/3	1/3	1/3
123	RGDU07097-26-5M	3	3	3	1/3	1/3	1/3
124	RGDU07097-26-6MKPS	1	3	3	3	3	3
125	RGDU07097-26-7M	1/3	1/3	1/3	1/3	1/3	1/3
126	RGDU07097-26-8M	3	1	1	1	1	1
127	RGDU07097-26-9M	3	1/3	1/3	1/3	1/3	1/3
128	RGDU07097-26-10M	3	1/3	1	1	1	1
129	RGDU07097-26-11M	1/3	1	1/3	1/3	1/3	1/3
130	RGDU07097-26-12M	1	1	1/3	1/3	1/3	1/3
131	RGDU07097-26-13MKPS	1	1/3	3	3	3	1/3
132	RGDU07097-26-14M	3	1/3	1/3	1	1	1
133	RGDU07097-26-15M	1/3	1	1/3	3	3	1
134	RGDU07097-26-16M	1/3	1/3	1/3	3	3	3
135	RGDU07097-26-17M	1/3	1	1	1/3	1/3	1/3
136	RGDU07097-26-18MKPS	1/3	1/3	3	1/3	1/3	1/3
137	RGDU07097-26-19	1/3	1/3	1	1/3	1/3	1/3
138	RGDU07097-26-20MKPS	3	1/3	1/3	1/3	1/3	1/3
139	RGDU07097-26-21M	3	1/3	1/3	1/3	1/3	1/3
140	RGDU07097-26-22M	1/3	1/3	1/3	1/3	1/3	1

Appendix Table 6 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
141	RGDU07097-27-1M	1	1	1/3	3	3	3
142	RGDU07097-27-2M	1/3	3	3	1/3	1/3	1/3
143	RGDU07097-27-3M	1/3	3	3	3	3	3
144	RGDU07097-27-4M	3	1	1/3	1	1	1
145	RGDU07097-27-5M	1/3	1/3	1/3	3	3	3
146	RGDU07097-27-6M	1/3	1	1	1/3	1/3	1/3
147	RGDU07097-27-7M	1/3	1/3	1	1/3	1/3	1/3
148	RGDU07097-27-8M	3	3	3	1/3	1/3	1/3
149	RGDU07097-27-9M	3	1	1/3	3	3	3
150	RGDU07097-27-10M	1/3	1/3	1/3	3	3	3
151	RGDU07097-27-11M	1/3	1/3	1/3	1/3	1/3	1/3
152	RGDU07097-27-12M	3	1/3	1/3	1	1	1
153	RGDU07097-27-13M	3	3	3	1/3	1/3	1/3
154	RGDU07097-27-14M	1	1/3	1/3	3	3	3
155	RGDU07097-27-15M	3	1/3	1/3	3	3	3
156	RGDU07097-27-16M	1	3	3	1/3	1/3	1/3
157	RGDU07097-27-17MKPS	1	3	3	1	1	1
158	RGDU07097-27-18M	1/3	1/3	1/3	3	3	3
159	RGDU07097-27-19M	1/3	1/3	1	3	3	3
160	RGDU07097-27-20M	13	1	1	1/3	1/3	1/3
161	RGDU07097-27-21M	3	1/3	1/3	1/3	1/3	1/3
162	RGDU07097-27-22M	1/3	1/3	1/3	3	3	3
163	RGDU07097-27-23M	1/3	3	3	1/3	1/3	1/3
164	RGDU07097-27-24M	1	1/3	1/3	1	1	1
165	RGDU07097-27-25M	1/3	1/3	1/3	1/3	1/3	1/3
166	RGDU07097-27-26M	1/3	1/3	1/3	1/3	1/3	1/3
167	RGDU07097-27-27M	1	1/3	1	1/3	1/3	1/3
168	RGDU07097-27-28M	3	1	1	1/3	1/3	1/3
169	RGDU07097-27-29M	1	1	1	1	1	1
170	RGDU07097-27-30M	1	1	1	1/3	1/3	1/3
171	RGDU07097-27-31M	1	1/3	1/3	1/3	1/3	1/3
172	RGDU07097-27-32M	1/3	1/3	1/3	1/3	1/3	1/3
173	RGDU07097-27-33M	3	1	1	1/3	1/3	3
174	RGDU07097-27-34M	1/3	1/3	1/3	1/3	1/3	1/3
175	RGDU07097-27-35M	1	1/3	3	1	1	1
176	RGDU07097-27-36M	3	1/3	1/3	1/3	1/3	1
177	RGDU07097-27-37M	3	1/3	1/3	3	3	3
178	RGDU07097-27-38M	1/3	1/3	1	1/3	3	3
179	RGDU07097-28-1M	1/3	1	1/3	1/3	1/3	1/3
180	RGDU07097-28-2M	1/3	3	3	1	1	1
181	RGDU07097-28-3M	3	1	1	3	3	3
182	RGDU07097-28-4M	1	3	3	1	1	13
183	RGDU07097-28-5M	3	1/3	13	13	13	13
184	RGDU07097-28-6M	3	1/3	1	3	3	3*
185	RGDU07097-28-7M	1/3	1/3	1	3	3	3
186	RGDU07097-28-8M	1/3	3	3	3	3	3
187	RGDU07097-28-9M	1	1	1/3	1	1	1
188	RGDU07097-28-10M	1/3	1/3	1/3	1/3	1/3	1/3
189	RGDU07097-28-11M	1/3	1	1/3	1/3	1/3	1/3
190	RGDU07097-28-12M	1/3	3	3	3	3	3

Appendix Table 6 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
191	RGDU07097-28-13M	3	1/3	13	1	1	1
192	RGDU07097-28-14M	3	3	3	1	1	1
193	RGDU07097-28-15M	3	1/3	1/3	1/3	1/3	1/3
194	RGDU07097-28-16M	3	3	3	1/3	1/3	1/3
195	RGDU07097-28-17M	1	1/3	3	1/3	1/3	3
196	RGDU07097-28-18M	1/3	1/3	1/3	1/3	1/3	1/3
197	RGDU07097-28-19M	1/3	1/3	1/3	1/3	1/3	1/3
198	RGDU07097-28-20M	1	1/3	3	1	1	1
199	RGDU07097-28-21M	1	3	1/3	3	3	3
200	RGDU07097-28-22M	3	1	1	3	3	3
201	RGDU07097-28-23M	1/3	3	3	3	3	3
202	RGDU07097-28-24M	1	1	1	1/3	1	1
203	RGDU07097-28-25M	3	1	1	1/3	1/3	1/3
204	RGDU07097-28-26M	3	1/3	1/3	1/3	1/3	1/3
205	RGDU07097-28-27M	3	1/3	1/3	1/3	1/3	1/3
206	RGDU07097-28-28M	1/3	3	1/3	1/3	1/3	1/3
207	RGDU07097-28-29M	1/3	1/3	1/3	1	1	1
208	RGDU07097-28-30M	1/3	1/3	1/3	1/3	1/3	1/3
209	RGDU07097-28-31M	1/3	1/3	1/3	1/3	1/3	3
210	RGDU07097-28-32M	1	3	3	1	1	1
211	RGDU07097-28-33M	1/3	1/3	1/3	1	1/3	1/3
212	RGDU07097-28-34M	1/3	1/3	1	1/3	1/3	1/3
213	RGDU07097-28-35M	1/3	1/3	1	3	3	3
214	RGDU07097-28-36M	1	1	1	3	3	3
215	RGDU07097-28-37M	1/3	1/3	3	1/3	1/3	1/3
216	RGDU07097-28-38M	3	1/3	1/3	3	3	3
217	RGDU07097-28-39M	3	1/3	1/3	1	1	1/3
218	RGDU07097-28-40M	1/3	3	3	3	3	3
219	RGDU07097-28-41M	3	1/3	1/3	1/3	1/3	1/3
220	RGDU07097-28-42M	1/3	3	3	3	3	13
221	RGDU07097-28-43M	1	1/3	1/3	1/3	1/3	1/3
222	RGDU07097-28-44M	1/3	1/3	1	1	1	1
223	RGDU07097-28-45M	1	1/3	1/3	1/3	1/3	1/3
224	RGDU07097-28-46M	1	1	1	1/3	1/3	1/3
225	RGDU07097-28-47MKPS	1/3	1/3	1/3	1/3	1/3	1/3
226	RGDU07097-28-48M	1	1/3	3	1/3	3	1
227	RGDU07097-28-49M	1/3	1/3	1/3	1/3	1/3	1/3
228	RGDU07097-28-50M	1	1	1/3	1/3	1/3	1/3
229	RGDU07097-28-51M	1/3	1/3	1/3	1/3	1/3	1/3
230	RGDU07097-28-52M	1/3	3	3	1/3	1/3	1/3
231	RGDU07097-28-53M	1/3	3	3	1	1	1*
232	RGDU07097-28-54M	1/3	1/3	1/3	1/3	1/3	1/3
233	RGDU07097-28-55M	1/3	1/3	1/3	1/3	1/3	1/3
234	RGDU07099-1-1M	1/3	1/3	1/3	1/3	1/3	1/3
235	RGDU07099-1-2M	3	1	1/3	1/3	1/3	1/3
236	RGDU07099-1-3M	1	1	1	1/3	1/3	1
237	RGDU07099-1-4M	1/3	3	3	1/3	1/3	1/3
238	RGDU07099-1-5M	1	1	1/3	3	3	3
239	RGDU07099-1-6M	1/3	3	1/3	1/3	1/3	1/3
240	RGDU07099-1-7M	1/3	1	1/3	1	1	1

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
241	RGDU07099-1-8MKPS	1	1	1	1	1	1
242	RGDU07099-1-9M	1/3	1/3	1/3	1	1	1
243	RGDU07099-1-10M	1/3	1/3	1/3	1/3	1/3	1/3
244	RGDU07099-1-11M	1	1/3	1/3	1/3	1/3	1/3
245	RGDU07099-1-12MKPS	1/3	1/3	1	1/3	1/3	1/3
246	RGDU07099-1-13M	1/3	1/3	3	1/3	1/3	1/3
247	RGDU07099-1-14M	1/3	1	1	1/3	1/3	1/3
248	RGDU07099-1-15M	1/3	1/3	1	3	3	3
249	RGDU07099-1-16M	1/3	3	3	1/3	1/3	1/3
250	RGDU07099-1-17M	1	1/3	1	1	1	1
251	RGDU07099-1-18M	1	1	1/3	3	3	3
252	RGDU07099-1-19MKPS	3	1	1/3	3	3	3
253	RGDU07099-1-20M	1/3	1	1	3	3	3
254	RGDU07099-1-21M	1/3	1	1	3	3	3
255	RGDU07099-1-22M	1/3	1/3	1	1/3	1/3	3
256	RGDU07099-1-23M	1/3	1/3	1/3	1/3	1/3	1/3
257	RGDU07099-1-24M	1	1/3	3	3	3	3
258	RGDU07099-1-25M	1/3	1	1	1/3	1/3	1/3
259	RGDU07099-1-26M	3	1	1	1/3	1/3	1/3
260	RGDU07099-1-27M	1	1/3	1/3	3	3	3
261	RGDU07099-1-28MKPS	1	1	1	1/3	1/3	1/3
262	RGDU07099-1-29M	1/3	1/3	1	1	1	1
263	RGDU07099-1-30MKPS	3	1/3	1/3	1	1	1
264	RGDU07099-1-31M	3	1/3	1/3	1	1	1/3
265	RGDU07099-1-32M	1/3	1/3	1/3	3	3	3
266	RGDU07099-1-33M	3	1/3	1	1/3	1/3	1/3
267	RGDU07099-1-34M	3	1	3	1/3	1/3	1/3
268	RGDU07099-1-35M	1/3	1	1/3	1	1	1
269	RGDU07099-2-1M	3	1/3	1/3	1/3	1/3	1/3
270	RGDU07099-2-2M	1/3	1	1	3	3	3
271	RGDU07099-2-3M	3	1/3	1/3	3	3	13
272	RGDU07099-2-4M	1/3	3	3	1	1	1
273	RGDU07099-2-5M	1/3	1/3	1/3	1/3	1/3	1/3
274	RGDU07099-2-6M	3	3	3	1/3	1/3	3
275	RGDU07099-2-7M	1	3	3	1/3	1/3	1/3
276	RGDU07099-2-8M	3	1	1/3	1	1	1
277	RGDU07099-2-9M	1/3	3	1	3	3	3
278	RGDU07099-2-10M	1/3	1/3	1	1/3	1/3	1/3
279	RGDU07099-2-11M	1/3	3	1/3	3	3	3
280	RGDU07099-2-12M	1/3	1	3	1	1	1
281	RGDU07099-2-13M	1/3	1/3	1/3	3	3	3
282	RGDU07099-2-14MKPS	1/3	1/3	1/3	1	1/3	1/3
283	RGDU07099-2-15M	1	1	1	1/3	1/3	1/3
284	RGDU07099-2-16M	1	3	3	1/3	1/3	1/3
285	RGDU07099-2-17M	1/3	3	3	1/3	1/3	1/3
286	RGDU07099-2-18M	1/3	1	1	1	1	1/3
287	RGDU07099-2-19M	1/3	1	1/3	3	3	3
288	RGDU07099-2-20M	1	1/3	1/3	3	3	3
289	RGDU07099-2-21M	1/3	3	3	3	3	1/3
290	RGDU07099-2-22MKPS	1/3	1/3	1/3	1/3	1/3	1/3

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
291	RGDU07099-2-23M	1/3	3	1/3	1/3	1/3	1/3
292	RGDU07099-2-24M	1/3	1/3	1	1/3	1/3	1/3
293	RGDU07099-2-25M	3	1	1	1	1	1
294	RGDU07099-2-26M	1	1	1	1/3	1/3	1/3
295	RGDU07099-2-27M	3	1/3	3	1/3	1/3	1/3
296	RGDU07099-2-28M	1/3	1	1	3	3	3
297	RGDU07099-2-29M	1/3	1/3	1/3	3	3	3
298	RGDU07099-2-30M	1/3	1/3	1	3	1/3	1/3
299	RGDU07099-2-31M	1	1	1	1/3	1/3	1/3
300	RGDU07099-2-32M	1/3	1	1	3	3	3
301	RGDU07099-2-33M	1/3	1/3	1/3	1/3	1/3	1/3
302	RGDU07099-2-34M	1	1/3	1/3	1/3	1/3	1/3
303	RGDU07099-2-35M	1/3	1/3	1/3	1	1	1
304	RGDU07099-2-36M	1	1	1	1	1/3	1/3
305	RGDU07099-2-37M	1/3	3	3	3	3	3
306	RGDU07099-2-38M	1/3	3	1/3	1/3	1/3	1/3
307	RGDU07099-2-39M	1	1	1	1	1	1
308	RGDU07099-2-40M	3	3	1/3	3	3	3
309	RGDU07099-2-41M	1/3	1	1	1/3	1/3	1/3
310	RGDU07099-3-1M	1/3	1/3	1/3	3	3	3
311	RGDU07099-3-2M	1/3	1	1	1	1	1
312	RGDU07099-3-3M	1/3	1/3	1/3	1/3	1/3	1/3
313	RGDU07099-3-4M	1/3	1/3	3	3	3	3
314	RGDU07099-3-5MKPS	1	1/3	1/3	1	1	1
315	RGDU07099-3-6M	1	1	1	1/3	1/3	1/3
316	RGDU07099-3-7M	1/3	3	3	1	1	1
317	RGDU07099-3-8M	3	1	1	1	1	1
318	RGDU07099-3-9M	1/3	3	3	1/3	1/3	1/3
319	RGDU07099-3-10M	1	1/3	3	1	1	1
320	RGDU07099-3-11M	1/3	3	3	3	3	3
321	RGDU07099-3-12M	1/3	1	1/3	1/3	1/3	1/3
322	RGDU07099-3-13M	1	1/3	1/3	1/3	1/3	1/3
323	RGDU07099-3-14M	1/3	1	1	1	1	1
324	RGDU07099-3-15M	1/3	3	3	1/3	1/3	1/3
325	RGDU07099-3-16MKPS	1/3	3	3	3	3	3
326	RGDU07099-3-17M	1/3	3	3	1	1	1
327	RGDU07099-3-18M	1/3	1	1	1/3	1/3	1/3
328	RGDU07099-3-19M	1/3	1	1	1/3	1/3	1/3
329	RGDU07099-3-20M	3	1/3	1/3	1/3	1/3	1/3
330	RGDU07099-3-21M	3	1	1	1	1	1
331	RGDU07099-3-22MKPS	3	1/3	1/3	1	1	1/3
332	RGDU07099-3-23M	1/3	1/3	3	1/3	1/3	1/3
333	RGDU07099-3-24M	1/3	1/3	1/3	1/3	1/3	1/3
334	RGDU07099-3-25M	3	1/3	1	3	3	3
335	RGDU07099-3-26M	3	1	1	1/3	1/3	1/3
336	RGDU07099-3-27M	1/3	1/3	1	3	3	3
337	RGDU07099-3-28M	3	3	3	3	3	3
338	RGDU07099-3-29M	3	1	1	3	3	3
339	RGDU07099-3-30M	1	1/3	1/3	3	3	3
340	RGDU07099-3-31M	1/3	3	3	3	3	3

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
341	RGDU07099-3-32M	1/3	1/3	1	3	3	3
342	RGDU07099-3-33M	1/3	1/3	1	3	3	3
343	RGDU07099-3-34M	3	3	1/3	1/3	1/3	1/3
344	RGDU07099-3-35M	3	1	1	3	3	3
345	RGDU07099-3-36M	1/3	3	3	1/3	1/3	1/3
346	RGDU07099-3-37M	1/3	1/3	1/3	1/3	1/3	1/3
347	RGDU07099-3-38M	1/3	1	1	1	1	1
348	RGDU07099-3-39M	1/3	3	3	3	3	3
349	RGDU07099-3-40M	1/3	1/3	1/3	1/3	1/3	1/3
350	RGDU07099-3-41MKPS	1	1/3	3	1/3	1/3	1/3
351	RGDU07099-3-42M	3	1/3	1/3	1	1	1
352	RGDU07099-3-43M	1/3	1/3	1/3	1/3	1/3	1/3
353	RGDU07099-3-44M	1/3	1/3	1/3	1/3	1/3	1/3
354	RGDU07099-3-45M	1/3	3	3	1/3	1/3	1/3
355	RGDU07099-3-46M	1/3	1/3	1/3	1	1	1
356	RGDU07099-3-47MKPS	1/3	1/3	1/3	1	1	1
357	RGDU07099-5-1MKPS	1/3	1	1	1/3	1/3	1/3
358	RGDU07099-5-2M	3	3	3	1	1	1
359	RGDU07099-5-3M	1	1	1	1	1	1
360	RGDU07099-5-4M	1/3	1/3	1	3	3	1/3
361	RGDU07099-5-5M	1/3	1/3	1	1/3	1/3	1/3
362	RGDU07099-5-6M	1/3	1/3	1/3	1/3	1/3	1/3
363	RGDU07099-5-7M	1	1/3	1/3	3	3	3
364	RGDU07099-5-8M	1/3	1	1	1/3	1/3	1/3
365	RGDU07099-5-9M	3	1	1/3	1/3	1/3	1/3
366	RGDU07099-5-10M	3	3	3	1/3	1	1
367	RGDU07099-5-11M	1/3	1/3	1/3	1/3	1/3	1/3
368	RGDU07099-5-12M	3	1	1	1/3	1/3	1/3
369	RGDU07099-5-13M	3	1/3	1/3	1	1	1
370	RGDU07099-5-14M	1/3	1	1/3	1/3	1/3	1/3
371	RGDU07099-5-15M	1	1/3	1/3	1/3	1/3	1/3
372	RGDU07099-5-16MKPS	1/3	1	3	1/3	1/3	1/3
373	RGDU07099-5-17M	1/3	1/3	1/3	3	3	3
374	RGDU07099-5-18M	3	3	3	1	1	1
375	RGDU07099-5-19M	1/3	1/3	1	1/3	1/3	1/3
376	RGDU07099-5-20M	1/3	1	1/3	3	3	3
377	RGDU07099-5-21M	3	1	1	1/3	1/3	1/3
378	RGDU07099-5-22M	1	1/3	3	1	1	1
379	RGDU07099-5-23M	1/3	1/3	1/3	1/3	1/3	1/3
380	RGDU07099-5-24M	1/3	1	1	3	3	3
381	RGDU07099-5-25M	3	1/3	1/3	1/3	1/3	1/3
382	RGDU07099-5-26M	1	1/3	1/3	1/3	1/3	1/3
383	RGDU07099-5-27M	1/3	1	1	1/3	1/3	1/3
384	RGDU07099-5-28M	1	1/3	1/3	3	3	3
385	RGDU07099-5-29M	1	1/3	1/3	1/3	1/3	1
386	RGDU07099-5-30M	1/3	1	1	1	1	1
387	RGDU07099-5-31M	1	1/3	1/3	1/3	1/3	1/3
388	RGDU07099-5-32M	1/3	1	1	1	1	1
389	RGDU07099-5-33M	1/3	3	1/3	1/3	1/3	1/3
390	RGDU07099-5-34M	3	1	1	1/3	1/3	1/3

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
391	RGDU07099-5-35M	1/3	1/3	3	1/3	1/3	1/3
392	RGDU07099-5-36M	1/3	1	1/3	1/3	1/3	1/3
393	RGDU07099-5-37M	3	1/3	1/3	1	1	1
394	RGDU07099-5-38M	1/3	1/3	3	1	1	1
395	RGDU07099-5-39M	1/3	1	1	1/3	1/3	1/3
396	RGDU07099-5-40M	1/3	3	1/3	1/3	1/3	1/3
397	RGDU07099-5-41M	3	3	3	1/3	1/3	3
398	RGDU07099-5-42M	3	1/3	1/3	1/3	1/3	1/3
399	RGDU07099-5-43M	1	3	3	3	3	3
400	RGDU07099-5-44M	1/3	1/3	1/3	1/3	1/3	3
401	RGDU07099-5-45M	1/3	1	1/3	1/3	1/3	1/3
402	RGDU07099-5-46M	1/3	3	3	1	1	1
403	RGDU07099-5-47M	1/3	1/3	1/3	1	1	1
404	RGDU07099-5-48M	3	1/3	1/3	3	3	3
405	RGDU07099-5-49M	3	1	1/3	1/3	1/3	1/3
406	RGDU07099-5-50M	1/3	1	1	3	3	1/3
407	RGDU07099-5-51M	3	3	1/3	1	1	1
408	RGDU07099-5-52M	1/3	3	1/3	3	3	3
409	RGDU07099-5-53M	3	1/3	1/3	1/3	1/3	1/3
410	RGDU07099-5-54M	3	1	1/3	1/3	1/3	1/3
411	RGDU07099-5-55M	3	1	3	1/3	1/3	1
412	RGDU07099-5-56M	3	1/3	1/3	1	1	1
413	RGDU07099-5-57M	3	1/3	1/3	1	1	1
414	RGDU07099-5-58M	1/3	1/3	1/3	1	1	1
415	RGDU07099-5-59M	1/3	1	1	1	1	1
416	RGDU07099-5-60MKPS	3	3	3	1/3	1/3	1/3
417	RGDU07099-5-61MKPS	1/3	3	1/3	1	1	1/3
418	RGDU07099-5-62M	1	1/3	3	1/3	1/3	1/3
419	RGDU07099-5-63M	1/3	1/3	1/3	3	3	3
420	RGDU07099-5-64M	3	1/3	3	1/3	1/3	1/3
421	RGDU07099-6-1M	3	1/3	3	1/3	1/3	1/3
422	RGDU07099-6-2M	1/3	1/3	3	1/3	1/3	1/3
423	RGDU07099-6-3M	1	1	1	1/3	1/3	1/3
424	RGDU07099-6-4M	1	3	3	1/3	1/3	1/3
425	RGDU07099-6-5M	1/3	3	3	1	1	1
426	RGDU07099-6-6M	1	1/3	1/3	1/3	1/3	1/3
427	RGDU07099-6-7M	1/3	1/3	1	1/3	1/3	1/3
428	RGDU07099-6-8M	3	3	3	1	1	1
429	RGDU07099-6-9M	1	1	1	1/3	1/3	1/3
430	RGDU07099-6-10M	1/3	3	3	1	1	1/3
431	RGDU07099-6-11M	1/3	3	1/3	1	1	1
432	RGDU07099-6-12M	1/3	1/3	1	3	3	3
433	RGDU07099-6-13M	1	1/3	1/3	1/3	1/3	1/3
434	RGDU07099-6-14M	1/3	1/3	3	1/3	1/3	1/3
435	RGDU07099-6-15M	1/3	3	1/3	3	3	3
436	RGDU07099-6-16M	3	1/3	3	1/3	1/3	1/3
437	RGDU07099-6-17M	1/3	1/3	3	1/3	1/3	1/3
438	RGDU07099-6-18M	1/3	1/3	1/3	1	1	1
439	RGDU07099-6-19M	1	1/3	3	3	3	3
440	RGDU07099-6-20M	1	1	1	3	1/3	1/3

Appendix Table 6 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
441	RGDU07099-6-21M	1	3	3	1/3	1/3	1/3
442	RGDU07099-6-22M	1	1/3	1/3	1	1	1
443	RGDU07099-6-23M	3	1	1	1/3	1/3	1/3
444	RGDU07099-6-24M	3	1	1	1/3	1/3	1
445	RGDU07099-6-25M	3	3	3	3	3	3
446	RGDU07099-6-26M	1	1	1/3	1/3	1/3	1/3
447	RGDU07099-6-27M	1/3	1/3	1/3	1	1	1
448	RGDU07099-6-28M	1/3	3	3	3	3	3
449	RGDU07099-6-29M	1/3	3	3	1/3	1/3	1/3
450	RGDU07099-6-30M	1	1/3	1/3	1/3	1/3	1/3
451	RGDU07099-6-31M	1/3	1/3	3	1	1	1
452	RGDU07099-6-32M	3	3	1/3	1/3	1/3	3
453	RGDU07099-6-33M	1/3	1/3	3	1	1	1
454	RGDU07099-6-34M	1/3	1/3	1/3	1	1	1
455	RGDU07099-6-35M	1/3	1/3	1/3	1/3	1/3	1/3
456	RGDU07099-6-36M	1/3	1/3	1/3	1/3	1/3	1/3
457	RGDU07099-6-37M	1/3	1/3	1/3	1	1	1
458	RGDU07099-6-38M	1/3	1/3	1/3	1/3	1/3	1/3
459	RGDU07099-6-39M	1/3	1/3	1/3	1/3	1/3	1/3
460	RGDU07099-6-40M	3	3	1/3	1/3	1/3	1/3
461	RGDU07099-6-41M	1/3	1/3	3	1	1	1/3
462	RGDU07099-6-42M	1/3	1/3	3	3	3	1/3
463	RGDU07099-6-43M	1/3	1/3	3	1/3	1/3	1/3
464	RGDU07099-6-44M	1/3	1	1/3	1/3	1/3	1/3
465	RGDU07099-6-45M	3	3	1/3	1/3	1/3	1/3
466	RGDU07099-6-46M	3	3	1/3	1/3	1/3	1/3
467	RGDU07099-6-47M	1	1	1/3	1/3	1/3	1/3
468	RGDU07099-6-48M	1/3	1/3	1/3	1/3	1/3	1/3
469	RGDU07099-6-49M	3	3	1/3	1	1	1
470	RGDU07099-6-50M	1/3	1/3	1/3	1/3	1/5	1/3
471	RGDU07099-8-1M	1/3	1/3	1	1/3	1/3	1/3
472	RGDU07099-8-2M	1/3	1	3	3	3	3
473	RGDU07099-8-3M	1	1	1/3	13	1	13
474	RGDU07099-8-4M	1/3	1/3	1	3	3	13
475	RGDU07099-8-5M	1/3	1	1	1	1	1
476	RGDU07099-8-6M	1/3	13	3	1/3	1/3	1
477	RGDU07099-8-7M	1/3	3	1/3	1	1	1/3
478	RGDU07099-8-8M	1/3	1/3	1/3	1/3	1/3	1/3
479	RGDU07099-8-9M	1/3	1/3	1/3	1	1	1
480	RGDU07099-8-10M	1/3	1/3	3	1	1	1
481	RGDU07099-8-11M	1/3	1/3	1/3	1/3	1/3	1/3
482	RGDU07099-8-12M	1/3	1	1	1	1	1
483	RGDU07099-8-13M	1	1/3	1	1/3	1/3	1/3
484	RGDU07099-8-14M	1/3	1/3	1/3	1/3	1/3	1
485	RGDU07099-8-15M	1/3	1/3	1/3	1/3	1/3	1/3
486	RGDU07099-8-16M	1/3	1	1	1/3	1/3	1/3
487	RGDU07099-8-17M	1/3	1/3	1	1/3	1/3	1/3
488	RGDU07099-8-18M	1	1	1/3	1	1	1
489	RGDU07099-8-19MKPS	1	3	3	1/3	1/3	3
490	RGDU07099-8-20MKPS	3	3	1/3	1/3	1/3	1/3

Appendix Table 6 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
491	RGDU07099-8-21M	1	3	3	3	3	3
492	RGDU07099-8-22M	3	1/3	1/3	1/3	1/3	1/3
493	RGDU07099-8-23M	1/3	3	3	1/3	1/3	1/3
494	RGDU07099-8-24M	3	1/3	1/3	1	1	1
495	RGDU07099-8-25M	1/3	3	3	1/3	1/3	1/3
496	RGDU07099-8-26M	3	3	3	3	3	3
497	RGDU07099-8-27MKPS	1	1	1	1	1	1
498	RGDU07099-8-28M	1/3	1/3	3	1	1	1
499	RGDU07099-8-29M	1/3	1/3	1/3	1	1	1
500	RGDU07099-8-30M	1/3	3	3	1/3	1/3	1/3

Appendix Table 7 Genotypes of 392 F_3 individuals from the cross between Py-*xa5/Xa21/qBB11* and Py-*xa33(t)/Xa34(t)*.

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
	KDML105	3	3	5	3	3	3
	IR1188	3	**1**	**1**	3	5	1
	Ba7	3	4	7	**1**	**1**	**1**
	IR62266	**1**	3	9	3	7	5
	PK	3	3	**3**	3	3	3
	104-4-1-19-7	3	**1**	**1**	3	3	3
1	RGDU07099-2-12M-1	1/3	1	3	1	1	1
2	RGDU07099-2-12M-2	1/3	1	3	1	1	1
3	RGDU07099-2-12M-3	1/3	1	3	1	1	1
4	RGDU07099-2-12M-4	1/3	1	3	1	1	1
5	RGDU07099-2-12M-5	3	1	3	1	1	1
6	RGDU07099-2-12M-6	1/3	1	3	1	1	1
7	RGDU07099-2-12M-7	1/3	1	3	1	1	1
8	RGDU07099-2-12M-8	1/3	1	3	1	1	1
9	RGDU07099-2-12M-9	3	1	3	1	1	1
10	RGDU07099-2-12M-10	1	1	3	1	1	1
11	RGDU07099-2-12M-11	1	1	3	1	1	1
12	RGDU07099-2-12M-12	1/3	1	3	1	1	1
13	RGDU07099-2-12M-13	1	1	3	1	1	1
14	RGDU07099-2-12M-14	1/3	1	3	1	1	1
15	RGDU07099-2-12M-15	1/3	1	3	1	1	1
16	RGDU07099-2-12M-16	3	1	3	1	1	1
17	RGDU07099-2-12M-17	1/3	1	3	1	1	1
18	RGDU07099-2-12M-18	2	1	3	1	1	1
19	RGDU07099-2-12M-19	3	1	3	1	1	1
20	RGDU07099-2-12M-20	1	1	3	1	1	1
21	RGDU07099-2-12M-21	1/3	1	3	1	1	1
22	RGDU07099-2-12M-22	1/3	1	3	1	1	1
23	RGDU07099-2-12M-23	1/3	1	3	1	1	1
24	RGDU07099-2-12M-24	1/3	1	3	1	1	1
25	RGDU07099-2-12M-25	1/3	1	3	1	1	1
26	RGDU07099-2-12M-26	1/3	1	3	1	1	1
27	RGDU07099-2-12M-27	3	1	3	1	1	1
28	RGDU07099-2-12M-28	1/3	1	3	1	1	1
29	RGDU07099-2-12M-29	1/3	1	3	1	1	1
30	RGDU07099-2-12M-30	3	1	3	1	1	1
31	RGDU07099-2-12M-31	1/3	1	3	1	1	1
32	RGDU07099-2-12M-32	3	1	3	1	1	1
33	RGDU07099-2-12M-33	3	1	3	1	1	1
34	RGDU07099-2-12M-34	1/3	1	3	1	1	1
35	RGDU07099-2-12M-35	1/3	1	3	1	1	1
36	RGDU07099-2-12M-36	1/3	1	3	1	1	1
37	RGDU07099-2-12M-37	1/3	1	3	1	1	1
38	RGDU07099-2-12M-38	1/3	1	3	1	1	1
39	RGDU07099-2-12M-39	3	1	3	1	1	1
40	RGDU07099-2-12M-40	1	1	3	1	1	1

Appendix Table 7 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
41	RGDU07099-2-12M-41	1/3	1	3	1	1	1
42	RGDU07099-2-12M-42	1	1	3	1	1	1
43	RGDU07099-2-12M-43	1/3	1	3	1	1	1
44	RGDU07099-2-12M-44	3	1	3	1	1	1
45	RGDU07099-2-12M-45	1/3	1	3	1	1	1
46	RGDU07099-2-12M-46	1	1	3	1	1	1
47	RGDU07099-2-12M-47	3	1	3	1	1	1
48	RGDU07099-2-12M-48	1	1	3	1	1	1
49	RGDU07099-2-12M-49	1/3	1	3	1	1	1
50	RGDU07099-2-12M-50	3	1	3	1	1	1
51	RGDU07099-2-12M-51	3	1	3	1	1	1
52	RGDU07099-2-12M-52	3	1	3	1	1	1
53	RGDU07099-2-12M-53	3	1	3	1	1	1
54	RGDU07099-2-12M-54	1/3	1	3	1	1	1
55	RGDU07099-2-12M-55	1/3	1	3	1	1	1
56	RGDU07099-2-12M-56	1/3	1	3	1	1	1
57	RGDU07099-2-12M-57	1	1	3	1	1	1
58	RGDU07099-2-12M-58	3	1	3	1	1	1
59	RGDU07099-1-17M-1	1	1	1	1	1	1
60	RGDU07099-1-17M-2	1	3	1	1	1	1
61	RGDU07099-1-17M-3	1	1/3	1	1	1	1
62	RGDU07099-1-17M-4	1	1/3	1	1	1	1
63	RGDU07099-1-17M-5	1	1/3	1	1	1	1
64	RGDU07099-1-17M-6	1	3	1	1	1	1
65	RGDU07099-1-17M-7	1	1/3	1	1	1	1
66	RGDU07099-1-17M-8	1	3	1	1	1	1
67	RGDU07099-1-17M-9	1	3	1	1	1	1
68	RGDU07099-1-17M-10	1	1	1	1	1	1
69	RGDU07099-1-17M-11	1	1	1	1	1	1
70	RGDU07099-1-17M-12	1	3	1	1	1	1
71	RGDU07099-1-17M-13	1	3	1	1	1	1
72	RGDU07099-1-17M-14	1	3	1	1	1	1
73	RGDU07099-1-17M-15	1	1	1	1	1	1
74	RGDU07099-1-17M-16	1	1	1	1	1	1
75	RGDU07099-1-17M-17	1	1	1	1	1	1
76	RGDU07099-1-17M-18	1	3	1	1	1	1
77	RGDU07099-1-17M-19	1	1/3	1	1	1	1
78	RGDU07099-1-17M-20	1	1	1	1	1	1
79	RGDU07099-1-17M-21	1	1/3	1	1	1	1
80	RGDU07099-1-17M-22	1	3	1	1	1	1
81	RGDU07099-1-17M-23	1	3	1	1	1	1
82	RGDU07099-1-17M-24	1	1	1	1	1	1
83	RGDU07099-1-17M-25	1	1/3	1	1	1	1
84	RGDU07099-1-17M-26	1	1/3	1	1	1	1
85	RGDU07099-1-17M-27	1	1/3	1	1	1	1
86	RGDU07099-1-17M-28	1	1	1	1	1	1
87	RGDU07099-1-17M-29	1	-	1	1	1	1
88	RGDU07099-1-17M-30	1	3	1	1	1	1
89	RGDU07099-1-17M-31	1	1/3	1	1	1	1
90	RGDU07099-1-17M-32	1	1/3	1	1	1	1

Appendix Table 7 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
91	RGDU07099-1-17M-33	1	1/3	1	1	1	1
92	RGDU07099-1-17M-34	1	1/3	1	1	1	1
93	RGDU07099-1-17M-35	1	1	1	1	1	1
94	RGDU07099-1-17M-36	1	3	1	1	1	1
95	RGDU07099-1-17M-37	1	1	1	1	1	1
96	RGDU07099-1-17M-38	1	1/3	1	1	1	1
97	RGDU07099-1-17M-39	1	1/3	1	1	1	1
98	RGDU07099-1-17M-40	1	3	1	1	1	1
99	RGDU07099-1-17M-41	1	3	1	1	1	1
100	RGDU07099-1-17M-42	1	1	1	1	1	1
101	RGDU07099-1-17M-43	1	1/3	1	1	1	1
102	RGDU07099-1-17M-44	1	1/3	1	1	1	1
103	RGDU07099-1-17M-45	1	3	1	1	1	1
104	RGDU07099-1-17M-46	1	1/3	1	1	1	1
105	RGDU07099-1-17M-47	1	1/3	1	1	1	1
106	RGDU07099-1-17M-48	1	1/3	1	1	1	1
107	RGDU07099-1-17M-49	1	1/3	1	1	1	1
108	RGDU07099-1-17M-50	1	1	1	1	1	1
109	RGDU07099-1-17M-51	1	1/3	1	1	1	1
110	RGDU07099-1-17M-52	1	1/3	1	1	1	1
111	RGDU07099-1-17M-53	1	1/3	1	1	1	1
112	RGDU07099-1-17M-54	1	1/3	1	1	1	1
113	RGDU07099-1-17M-55	1	1/3	1	1	1	1
114	RGDU07099-1-24-1	1	1/3	3	3	3	3
115	RGDU07099-1-24-2	1	1	3	3	3	3
116	RGDU07099-1-24-3	1	1/3	3	3	3	3
117	RGDU07099-1-24-4	1	1/3	3	3	3	3
118	RGDU07099-1-24-5	1	1/3	3	3	3	3
119	RGDU07099-1-24-6	1	1	3	3	3	3
120	RGDU07099-1-24-7	1	1/3	3	3	3	3
121	RGDU07099-1-24-8	1	1/3	3	3	3	3
122	RGDU07099-1-24-9	1	1	3	3	3	3
123	RGDU07099-1-24-10	1	1	3	3	3	3
124	RGDU07099-1-24-11	1	1	3	3	3	3
125	RGDU07099-1-24-12	1	1/3	3	3	3	3
126	RGDU07099-1-24-13	1	1/3	3	3	3	3
127	RGDU07099-1-24-14	1	1/3	3	3	3	3
128	RGDU07099-1-24-15	1	1/3	3	3	3	3
129	RGDU07099-1-24-16	1	1/3	3	3	3	3
130	RGDU07099-1-24-17	1	1/3	3	3	3	3
131	RGDU07099-1-24-18	1	1/3	3	3	3	3
132	RGDU07099-1-24-19	1	3	3	3	3	3
133	RGDU07099-1-24-20	1	1/3	3	3	3	3
134	RGDU07099-1-24-21	1	3	3	3	3	3
135	RGDU07099-1-24-22	1	1	3	3	3	3
136	RGDU07099-1-24-23	1	1	3	3	3	3
137	RGDU07099-1-24-24	1	3	3	3	3	3
138	RGDU07099-1-24-25	1	3	3	3	3	3
139	RGDU07099-1-24-26	1	1/3	3	3	3	3
140	RGDU07099-1-24-27	1	1/3	3	3	3	3

Appendix Table 7 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
141	RGDU07099-1-24-28	1	3	3	3	3	3
142	RGDU07099-1-24-29	1	1/3	3	3	3	3
143	RGDU07099-1-24-30	1	1/3	3	3	3	3
144	RGDU07099-1-24-31	1	1/3	3	3	3	3
145	RGDU07099-1-24-32	1	1/3	3	3	3	3
146	RGDU07099-1-24-33	1	1/3	3	3	3	3
147	RGDU07099-1-24-34	1	1/3	3	3	3	3
148	RGDU07099-1-24-35	1	1/3	3	3	3	3
149	RGDU07099-1-24-36	1	1/3	3	3	3	3
150	RGDU07099-1-24-37	1	3	3	3	3	3
151	RGDU07099-1-24-38	1	1/3	3	3	3	3
152	RGDU07099-1-24-39	1	1/3	3	3	3	3
153	RGDU07099-1-24-40	1	1/3	3	3	3	3
154	RGDU07097-1-26M-1	1	1/3	3	3	3	3
155	RGDU07097-1-26M-2	1	3	3	3	3	3
156	RGDU07097-1-26M-3	1	3	3	3	3	3
157	RGDU07097-1-26M-4	1	1/3	3	3	3	3
158	RGDU07097-1-26M-5	1	1/3	3	3	3	3
159	RGDU07097-1-26M-6	1	1	3	3	3	3
160	RGDU07097-1-26M-7	1	1/3	3	3	3	3
161	RGDU07097-1-26M-8	1	3	3	3	3	3
162	RGDU07097-1-26M-9	1	1	3	3	3	3
163	RGDU07097-1-26M-10	1	3	3	3	3	3
164	RGDU07097-1-26M-11	1	1/3	3	3	3	3
165	RGDU07097-1-26M-12	1	1	3	3	3	3
166	RGDU07097-1-26M-13	1	3	3	3	3	3
167	RGDU07097-1-26M-14	1	1	3	3	3	3
168	RGDU07097-1-26M-15	1	1	3	3	3	3
169	RGDU07097-1-26M-16	1	1/3	3	3	3	3
170	RGDU07097-1-26M-17	1	1/3	3	3	3	3
171	RGDU07097-1-26M-18	1	1/3	3	3	3	3
172	RGDU07097-1-26M-19	1	3	3	3	3	3
173	RGDU07097-1-26M-20	1	1	3	3	3	3
174	RGDU07099-8-2M-1	1/3	1	3	3	3	3
175	RGDU07099-8-2M-2	1/3	1	3	3	3	3
176	RGDU07099-8-2M-3	1	1	3	3	3	3
177	RGDU07099-8-2M-4	1/3	1	3	3	3	3
178	RGDU07099-8-2M-5	1	1	3	3	3	3
179	RGDU07099-8-2M-6	3	1	3	3	3	3
180	RGDU07099-8-2M-7	3	1	3	3	3	3
181	RGDU07099-8-2M-8	1	1	3	3	3	3
182	RGDU07099-8-2M-9	1	1	3	3	3	3
183	RGDU07099-8-2M-10	1	1	3	3	3	3
184	RGDU07099-8-2M-11	3	1	3	3	3	3
185	RGDU07099-8-2M-12	1/3	1	3	3	3	3
186	RGDU07099-8-2M-13	3	1	3	3	3	3
187	RGDU07099-8-2M-14	1/3	1	3	3	3	3
188	RGDU07099-8-2M-15	3	1	3	3	3	3
189	RGDU07099-8-2M-16	1/3	1	3	3	3	3
190	RGDU07099-8-2M-17	1	1	3	3	3	3

Appendix Table 7 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
191	RGDU07099-8-2M-18	1	1	3	3	3	3
192	RGDU07099-8-2M-19	1/3	1	3	3	3	3
193	RGDU07099-8-2M-20	1	1	3	3	3	3
194	RGDU07099-6-19M-1	1	1/3	3	3	3	3
195	RGDU07099-6-19M-2	1	1/3	3	3	3	3
196	RGDU07099-6-19M-3	1	1/3	3	3	3	3
197	RGDU07099-6-19M-4	1	3	3	3	3	3
198	RGDU07099-6-19M-5	1	1/3	3	3	3	3
199	RGDU07099-6-19M-6	1	3	3	3	3	3
200	RGDU07099-6-19M-7	1	1/3	3	3	3	3
201	RGDU07099-6-19M-8	1	1/3	3	3	3	3
202	RGDU07099-6-19M-9	1	1/3	3	3	3	3
203	RGDU07099-6-19M-10	1	3	3	3	3	3
204	RGDU07099-6-19M-11	1	1	3	3	3	3
205	RGDU07099-6-19M-12	1	1	3	3	3	3
206	RGDU07099-6-19M-13	1	1/3	3	3	3	3
207	RGDU07099-6-19M-14	1	1/3	3	3	3	3
208	RGDU07099-6-19M-15	1	1/3	3	3	3	3
209	RGDU07099-6-19M-16	1	1/3	3	3	3	3
210	RGDU07099-6-19M-17	1	1/3	3	3	3	3
211	RGDU07099-6-19M-18	1	1	3	3	3	3
212	RGDU07099-6-19M-19	1	1/3	3	3	3	3
213	RGDU07099-6-19M-20	1	3	3	3	3	3
214	RGDU07096-2-12M-1	1	3	1	3	3	3
215	RGDU07096-2-12M-2	1	3	1/3	3	3	3
216	RGDU07096-2-12M-3	1	3	1/3	3	3	3
217	RGDU07096-2-12M-4	1	3	1	3	3	3
218	RGDU07096-2-12M-5	1	3	3	3	3	3
219	RGDU07096-2-12M-6	1	3	1/3	3	3	3
220	RGDU07096-2-12M-7	1	3	1/3	3	3	3
221	RGDU07096-2-12M-8	1	3	1/3	3	3	3
222	RGDU07096-2-12M-9	1	3	1/3	3	3	3
223	RGDU07096-2-12M-10	1	3	1	3	3	3
224	RGDU07096-2-12M-11	1	3	1/3	3	3	3
225	RGDU07096-2-12M-12	1	3	1/3	3	3	3
226	RGDU07096-2-12M-13	1	3	3	3	3	3
227	RGDU07096-2-12M-14	1	3	1/3	3	3	3
228	RGDU07096-2-12M-15	1	3	1	3	3	3
229	RGDU07096-2-12M-16	1	3	1	3	3	3
230	RGDU07096-2-12M-17	1	3	1/3	3	3	3
231	RGDU07096-2-12M-18	1	3	1/3	3	3	3
232	RGDU07096-2-12M-19	1	3	1/3	3	3	3
233	RGDU07096-2-12M-20	1	3	1/3	3	3	3
234	RGDU07097-1-47M-1	1	3	1/3	3	3	3
235	RGDU07097-1-47M-2	1	3	1/3	3	3	3
236	RGDU07097-1-47M-3	1	3	3	3	3	3
237	RGDU07097-1-47M-4	1	3	1/3	3	3	3
238	RGDU07097-1-47M-5	1	3	1	3	3	3
239	RGDU07097-1-47M-6	1	3	3	3	3	3
240	RGDU07097-1-47M-7	1	3	1	3	3	3

Appendix Table 7 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
241	RGDU07097-1-47M-8	1	3	1/3	3	3	3
242	RGDU07097-1-47M-9	1	3	1	3	3	3
243	RGDU07097-1-47M-10	1	3	1/3	3	3	3
244	RGDU07097-1-47M-11	1	3	1/3	3	3	3
245	RGDU07097-1-47M-12	1	3	3	3	3	3
246	RGDU07097-1-47M-13	1	3	1/3	3	3	3
247	RGDU07097-1-47M-14	1	3	1/3	3	3	3
248	RGDU07097-1-47M-15	1	3	1	3	3	3
249	RGDU07097-1-47M-16	1	3	1/3	3	3	3
250	RGDU07097-1-47M-17	1	3	1/3	3	3	3
251	RGDU07097-1-47M-18	1	3	3	3	3	3
252	RGDU07097-1-47M-19	1	3	3	3	3	3
253	RGDU07097-1-47M-20	1	3	1	3	3	3
254	RGDU07097-1-1M-1	1	3	1/3	3	3	3
255	RGDU07097-1-1M-2	1	3	1/3	3	3	3
256	RGDU07097-1-1M-3	1	3	1/3	3	3	3
257	RGDU07097-1-1M-4	1	3	1/3	3	3	3
258	RGDU07097-1-1M-5	1	3	1	3	3	3
259	RGDU07097-1-1M-6	1	3	1	3	3	3
260	RGDU07097-1-1M-7	1	3	1/3	3	3	3
261	RGDU07097-1-1M-8	1	3	1	3	3	3
262	RGDU07097-1-1M-9	1	3	3	3	3	3
263	RGDU07097-1-1M-10	1	3	3	3	3	3
264	RGDU07097-1-1M-11	1	3	3	3	3	3
265	RGDU07097-1-1M-12	1	3	1	3	3	3
266	RGDU07097-1-1M-13	1	3	1/3	3	3	3
267	RGDU07097-1-1M-14	1	3	1/3	3	3	3
268	RGDU07097-1-1M-15	1	3	3	3	3	3
269	RGDU07097-1-1M-16	1	3	1/3	3	3	3
270	RGDU07097-1-1M-17	1	3	1/3	3	3	3
271	RGDU07097-1-1M-18	1	3	3	3	3	3
272	RGDU07097-1-1M-19	1	3	1	3	3	3
273	RGDU07097-1-1M-20	1	3	1/3	3	3	3
274	RGDU07097-15-12M-1	3	1/3	3	3	3	3
275	RGDU07097-15-12M-2	3	1/3	3	3	3	3
276	RGDU07097-15-12M-3	3	1	3	3	3	3
277	RGDU07097-15-12M-4	3	1	3	3	3	3
278	RGDU07097-15-12M-5	3	3	3	3	3	3
279	RGDU07097-15-12M-6	3	1	3	3	3	3
280	RGDU07097-15-12M-7	3	1	3	3	3	3
281	RGDU07097-15-12M-8	3	1	3	3	3	3
282	RGDU07097-15-12M-9	3	1/3	3	3	3	3
283	RGDU07097-15-12M-10	3	1/3	3	3	3	3
284	RGDU07097-15-12M-11	3	1/3	3	3	3	3
285	RGDU07097-15-12M-12	3	1	3	3	3	3
286	RGDU07097-15-12M-13	3	1/3	3	3	3	3
287	RGDU07097-15-12M-14	3	1/3	3	3	3	3
288	RGDU07097-15-12M-15	3	1/3	3	3	3	3
289	RGDU07097-15-12M-16	3	3	3	3	3	3
290	RGDU07097-15-12M-17	3	1	3	3	3	3

Appendix Table 7 (Continued)

Entry	**Pedigree**	***xa5***	***Xa21***	***Xa34(t) or qBB11***	***xa33(t)***		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
291	RGDU07097-15-12M-18	3	1/3	3	3	3	3
292	RGDU07097-15-12M-19	3	1/3	3	3	3	3
293	RGDU07097-15-12M-20	3	1	3	3	3	3
294	RGDU07097-15-12M-21	3	1/3	3	3	3	3
295	RGDU07097-15-12M-22	3	3	3	3	3	3
296	RGDU07097-15-12M-23	3	1/3	3	3	3	3
297	RGDU07097-15-12M-24	3	1	3	3	3	3
298	RGDU07097-15-12M-25	3	1/3	3	3	3	3
299	RGDU07097-15-12M-26	3	1	3	3	3	3
300	RGDU07097-15-12M-27	3	1/3	3	3	3	3
301	RGDU07097-15-12M-28	3	1	3	3	3	3
302	RGDU07097-15-12M-29	3	1/3	3	3	3	3
303	RGDU07097-15-12M-30	3	1	3	3	3	3
304	RGDU07097-15-12M-31	3	1/3	3	3	3	3
305	RGDU07097-15-12M-32	3	1/3	3	3	3	3
306	RGDU07097-15-12M-33	3	1	3	3	3	3
307	RGDU07097-15-12M-34	3	1	3	3	3	3
308	RGDU07097-15-12M-35	3	1/3	3	3	3	3
309	RGDU07097-15-12M-36	3	1/3	3	3	3	3
310	RGDU07097-15-12M-37	3	3	3	3	3	3
311	RGDU07097-15-12M-38	3	1	3	3	3	3
312	RGDU07097-15-12M-39	3	1	3	3	3	3
313	RGDU07097-15-12M-40	3	1/3	3	3	3	3
314	RGDU07097-15-12M-41	3	3	3	3	3	3
315	RGDU07097-15-12M-42	3	1	3	3	3	3
316	RGDU07097-15-12M-43	3	1/3	3	3	3	3
317	RGDU07097-15-12M-44	3	1	3	3	3	3
318	RGDU07097-15-12M-45	3	1	3	3	3	3
319	RGDU07097-15-12M-46	3	1/3	3	3	3	3
320	RGDU07097-15-12M-47	3	3	3	3	3	3
321	RGDU07097-15-12M-48	3	3	3	3	3	3
322	RGDU07097-15-12M-49	3	1	3	3	3	3
323	RGDU07097-15-12M-50	3	3	3	3	3	3
324	RGDU07097-15-12M-51	3	1/3	3	3	3	3
325	RGDU07097-15-12M-52	3	1	3	3	3	3
326	RGDU07097-15-12M-53	3	1/3	3	3	3	3
327	RGDU07097-15-12M-54	3	3	3	3	3	3
328	RGDU07097-15-12M-55	3	1/3	3	3	3	3
329	RGDU07097-15-12M-56	3	1/3	3	3	3	3
330	RGDU07097-15-12M-57	3	1	3	3	3	3
331	RGDU07097-15-12M-58	3	1/3	3	3	3	3
332	RGDU07097-15-12M-59	3	1/3	3	3	3	3
333	RGDU07099-2-9M-1	1/3	3	1	3	3	3
334	RGDU07099-2-9M-2	1/3	3	1	3	3	3
335	RGDU07099-2-9M-3	3	3	1	3	3	3
336	RGDU07099-2-9M-4	1/3	3	1	3	3	3
337	RGDU07099-2-9M-5	3	3	1	3	3	3
338	RGDU07099-2-9M-6	3	3	1	3	3	3
339	RGDU07099-2-9M-7	1/3	3	1	3	3	3
340	RGDU07099-2-9M-8	1	3	1	3	3	3

Appendix Table 7 (Continued)

Entry	Pedigree	*xa5*	*Xa21*	*Xa34(t) or qBB11*	*xa33(t)*		
		PAxa5	**PB78**	**RM224**	**RM7243**	**RM5509**	**RM400**
341	RGDU07099-2-9M-9	1/3	3	1	3	3	3
342	RGDU07099-2-9M-10	1	3	1	3	3	3
343	RGDU07099-2-9M-11	1/3	3	1	3	3	3
344	RGDU07099-2-9M-12	1/3	3	1	3	3	3
345	RGDU07099-2-9M-13	1/3	3	1	3	3	3
346	RGDU07099-2-9M-14	3	3	1	3	3	3
347	RGDU07099-2-9M-15	1/3	3	1	3	3	3
348	RGDU07099-2-9M-16	1/3	3	1	3	3	3
349	RGDU07099-2-9M-17	1	3	1	3	3	3
350	RGDU07099-2-9M-18	3	3	1	3	3	3
351	RGDU07099-2-9M-19	3	3	1	3	3	3
352	RGDU07099-2-9M-20	3	3	1	3	3	3
353	RGDU07099-2-9M-21	1	3	1	3	3	3
354	RGDU07099-2-9M-22	1	3	1	3	3	3
355	RGDU07099-2-9M-23	3	3	1	3	3	3
356	RGDU07099-2-9M-24	1/3	3	1	3	3	3
357	RGDU07099-2-9M-25	1	3	1	3	3	3
358	RGDU07099-2-9M-26	1/3	3	1	3	3	3
359	RGDU07099-2-9M-27	1/3	3	1	3	3	3
360	RGDU07099-2-9M-28	1	3	1	3	3	3
361	RGDU07099-2-9M-29	1/3	3	1	3	3	3
362	RGDU07099-2-9M-30	1/3	3	1	3	3	3
363	RGDU07099-2-9M-31	1	3	1	3	3	3
364	RGDU07099-2-9M-32	1	3	1	3	3	3
365	RGDU07099-2-9M-33	1	3	1	3	3	3
366	RGDU07099-2-9M-34	3	3	1	3	3	3
367	RGDU07099-2-9M-35	3	3	1	3	3	3
368	RGDU07099-2-9M-36	1/3	3	1	3	3	3
369	RGDU07099-2-9M-37	1/3	3	1	3	3	3
370	RGDU07099-2-9M-38	1/3	3	1	3	3	3
371	RGDU07099-2-9M-39	1/3	3	1	3	3	3
372	RGDU07099-2-9M-40	3	3	1	3	3	3
373	RGDU07099-2-9M-41	1/3	3	1	3	3	3
374	RGDU07099-2-9M-42	1/3	3	1	3	3	3
375	RGDU07099-2-9M-43	1/3	3	1	3	3	3
376	RGDU07099-2-9M-44	1	3	1	3	3	3
377	RGDU07099-2-9M-45	1/3	3	1	3	3	3
378	RGDU07099-2-9M-46	1/3	3	1	3	3	3
379	RGDU07099-2-9M-47	3	3	1	3	3	3
380	RGDU07099-2-9M-48	1/3	3	1	3	3	3
381	RGDU07099-2-9M-49	1	3	1	3	3	3
382	RGDU07099-2-9M-50	1/3	3	1	3	3	3
383	RGDU07099-2-9M-51	1/3	3	1	3	3	3
384	RGDU07099-2-9M-52	1/3	3	1	3	3	3
385	RGDU07099-2-9M-53	1	3	1	3	3	3
386	RGDU07099-2-9M-54	1/3	3	1	3	3	3
387	RGDU07099-2-9M-55	1/3	3	1	3	3	3
388	RGDU07099-2-9M-56	3	3	1	3	3	3
389	RGDU07099-2-9M-57	1/3	3	1	3	3	3
390	RGDU07099-2-9M-58	3	3	1	3	3	3
391	RGDU07099-2-9M-59	1	3	1	3	3	3
392	RGDU07099-2-9M-60	1/3	3	1	3	3	3

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