

DISSERTATION

EXPLOITING RICE DIVERSITY TO UNCOVER DURABLE AND BROAD-SPECTRUM RESISTANCE

Submitted by

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ABSTRACT

EXPLOITING RICE DIVERSITY TO UNCOVER DURABLE AND BROAD-SPECTRUM RESISTANCE

Rice is the staple food for human consumption and feeds over half the world's population. Major constraints towards a sustainable productivity of this cereal are losses caused by bacterial diseases, such as bacterial blight (BB) and bacterial leaf streak (BLS). Therefore, strategies aimed at increasing the global production of rice are essential. BB and BLS are caused by *Xanthomonas oryzae* pvs. *oryzae* (*Xoo*) and *oryzicola* (*Xoc*), respectively. This study aims to identify novel, broad-spectrum and durable sources of resistance to BB and BLS, and to pinpoint potential candidate genes for further characterization. We screened an indica rice Multi-parent Advanced Generation Inter-Cross (MAGIC) population, a novel mapping resource that allows high-resolution detection for quantitative trait loci (QTL). A total of 14 disease resistance QTL effective against multiple *X. oryzae* strains were mapped, 11 confer resistance to both pathovars, i.e. broad-spectrum resistance (BSR), and three are pathovar-specific. We also detected specific alleles conferring disease resistance and susceptibility to these bacterial pathogens. Then, we combined diverse approaches to identify promising candidate genes, putatively involved in PAMP-triggered immunity (PTI) and effector triggered immunity (ETI), by (1) evaluating the presence and polymorphisms in defense-responsive *cis*-regulatory modules (CRMs) in gene promoters, (2) predicting gene promoters targeted by multiple *X. oryzae* strains, and (3) assessing the presence of SNP markers associated with resistance to *X. oryzae* strains. We also analyzed a cluster of *MATH-BTB* genes in a rice BSR QTL on chromosome 4 for polymorphisms between

resistant and susceptible MAGIC lines. As a parallel approach to identify sources of durable resistance, the indica MAGIC population was also screened with an *Xoo* strain containing Tal7b, a transcription activator-like (TAL) virulence effector that is common to many *Xoo* strains. We mapped disease resistance QTL unique to this specific virulence factor and hypothesize that the mechanism of resistance conferred by one QTL is through a loss of susceptibility. BSR QTL and QTL specifically effective against virulence enhancing TALs may offer increased durability in the field. Because MAGIC lines are derived from elite cultivars, the use of identified QTL will be facilitated for the development of improved varieties.

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CHAPTER 1

INTRODUCTION

1.1. BACTERIAL DISEASES OF RICE: A THREAT TO WORLDWIDE AGRICULTURE

Rice (*Oryza sativa* L.) is the most genetically diverse cereal and has been cultivated for over 10,000 years (Kush, 1997, Vitte et al., 2004). It is grown worldwide with hundreds of varieties from different genetic backgrounds and agronomic traits (Kush, 1997). Importantly, rice is one of the most essential crops for food security, feeding over 60% of the world's population, and providing 23% of the global human caloric intake (Sharma et al., 2012, Ke et al., 2017). The growing human demand, together with losses caused by pathogens worldwide, require novel strategies and agricultural practices aimed at increasing global production of rice.

Major bacterial diseases of rice are bacterial blight (BB) and bacterial leaf streak (BLS). The causal agents of BB and BLS are the closely related bacterial pathogens *Xanthomonas oryzae* pvs. *oryzae* (*Xoo*) and *oryzicola* (*Xoc*), respectively. BB was originally discovered in Japan in 1884 (Ou, 1972), and since then has become the most destructive bacterial disease of rice. It is widespread in both irrigated and rainfed rice environments of tropical and temperate zones of Asia, West Africa, and Australia (Mew et al., 1992, Nino-Liu et al., 2006). Under conducive conditions, it can cause up to 70% yield loss (Kang et al., 2008, Reddy et al., 1979). BLS is an emerging disease; although first observed in the Philippines in 1918 (Ou, 1972), its incidence has recently increased in China and Africa (Gonzalez et al., 2007, Verdier et al., 2012). BLS is present

in tropical and subtropical Asia, northern Australia and West Africa, causing up to 20% yield loss (Ou, 1985, Gonzalez et al., 2007, Wonni et al., 2011).

Both *Xoo* and *Xoc* represent significant threats to agriculture and global food security, and because of this are considered quarantine organisms in many rice producing countries (Verdier et al., 2012, Nino-Liu et al., 2006). Host resistance is the most effective and sustainable way to control bacterial diseases, such as BB and BLS. Historically, deployment of rice varieties resistant to *Xoo* has been widely used in Asia; however, these genotypes usually target very specific strains (races) of the pathogen, and thus, can be easily overcome due to the high degree of pathogenic variation (Tang et al., 2000, Verdier et al., 2012). Because of the instability of resistance, the search for new sources of resistance is a constant demand for breeding programs. In Africa, sources of resistance for BB and BLS are critically needed (Wonni et al., 2015).

1.2. TWO CLOSELY RELATED BUT DISTINCT PATHOGENS

Despite the high sequence similarity shared between *Xoo* and *Xoc*, the pathogens have distinct lifestyles and differ in tissue colonization and symptoms caused in the host, particularly in early stages of colonization (Sharma & Patil, 2011, Hajri et al., 2012). *Xoo* is a vascular pathogen that enters via hydathodes or wounds, colonizing the xylem and causing a systemic infection (Tabei, 1977). It induces a wilt at early stages of crop growth and leaf blight at later stages, and can affect grain quality by interfering with maturation (Ou, 1985). *Xoc* is a non-vascular pathogen that infects rice leaves through stomata or wounds and colonizes intercellular spaces of mesophyll parenchyma (Ou, 1985). Lesions expand along the leaf between the veins, thus resulting in streaks (Nino-Liu et al., 2006).

For each pathovar, endemic isolates from Asia and Africa exist (Hajri et al., 2012). Genetic diversity analyses have differentiated each group according to the geographical origin. Thus, Asian and African *Xoo* strains are well separated into two clades. African *Xoo* are more closely related to *Xoc* isolates in general. Asian and African *Xoc* are also differentiated with some but not all methodologies tested (Hajri et al., 2012). Altogether, African and Asian *Xoo* and *Xoc* strains have diverse evolutionary histories which may translate into differences in the control measures that need to be implemented in each continent.

1.3. PLANT IMMUNITY AND RICE – *X. oryzae* INTERACTIONS

Plant immunity consists of two branches, basal or non-host resistance and race-specific resistance (Jones & Dangl, 2006). Basal resistance entails the recognition of common and slowly evolving features of microbial pathogens, such as the bacterial protein flagellin; these features are termed microbial or pathogen-associated molecular patterns (MAMPs or PAMPs). PAMP perception is achieved by transmembrane pattern recognition receptors (PRRs), which initiate PAMP-triggered immunity (PTI). Successful pathogens secrete effector proteins to suppress the immune response induced by PRRs and promote infection, also known as effector-triggered susceptibility (ETS). Plants have acquired nucleotide-binding leucine-rich repeat (NLR) proteins which monitor directly or indirectly the presence of the pathogen effectors, and activate the effector-triggered immunity (ETI). These host surveillance proteins are encoded by resistance (*R*) genes (Chisholm et al., 2006, Jones & Dangl, 2006, Stuart et al., 2013). PTI is a weak resistance effective against multiple and diverse pathogens, whereas ETI confers a stronger response to specific races of a pathogen species (Ke et al., 2017). Although PTI and ETI are both aimed at preventing pathogen colonization, they differ in strength, duration and timing of activation (Li et

al., 2016). However, significant overlap in defense response (DR) gene induction after perception of PAMPs or effectors has been described (Navarro et al., 2004). DR-genes can respond either transcriptionally or posttranslationally to pathogen infection (Ke et al., 2017).

In the rice-*Xoo* pathosystem, over 40 *R* genes have been identified (Hutin et al., 2015b, Kim et al., 2015). While the prevalent class of *R* genes in plants encode NLR proteins, rice *R* genes conferring resistance to *Xoo* encode various types of proteins (Kim et al., 2015). *Xa1* encodes an NLR protein (Yoshimura et al., 1998). *Xa21* and *Xa3/26* code for leucine-rich repeat (LRR) receptor kinase-like proteins (Sun et al., 2004, Song et al., 1995). *Xa10* and *Xa27* encode novel proteins with trans-membrane domains (Gu et al., 2004, Tian et al., 2014). The recessive *R* gene *xa5* encodes the gamma subunit of transcription factor IIA (Iyer & McCouch, 2004). Almost one third of the mapped *R* genes to *Xoo* are recessive (Verdier et al., 2012).

A unique type of *Xanthomonas* effector proteins secreted by a type III secretion system (TTSS) are the transcription activator-like (TAL) effectors. Upon injection into the cytoplasm, TAL are translocated into the nucleus where they activate transcription of host genes required for infection success. This is achieved by a sequence-specific binding to host promoter sequences, the effector binding elements (EBEs) (Boch et al., 2009, Moscou & Bogdanove, 2009). Rice genes activated by TAL effectors to promote infection are considered susceptibility (*S*) genes (Boch et al., 2014). For instance, the *SWEET* sucrose transporter genes are targets of multiple *X. oryzae* TAL effectors (Hutin et al., 2015a). Conversely, TAL effectors can activate “executor” *R* genes, which elicit a strong defense response and restrict pathogen colonization (Zhang et al., 2015). Both *Xoo* and *Xoc* employ TAL as their major virulence factors, but differ in their TAL repertoires. Asian and African *Xoo* strains have up to 19 and nine TAL, respectively, whereas Asian and African

Xoc have up to 28 and 24, respectively (Gonzalez et al., 2007, Wilkins et al., 2015). So far, different targets have been characterized for each pathovar, with *Xoo* targeting sucrose transporters and transcription factors (Chen et al., 2010, Sugio et al., 2007), and *Xoc* targeting sulfate transporters (Cernadas et al., 2014).

1.4. QUANTITATIVE TRAIT LOCI AND BROAD-SPECTRUM DISEASE RESISTANCE

An alternative classification of plant defense responses is explained by qualitative and quantitative types of resistance. Qualitative resistance is governed by a single *R* gene and it is usually race-specific. Quantitative resistance is controlled by multiple genes, i.e., quantitative trait loci (QTL), and can be effective against diverse pathogen species. As QTL confer a partial resistance and exert less pressure on pathogen evolution, quantitative resistance is considered a more durable and broad-spectrum source of resistance (BSR) (Wisser et al., 2005, Boyd et al., 2013). Current interest of breeders is to develop long-lasting resistant crops by pyramiding *R* genes and QTL for resistance (Boyd et al., 2013). As host resistance is the most sustainable and effective method to control bacterial diseases, BSR sources are ideal in regions where more than one disease is present, as is the case for BB and BLS of rice.

Traditional QTL mapping is based on bi-parental populations, which have limited genetic diversity, provide limited resolution, and restrict the number of traits to study (Bohra, 2013). Novel mapping resources, such as the Multi-parent Advanced Generation Inter-Cross (MAGIC) populations, bypass these constraints. As indicated in their name, MAGIC populations are generated from multiple founders, increasing the genetic diversity integrated into the resulting progeny. Through several crossing events, an increased recombination is achieved, reducing the

linkage disequilibrium and thus, allowing higher resolution for QTL detection. Importantly, these novel populations allow the study of multiple traits in a single population (Cavanagh et al., 2008). In this study, we use a MAGIC population that was generated from eight elite founders from the indica subspecies of rice (Bandillo et al., 2013).

1.5. SCOPE OF DISSERTATION

The overarching goal of this dissertation is to identify novel, broad-spectrum and durable sources of resistance to BLS and BB, by exploiting the diversity and increased recombination achieved in the indica MAGIC population.

In Chapter 2, I screen early and advanced selfed generations of MAGIC advanced intercross lines (AILs) to identify novel and broad-spectrum sources of resistance to BB and BLS. In particular, I map 11 BSR QTL and detect alleles conferring resistance and susceptibility to these diseases.

In Chapter 3, I select candidates of rice DR-genes putatively involved in PTI and ETI to BB and BLS, that were identified in the indica MAGIC population. I focus on candidate gene promoters to evaluate the presence and polymorphisms in *cis*-regulatory modules (CRMs), as well as putative EBE targets for multiple *X. oryzae* strains. In addition, I also evaluate SNP markers associated with resistance to *X. oryzae* strains in coding or promoter sequences.

In Chapter 4, I detect polymorphisms in coding and promoter sequences of a cluster of *MATH-BTB* genes in a rice BSR QTL between resistant and susceptible MAGIC lines, which could explain phenotypic differences among these genotypes.

In Appendix A, I collaborate to screen an advanced selfed generation of MAGIC AILs to identify resistance sources to a specific *Xoo* virulence factor, Tal7b, and hypothesize the mechanism of resistance of one QTL.

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CHAPTER 2

ALLELIC VARIATION FOR BROAD-SPECTRUM RESISTANCE AND SUSCEPTIBILITY TO BACTERIAL PATHOGENS IDENTIFIED IN A RICE MAGIC POPULATION¹

OVERVIEW

Quantitative trait loci (QTL) that confer broad-spectrum resistance (BSR), or resistance that is effective against multiple and diverse plant pathogens, have been elusive targets of crop breeding programs. Multi-parent Advanced Generation Inter-Cross (MAGIC) populations, with their diverse genetic composition and high levels of recombination, are potential resources for identification of QTL for BSR. In this study, a rice MAGIC population was used to map QTL conferring BSR to two major rice diseases, bacterial leaf streak (BLS) and bacterial blight (BB), caused by *Xanthomonas oryzae* pathovars (pv.) *oryzicola* (*Xoc*) and *oryzae* (*Xoo*), respectively. Controlling these diseases is particularly important in Sub-Saharan Africa, where no sources of BSR are currently available in deployed varieties. The MAGIC founders and lines were genotyped by sequencing and phenotyped in the greenhouse and field by inoculation with multiple strains

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of *Xoc* and *Xoo*. A combination of genome-wide association studies (GWAS) and interval mapping analyses revealed 11 BSR QTL, effective against both diseases, and three pathovar-specific QTL. The most promising BSR QTL (qXO-2-1, qXO-4-1 and qXO-11-2) conferred resistance to more than nine *Xoc* and *Xoo* strains. GWAS detected 369 significant SNP markers with distinguishable phenotypic effects, allowing the identification of alleles conferring disease resistance and susceptibility. The BSR and susceptibility QTL will improve our understanding of the mechanisms of both resistance and susceptibility in the long term, and will be immediately useful resources for rice breeding programs.

2.1. INTRODUCTION

Disease resistance in rice (*Oryza sativa* L.) is classified into two main categories, qualitative and quantitative. Qualitative resistance is controlled by a single resistance (*R*) gene, and is usually effective against only certain strains of a pathogen species. As it imposes a greater selection pressure on pathogen evolution, this type of resistance can be more readily overcome. Conversely, quantitative resistance is conferred by quantitative trait loci (QTL), encompassing multiple genes, and is frequently associated with partial but durable resistance to an entire pathogen species or even different pathogen genera (Boyd et al., 2013; Wisser et al., 2005). Quantitative resistance is frequently referred to as broad-spectrum resistance (BSR), because of the breadth of pathogen groups it affects (Wisser et al., 2005).

The deployment of disease resistance QTL in rice has been limited due to its complex genetic control and the lack of knowledge on the function of genes underlying the QTL (Ramalingam et al., 2003). Recently, novel resources for association and interval mapping studies

in rice, the Multi-parent Advanced Generation Inter-Cross (MAGIC) populations, were developed and demonstrated to expedite identification of QTL (Bandillo et al., 2013; Cavanagh et al., 2008; Raghavan et al., 2017). Each rice MAGIC population was generated from multiple founder lines, selected for their different agronomic traits and genetic background. The founders were crossed in a design that ensured an equal representation of each founder in the population. Benefits of MAGIC populations to QTL mapping are increased recombination, transgressive segregation events revealing novel phenotypes, and capacity for fine-mapping, which expedite the discovery of new resistance sources against pathogens (Bandillo et al., 2013; Raghavan et al., 2017).

Bacterial leaf streak (BLS) and bacterial blight (BB) are devastating diseases of rice that cause considerable losses and yield reductions, especially in Asia and Africa (Cernadas et al., 2014; Mew et al., 1992). In Africa, the expansion and intensification of crop cultivation, coupled with the absence of appropriate phytosanitary controls, have contributed to the increased incidence of BLS and BB and the emergence of more virulent pathogen strains (Verdier et al., 2012; Wonni et al., 2014). BB has been an important threat in Africa since 1980, causing up to 50% yield loss, while BLS is a more recently observed disease, causing up to 20% yield loss (Kang et al., 2008; Reddy et al., 1979; Wonni et al., 2015). In Asia, the use of resistant varieties is considered the most effective and sustainable way to control these diseases (Tang et al., 2000; Verdier et al., 2012), but sources of resistance for BLS and BB in Africa are lacking (Wonni et al., 2015). BLS and BB are caused by two closely related pathogens, *Xanthomonas oryzae* pv. *oryzicola* (Xoc), and *Xanthomonas oryzae* pv. *oryzae* (Xoo), respectively. Xoc is a non-vascular pathogen that enters the plant through stomata or wounds and colonizes intercellular spaces of mesophyll parenchyma (Ou, 1985), while Xoo is a vascular pathogen that enters through

hydathodes or wounds, causing a systemic infection (Tabei, 1977). Although African *Xoc* and *Xoo* strains elicit similar symptoms to their Asian counterparts, they display several genetic differences, and are grouped into distinct phylogenetic clades (Gonzalez et al., 2007; Wonni et al., 2014).

Over 40 *R* genes against Asian *Xoo* strains have been mapped (Hutin et al., 2015; Kim et al., 2015), however, most of these *R* genes are not effective in controlling the distinct strains of *Xoc* and *Xoo* present in Sub-Saharan Africa (Gonzalez et al., 2007). Djedatin *et al.* recently mapped disease resistance QTL effective against African *Xoo* strains, located on rice chromosomes 1, 7, 9, 10 and 11 (Djedatin et al., 2016). Interestingly, the QTL on chromosome 11 confers resistance to both Asian and African *Xoo*. QTL for Asian *Xoc* have also been identified (Tang et al., 2000; Xie et al., 2014), but no QTL to African *Xoc* have yet been detected. Despite numerous efforts, only two resistance loci to *Xoc* are currently known in rice. These include the recessive resistance gene *bls1* effective against Asian *Xoc* (He et al., 2012), and the locus *Xo1* effective against multiple African *Xoc* and *Xoo* strains (Triplett et al., 2016). *Xo1* colocalizes with the *R* gene *Xa1*, which confers resistance to Asian *Xoo*, and work is in progress to determine whether they correspond to the same gene (Triplett et al., 2016). Additionally, *Rxo1*, a gene cloned from maize, confers non-host resistance in rice plants against *Xoc* (Zhao et al., 2005). Previous studies argued that resistance to BLS is mostly quantitative (Tang et al., 2000), possibly explaining why few single *R* loci have been detected so far (Makino et al., 2006). As related pathogens, *Xoc* and *Xoo* use transcription activator-like (TAL) effectors as their primary virulence factors to manipulate rice gene expression and invade the host (Bogdanove and Voytas, 2011). Rice genes that promote infection, such as some genes activated by TAL effectors, are considered susceptibility (*S*) genes

(Boch et al., 2014). A disease resistance-associated region can have either the alleles that contribute to a resistant phenotype, or the susceptible alleles which lead to increased disease. Because *S* gene activation is essential for *X. oryzae* virulence, the mutation of an *S* gene can decrease the ability to invade the host. The resulting resistance is therefore achieved by the loss of susceptibility (Boch et al., 2014).

For the present study, we selected a MAGIC population developed from eight indica founders (Appendix B1, Table S2.1). Indica is one of the eco-geographical subspecies of rice grown widely cultivated in the tropics and the subtropics, including African countries (Garris et al., 2005). Our goal was to use the indica MAGIC population to identify loci (QTL/genes) associated with resistance and susceptibility to BLS and BB of rice, and, specifically, to identify loci that confer BSR to both diseases. Our primary focus was on strains of *Xoc* and *Xoo* from Sub-Saharan Africa, due to the lack of effective BLS or BB resistance in currently cultivated germplasm in this region (Verdier et al., 2012). Indica MAGIC founders had not been previously screened for resistance to African *Xoc* and *Xoo* strains. In general, BSR effective against multiple bacterial pathogens is a powerful resource for enhancement of local elite varieties or advanced lines from regional breeding programs. Importantly, because highly useful new source materials for breeding programs can be extracted directly from MAGIC populations, this approach can significantly expedite the deployment of durable *X. oryzae*-resistant varieties.

2.2. RESULTS

Indica MAGIC population reveals sources of resistance to *Xoc* and *Xoo* strains

Two subsets of the MAGIC population were chosen at early (fourth, called S4) and advanced (sixth-eighth, called S8) selfed generations, consisting of 200 and 340 advanced intercross lines (AILs), respectively. Both subsets were used to map QTL/genes associated with resistance and susceptibility, and to evaluate the suitability of MAGIC populations for discovery of disease resistance-associated regions. In addition, the resolution of QTL detection was compared for each generation (early and advanced).

The MAGIC S4 subset was screened with two *Xoc* and two *Xoo* African strains (Appendix B1, Table S2.2). The responses to *Xoc* BAI5 and MAI3, and *Xoo* BAI3 and MAI1, measured as lesion length (LL), exhibited a large range of phenotypic variation when compared to the phenotypes of the founders (Appendix B1, Figure S2.1). The phenotypic variation was expected, due to the high degree of recombination in this population. A high number of resistant AILs ($0 < LL \leq 0.1$ cm for *Xoc* and $0 < LL < 5$ cm for *Xoo*) were observed for strains *Xoc* BA5 and MAI3, and *Xoo* MAI1, whereas *Xoo* BAI3 showed a more normal distribution of phenotypes. Overall, these results demonstrated potential sources of resistance for BLS and BB in the indica MAGIC population.

The MAGIC S8 subset was screened using a larger set of strains with diverse genetic backgrounds and isolated from different geographical regions. A total of 20 *X. oryzae* strains, nine *Xoc* and 11 *Xoo*, were used for screening the S8 AILs and founders in the greenhouse and under field conditions in Mali (Figure 2.1; Appendix B1, Figures S2.2 and S2.3; Table S2.2). Two common strains were used to phenotype the S4 and the S8 (*Xoc* BA5 and *Xoo* BAI3). Phenotypic responses

to most strains in both the greenhouse and the field displayed a right-skewed distribution, while some showed an approximately normal distribution (Figure 2.1; Appendix B1, Figures S2.2 and S2.3). As observed in the S4 screenings, founders responded differently to each strain, indicating different resistance sources. For strains *Xoc* BLS256 and *Xoo* MAI133, transgressive segregation for resistance was observed in the S8, showing AILs with more resistant phenotypes than any of the founders. Interestingly, for all the strains tested, transgressive segregation for susceptibility was observed in the MAGIC AILs (Figure 2.1; Appendix B1, Figures S2.2 and S2.3) thus positioning the indica MAGIC as a valuable population for studying susceptibility-associated loci.

Multiple disease resistance QTL identified in the indica MAGIC population

Founders and the S4 subset were genotyped using the genotyping by sequencing (GBS) method (Bandillo et al., 2013; Elshire et al., 2011), as were 1,316 MAGIC AILs of the S6:S8 generation (Raghavan et al., 2017). For this study, monomorphic SNP markers were excluded, therefore the final datasets contained SNPs for which at least one of the parents was polymorphic. Genome-wide association studies (GWAS) and interval mapping (IM) adapted to multiparent populations were conducted to detect genome-wide associations and QTL, using the SNP marker datasets for each bacterial strain and MAGIC population subset (Appendix B1, Table S2.3).

For GWAS, the founders were excluded, as this methodology considers individuals to be unrelated. The indica MAGIC population has a negligible population structure (Bandillo et al., 2013; Mackay and Powell, 2007), allowing these studies. A kinship matrix was generated for each subset-bacterial strain dataset and then analyses were performed using the mixed linear model

(MLM) for S4 and S8 subsets. Regions associated with resistance to *Xoc* or *Xoo* were detected for all bacterial strains screened in the S4, with 42 significant SNPs (P -value < 0.001), on chromosomes 4, 5, 8, 9 and 11 (Figure 2.2a; Appendix B1, Figures S2.4a, S2.4c, S4e; Table S2.4). GWAS on the S8 yielded 369 significant SNPs (P -value < 0.001) and identified additional regions for resistance to *Xoc* or *Xoo* in all 12 chromosomes, with the most significant associations found on chromosomes 2, 4, 5, 7, 10 and 11 (Figures 2.2c, 2.2e; Appendix B1, Figures S2.5 and S2.6; Table S2.5). The GWAS approach detected two loci on chromosome 11, at 6-8 Mpb and 26-29 Mbp, for resistance to four *Xoo* strains (Figure 2.2e; Appendix B1, Figures S2.6a, S2.6e, S2.6k). The majority of the 369 significant SNPs were located in or near gene promoters (40), coding sequences (185), introns (43), and untranslated (28) regions (Appendix B1, Table S2.5). The significance of the associations was notably higher in the S8 compared to the S4 for the same *X. oryzae* strain for three main reasons. The S8 is an advanced generation where alleles are fixed, as opposed to the S4 where alleles are still segregating, the number of the SNP markers used in the S8 was almost double that of the S4, and because a larger number of MAGIC AILs were screened in the S8 (Figures 2.2a, 2.2c; Appendix B1, Figures S2.4c, S2.6a).

For IM, genotypic and pedigree information from the AILs were used to generate a linkage map for each subset. QTL were determined using simple interval mapping, computing the founder effects between each pair of markers. A Wald test for the significance of all founder effects at each putative QTL position was performed. QTL were called when P -value < 0.001 and supporting intervals were calculated as the 95% confidence interval (1-LOD). A total of 19 disease resistance QTL were detected in the S4, located in almost all chromosomes, except 6 and 12 (Figure 2.2b; Appendix B1, Figures S2.4b, S2.4d, S2.4f; Table S2.6). As expected, the two mapping

approaches identified identical genetic regions, i.e., IM supporting intervals contained markers significantly associated by GWAS in the S4 (Appendix B1, Table S2.4). Overlapping genetic regions associated with disease resistance for both *X. oryzae* pathovars were mapped on chromosomes 4 for *Xoc* BAI5, MAI3 and *Xoo* BAI3, and on 11 for *Xoc* MAI3, and *Xoo* BAI3, at 30-32 Mbp and 27-29 Mbp, respectively (Appendix B1, Table S2.6). The region on chromosome 4 colocalizes with a recently detected locus *Xo1* that is effective against multiple *Xoc* and *Xoo* strains (Triplett et al., 2016), and the region on chromosome 11 was reported to contain resistance for *Xoo* but not for *Xoc* (Djedatin et al., 2016).

IM analyses on the S8, performed independently for each strain and using 14,475 SNP markers, detected significant associations in all chromosomes except chromosome 3 (Figures 2.2b, 2.2d, 2.2f; Appendix B1, Figures S2.5 and S2.6; Table S2.7), and revealed novel genetic regions associated with resistance to BLS and BB. More associated regions were mapped using IM than GWAS for each strain, with up to three QTL within a single chromosome (Appendix B1, Table S2.7). As observed in the S4, some identified loci were corroborated by the two approaches. A total of 37 strain-specific QTL were detected in the S8, with an average of five QTL per bacterial strain.

Overall, we identified multiple QTL associated with resistance to BLS and BB in both S4 and S8 subsets of the indica MAGIC population, many of which were confirmed by both GWAS and IM. While the earlier generation (S4) was sufficient to map regions associated with disease resistance, the S8 results yielded SNPs associated at lower *P*-values by GWAS, and provided more precision for determining the location of the QTL by IM. In fact, the size of the supporting

intervals detected in the S4 subset was notably reduced in the S8, for QTL on chromosomes 4, 5, 10 and 11 (Appendix B1, Table S2.8).

Indica MAGIC population uncovers multiple BSR QTL and allelic contributions to resistance and susceptibility

Integrating the results of GWAS and IM from the 20 *X. oryzae* strains in the S8, we identified 14 regions associated with resistance to multiple bacterial strains (Figure 2.3). Of these loci, 11 QTL, named qXO, are effective against both *Xoc* and *Xoo*, and three QTL, named qBLS and qBB, are specific to one pathovar. To define the limits of the pathovar-specific and BSR QTL, we selected the widest overlapping genetic region from IM analyses as the common QTL (Table 2.1; Appendix B1, Table S2.9). Most QTL were identified by both mapping approaches with the same pathogen strains; and some of these same QTL were detected by additional strains in GWAS. Four QTL were detected only by IM. Of the 369 significant SNPs yielded by GWAS across all strains, 103 SNPs were effective against multiple strains and located on QTL qXO-2-1, qXO-4-1, qXO-5-1, qBB-11-1 and qXO-11-2. Overall, we detected 51 QTL in the S8 (11 BSR QTL, three pathovar-specific and 37 strain-specific). From the 19 QTL detected in the S4, five overlapped with the BSR QTL qXO-2-2, qXO-4-1, qXO-5-2, qXO-10-1 and qXO-11-2 identified in the S8 (Appendix B1, Table S2.6). The locations of QTL common to the S4 and S8 as well as the QTL sizes were refined in the S8, largely due to an increased number of SNPs, a larger sample size, and the fact that the S8 is a more advanced generation where alleles are fixed (Appendix B1, Table S2.8).

One advantage of performing both GWAS and IM, beyond confirmation of the identified QTL, is that clusters of significant SNPs within the QTL can be identified to fine map the causal

genes. The most promising QTL in our study were qXO-2-1, qXO-4-1 and qXO-11-2, as they confer resistance to 12, 16 and nine *X. oryzae* strains, respectively. These QTL explained 6.3-13.2%, 7.0-39.5%, and 6.9-12.3% of the phenotypic variance to *X. oryzae* strains, respectively. Furthermore, for these three QTL, several SNPs were significantly associated with multiple strains (Appendix B1, Table S2.5). We selected the overlapping genetic region for each QTL where common SNPs were detected by different strains, 24.5-27.2 Mbp, 29.5-32.6 Mbp, 25.1-28.9 Mbp in chromosomes 2, 4 and 11, respectively. Linkage disequilibrium (LD) analyses performed within these regions identified haplotype blocks (Appendix B1, Figures S2.7, S2.8 and S2.9). More than five SNPs significantly associated with resistance to multiple *X. oryzae* strains were clustered in a few haplotype blocks in each chromosome (Appendix B1, Figures S2.7, S2.8 and S2.9; Tables S2.10, S2.11 and S2.12). These results provide useful information to narrow the genetic region associated with resistance for each one of these QTL. For instance, on chromosome 4, 26 out of the 39 common significant SNPs were located in haplotype blocks 6, 7 and 8. SNPs on blocks 7 and 8 were associated with resistance to more than 15 strains (Figure 2.4a; Appendix B1, Figure S2.8; Table S2.11), and the putative donor of the resistant alleles in this region was the founder IR4630-22-2-5-1-3 (Appendix B1, Table S2.11).

Integration of GWAS and IM in multiparent populations can help in assessing the phenotypic effects of single allelic variants at each SNP. All the SNP in the S4 and S8 subset are dimorphic, i.e. there are only two possible alleles for each marker. GWAS estimates the effect of each allele at a SNP; in this case, a negative effect indicates the “effect allele” is associated with shorter lesion lengths (thus associated with a more resistant phenotype) and a positive effect indicates the opposite. For the majority of the identified QTL, the effect (causal) alleles were

predicted to have negative effects (Appendix B1, Table S2.5). Interestingly, in qXO-2-1 and qXO-4-1 several alleles had positive effects, indicating their association with an increase in susceptibility. In qXO-4-1, 11 SNPs located in blocks 7 and 8 are associated with increased susceptibility to 12-15 *X. oryzae* strains (Figure 2.4b).

In summary, multiple BSR sources to *Xoc* and *Xoo* of particular importance to rice producing areas of Sub-Saharan Africa were identified. Moreover, our integration of GWAS and IM results enabled refinement of the mapped QTL. By detecting phenotypic effects of causal alleles, we have identified resources that will facilitate a better understanding of how the affected genes contribute to resistance or susceptibility.

2.3. DISCUSSION

MAGIC populations are powerful resources for discovery of novel, broad-spectrum disease resistance

In this study, we used an indica MAGIC population to identify QTL exhibiting broad-spectrum resistance to two bacterial diseases of rice, BLS and BB. Our results are particularly relevant for Sub-Saharan Africa, given the increasing incidence of these diseases and the lack of resistance in currently used rice germplasm. In total, we identified 14 disease resistance QTL effective against multiple *X. oryzae* strains; of these, 11 are BSR QTL (Figure 2.3 and Table 2.1). In addition, we identified 37 strain-specific QTL (Appendix B1, Table S2.7). Of the total 51 QTL, 49 were confirmed under field screening conditions, supporting their value in the development of improved varieties.

Three types of novel resistance QTL for BLS and BB disease resistance were identified in this study, including 25 strain-specific QTL (Appendix B1, Table S2.7), two pathovar-specific QTL (qBLS-8-1 for BLS and qBB-11-1 for BB), and three BSR QTL (qXO-1-1, qXO-5-2, XO-7-2). Although some of the identified BSR QTL colocalize with formerly described loci or QTL for Asian *X. oryzae* strains (e.g. qXO-2-1, qXO-2-2, qXO-5-1, qXO-5-3 and qXO-12-1), these regions were not shown previously to confer resistance to African *X. oryzae* strains. We used a larger and more diverse set of strains, including different *Xoo* races, and demonstrated a broader effectiveness for the previously identified loci qXO-4-1, qBB-7-1, qXO-10-1 and qXO-11-2 (Djedatin et al., 2016; Triplett et al., 2016). Two QTL, qXO-4-1 and qXO-11-2, coincide with clusters of *R* genes previously identified for Asian *Xoo* resistance on chromosome 4 (*Xa1*, *Xa2*, *Xa12*, *Xa14*, *Xa31* and *Xa38*) and chromosome 11 (*Xa3/26*, *Xa4*, *Xa10*, *Xa21*, *Xa22*, and *Xa23*) (Kim et al., 2015). *Xa4* and *xa5* are present in some of the MAGIC founders (Appendix B1, Table S2.1). However, these *R* genes are only reported to confer resistance to *Xoo*, and thus, they do not confer BSR. The BSR QTL qXO-4-1 and qXO-11-2, together with qXO-2-1, confer resistance to a large number of *X. oryzae* strains and are excellent targets for further validation and use in crop improvement programs.

MAGIC populations include multiple founders, which endows greater genetic diversity, and their construction involves several crossing events, which increases shuffling of the progeny's genomes. For these reasons, a single MAGIC population can be used to study multiple traits, and, as we observed in this study, can reveal more QTL than a single biparental population (Bohra, 2013). Multiparent populations also allow the possibility of using smaller sample sizes and earlier generations to identify traits of agricultural interest. We conducted QTL mapping in early and advanced generations, the S4 and S6:S8, respectively, and found that the former is suitable for

coarse mapping while the latter allows for fine mapping (Cavanagh et al., 2008), with reduced intervals, and confirmation of the associations found in the early generation (Appendix B1, Table S2.8). Moreover, by combining GWAS and IM approaches, we identified alleles associated with resistance and susceptibility, which will help assess the mechanisms of resistance in these QTL.

Understanding the resistance and susceptibility mechanisms to *X. oryzae* in rice

Despite advances in understanding how Asian *X. oryzae* elicit resistance or susceptibility in the host, the knowledge of resistance and susceptibility mechanisms to African *X. oryzae* is limited (Djedatin et al., 2016; Triplett et al., 2016). Both *Xoc* and *Xoo* contain and use TAL effectors for virulence, but their TAL repertoires are distinct (Cernadas et al., 2014). Moreover, rice gene expression patterns during infection with *Xoc* and *Xoo* are very different (Cernadas et al., 2014), suggesting that, in addition to differences in their tissue specificity, these pathogens differ in their virulence mechanisms. Rice *S* genes targeted by *Xoo* TAL effectors are different than those targeted by *Xoc* (Cai et al., 2017; Verdier et al., 2012). For instance, several *Xoo* TAL effectors target host sucrose transporter genes (Chen et al., 2010), while some *Xoc* TAL effectors target sulfur transporter genes (Cernadas et al., 2014).

Mutation of target *S* genes results in one type of host resistance, i.e., the loss of susceptibility (Boch et al., 2014). These mutations can occur in promoters, blocking the ability of the TAL to bind and activate, or in coding regions, changing how effectors interact with the susceptibility target (Huang et al., 2016). In our study, we found variants in promoters (40/369) and in coding regions (185/369) of potential *S* genes (Appendix B1, Table S2.5). In the near-term, these allelic variants can inform marker-assisted selection strategies for germplasm

improvement. These specific alleles pinpoint gene candidates for functional analysis, the next step to revealing how the allelic variants contribute to resistance and susceptibility.

Remaining questions are (1) whether the same or different genes within each QTL are involved in the defense response to each of the *X. oryzae* pathovars, (2) if there are QTL interactions that favor the defense response, and (3) how the QTL are transcriptionally modulated.

Few resistance sources effective against diverse pathogens (broad-spectrum resistance, BSR) are available for crop improvement programs. BSR providing protection to two important rice diseases, bacterial blight and bacterial leaf streak, is particularly needed for African rice producing areas, where resistance to both diseases are lacking. In this study we identified 11 BSR QTL to BLS and BB diseases using a rice indica MAGIC population. The QTL were confirmed in greenhouse and field studies. Our work shows that the implementation of multiparent populations for the study of disease resistance, in combination with genome-wide association and interval mapping analyses, can facilitate the discovery of BSR QTL. Moreover, the integration of these approaches are useful to refine QTL and to improve the understanding of their contributions to resistance or susceptibility. Because the MAGIC founders are elite varieties, the disease resistance QTL identified here can be rapidly incorporated into breeding programs to achieve more durable resistance to BLS and BB.

2.4. MATERIALS AND METHODS

Plant materials

The crossing strategy and development of the indica MAGIC mapping population used in this study were previously described (Bandillo et al., 2013). Briefly, the eight founders were intermated for a total of 28 bi-parental crosses. To derive 4-way crosses, the 28 F1's were then intercrossed, but only 70 crosses (out of the possible 210 crosses) were performed. The 8-way crosses were derived from intercrossing the 70 4-way crosses, but only 35 (out of the possible 105) 8-way crosses were done. From each of the 35 8-way crosses, approximately 60 seeds were advanced by selfing, achieving a population size of approximately 2,100 advanced intercross lines (AILs). At the fourth selfed generation, a subset of 200 AILs (S4 subset) was randomly selected for screening (Bandillo et al., 2013). At the sixth-eighth selfed generation (S6:S8), 340 AILs were selected (approximately 10 random lines from 33 8-way crosses) for screening (called the S8 subset).

Genotyping and filtering of S4 and S8 subsets

Founders and the S4 subset were genotyped using a 96-plex *ApeKI* genotyping by sequencing (GBS) protocol (Bandillo et al., 2013; Elshire et al., 2011). The Nipponbare reference genome was used for SNP calling by the TASSEL GBS analysis pipeline v. 3.0.147 (Glaubitz et al., 2014). The same procedure was repeated for the eight founders and 1316 MAGIC AILs of the S6:S8 generation (Raghavan et al., 2017); SNP calling was carried out using TASSEL GBS analysis pipeline v. 3.0.169 (Glaubitz et al., 2014).

Initial datasets of 634,103 and 396,361 SNP markers were obtained for the S4 and S8 subsets, respectively. Markers with missing calls, heterozygous and monomorphic markers in the founders were removed from both datasets. Missing calls were not imputed for any analysis. For the S4 subset, SNP markers for each AILs-bacterial strain dataset were filtered so that 80% of the AILs had a call and a minimum frequency of 0.05 for the minor allele, using TASSEL v 4.3.4 (Bradbury et al., 2007). Resulting SNP markers for each strain are listed in Appendix B1, Table S2.3. For the S8 subset, SNP markers were filtered so that 80% of the AILs had a call and a minimum frequency of 0.05 for the minor allele, resulting in a set of 14,475 SNP markers, using TASSEL v 5.0.2 (Bradbury et al., 2007). The same SNP datasets for each bacterial strain in S4 and S8 subsets were used for both GWAS and IM (Appendix B1, Table S2.3).

Greenhouse and field conditions

Plants screened in growth chamber and greenhouse were grown individually in pots containing 1: 1: 0.25 mixture of Pro-mix potting mix, peat moss and sand at Colorado State University. Fertilizer (Peters Excel 15-5-15 Cal-Mag (Scotts) 300mg/L) was applied twice per week, beginning at two weeks after germination.

The growth chamber conditions throughout the experiment were 16h light/8h dark at 28°C day/24°C night with an average relative humidity of 85% (used only for S4 screening of *Xoc* strains BAI5 and MAI3). The greenhouse conditions throughout the experiment were 16h light/8h dark at 30°C day/25°C night, with an average relative humidity of 75%. The S4-growth chamber screenings were conducted in July 2013 and the S4-greenhouse screenings on September 2013. The S8-greenhouse screenings were conducted in June 2014.

The screening of MAGIC AILs in field conditions was conducted at the agronomic research station IER Sotuba (Bamako, Mali) from June to September 2015. Seeds were sown in pots filled with local compost. About 5 g of DAP (18-46-0) were added to each pot on the 15th, 25th and 35th days after sowing. The average temperature was 28°C with a minimum of 23°C and maximum of 33°C. The total precipitation during this period was 680 mm with an average relative humidity of 74% (61% minimum to 88% maximum).

Inoculations and phenotyping

Cultures of *Xoc* and *Xoo* were incubated for 24 h on peptone-sucrose agar (PSA) medium (Karganilla et al., 1973) at 28°C. For inoculum, the bacteria were suspended in sterile water at an optical density (OD 600) of 0.2 (10^8 CFU/ml).

For *Xoc* screenings, four-week-old plants were inoculated by leaf infiltration, using a needleless syringe to introduce the bacterial suspension into the intercellular spaces of leaves (Reimers and Leach, 1991). One inoculation per leaf was done in three leaves of the central tiller. Lesion lengths (in millimeters) were measured 12 days post inoculation (dpi), and 4 mm (the size of the infiltration site) were subtracted for each single measurement.

For *Xoo* screenings, six-week old plants were inoculated by the leaf clipping method (Kauffman et al., 1973), cutting approximately 4 cm from the tip of the two fully expanded leaves of the central tiller with scissors dipped in bacterial suspensions. Lesion lengths (in centimeters) were measured 14 dpi.

Experimental design

For the S4 subset, four technical replicates of each MAGIC line were independently screened with each bacterial strain. The averages of the lesion lengths were calculated for each line and used for GWAS and IM.

For greenhouse studies of the S8 subset, separate experiments were conducted for each bacterial strain (treatment; *Xoc* BAI5, BLS256 and *Xoo* BAI3), using a randomized block design with three replications (blocked over time). For each experiment, the S8 subset MAGIC AILs (340 lines), founders and controls (Nipponbare and WAB 56-125) were randomly planted. Least-squares means (LS means) were calculated for each MAGIC line, using Proc Mixed (SAS Institute 2008). A random model (with ddfm = kr for degrees of freedom) was used, where lesion length was the response variable, and line and rep were the independent and blocking variables, respectively. The LS means were used for GWAS and IM.

For the AILs screened in the field, six technical replicates of each MAGIC line were independently screened with each bacterial strain. The averages of the lesion lengths were calculated and for each MAGIC line and used for GWAS and IM.

Genome-wide association studies

GWAS were performed using TASSEL (Bradbury et al., 2007). A kinship matrix (K) was generated for each SNP dataset and then analyses were performed using the (Q+K) mixed linear model (MLM). To account for the false discovery rate, q-values were calculated using the qvalue R-package (Storey and Tibshirani, 2003). Manhattan plots were constructed using the qqman R-package (Turner, 2014). For the S4 subset, TASSEL v 4.3.4 was used, and *P*-values < 0.001 were

considered significant (Appendix B1, Tables S2.3 and S2.4). For the S8 subset, TASSEL v 5.0.2 was used, and three levels of significance were considered (Appendix B1, Tables S2.3 and S2.5): (*) P -value < 0.001 and q -value > 0.05; (**) P -value < 0.001 and q -value < 0.05; (***) P -value < 0.0001 and q -value < 0.05.

Interval mapping analyses

The R package mpMap (Huang and George, 2011), a platform that allows QTL mapping for multi-parent populations, was used as described previously (Huang and George, 2011). SNP data for each subset of AILs and founders, as well as pedigree information of the AILs were used to generate a linkage map (Raghavan et al., 2017). QTL were determined using simple interval mapping from the *mpIM* function, computing the founder effects between each pair of markers. For the S4 subset, mpMap v 1.14 was used (Appendix B1, Figure S2.3), whereas for the S8 subset, mpMap v 2.0.2 was used (Figure 2.3; Appendix B1, S2.6 and S2.7). mpMap v 2.0.2 allowed the estimation of the percentage of phenotypic variation explained by each QTL.

Prediction of SNP location and annotation

Functional annotation of variants was performed using SnpEff software (Cingolani et al., 2012) using the MSU7 rice reference annotation (Kawahara et al., 2013). Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes.

Linkage disequilibrium and haplotype analyses

Linkage disequilibrium (LD) and haplotype analyses were performed using Gevalt software (Davidovich et al., 2007), through the SNIPlay3 web application (Dereeper et al., 2015).

Regions where multiple SNPs were significantly associated with resistance to several *X. oryzae* strains were defined on chromosomes 2, 4 and 11. The corresponding genotype data of the MAGIC population was then extracted and sent to Gevalt, which includes the visualization capabilities of Haploview (Barrett et al., 2005), for the construction of the LD patterns and haplotype blocks.

2.5. FIGURES

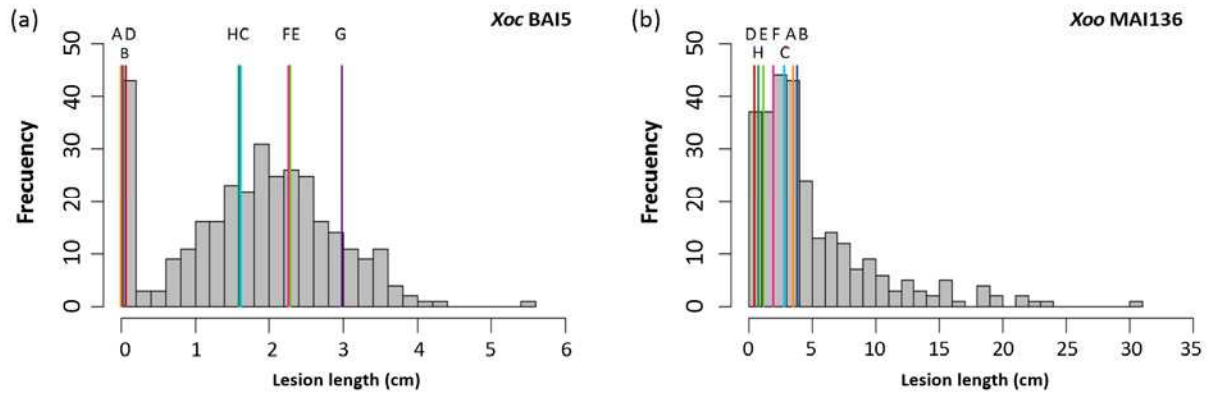


Figure 2.1. Distribution of lesion length (cm) of indica MAGIC founders and S8 subset. (a) Screening of 323 AILs in the greenhouse with *Xoc* BAI5. (b) Screening of 276 AILs in the field with *Xoo* MAI136. Histograms represent mean values of MAGIC lines. Mean lesion lengths of founders are indicated with vertical lines (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1). For *Xoo* MAI136, phenotypic value of founder PSBRc158 is missing due to lack of germination.

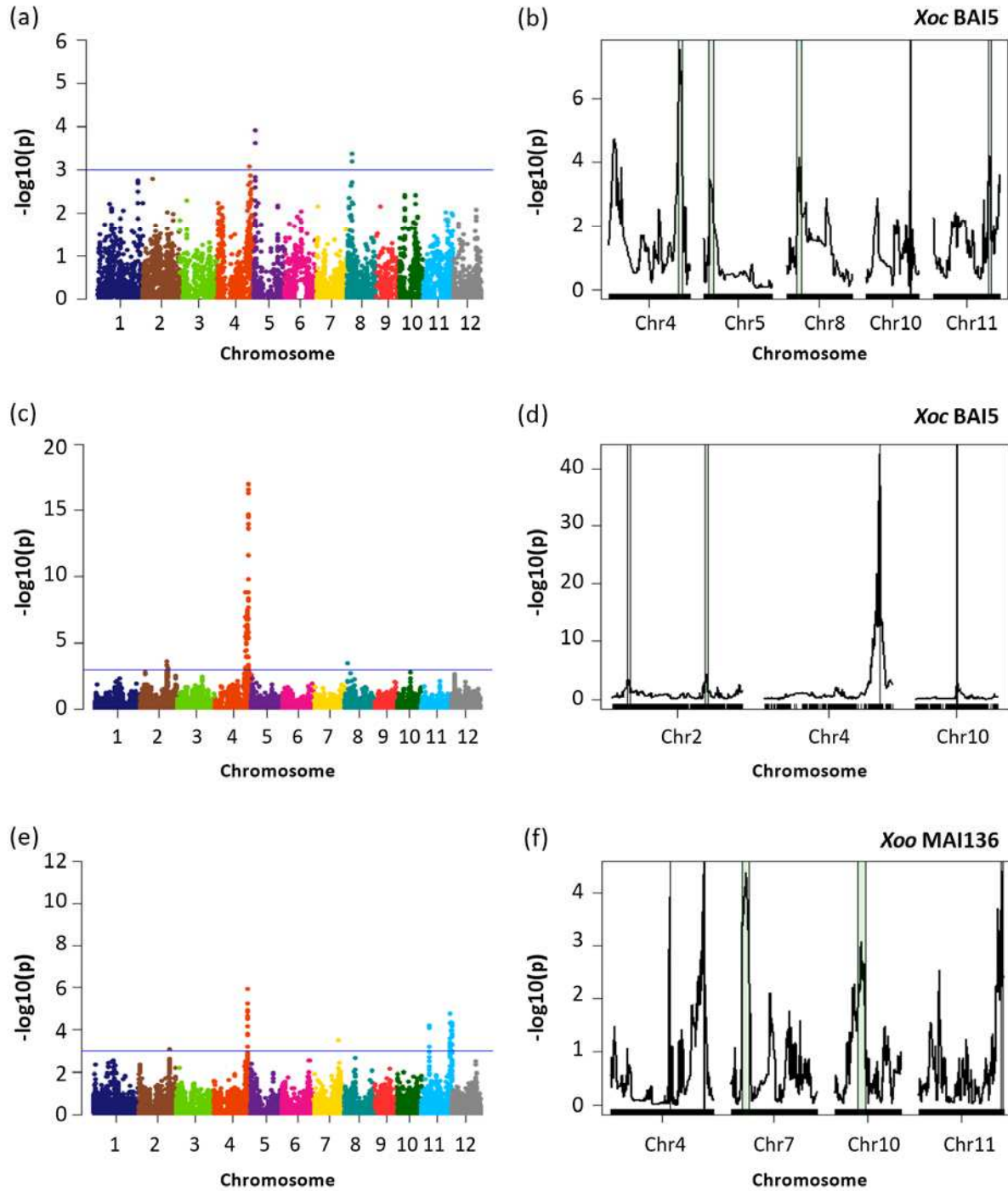


Figure 2.2. QTL detection for resistance to *Xoc* BAI5 and *Xoo* MAI136 in indica MAGIC S4 and S8 subsets. (a, b) *Xoc* BAI5 (markers=7,258), S4 subset. (c, d) *Xoc* BAI5 (markers=14,475), S8 subset. (e, f) *Xoo* MAI136 (markers =14,475), S8 subset. (a, c, e) Manhattan plots show the negative logarithm of the P -values for the mixed linear model, by chromosome. Solid blue line indicates significance threshold (P -value < 0.001). (b, d, f) Simple interval mapping showing chromosomes with significant QTL (P -value < 0.001). Green regions indicate 1-LOD support intervals.

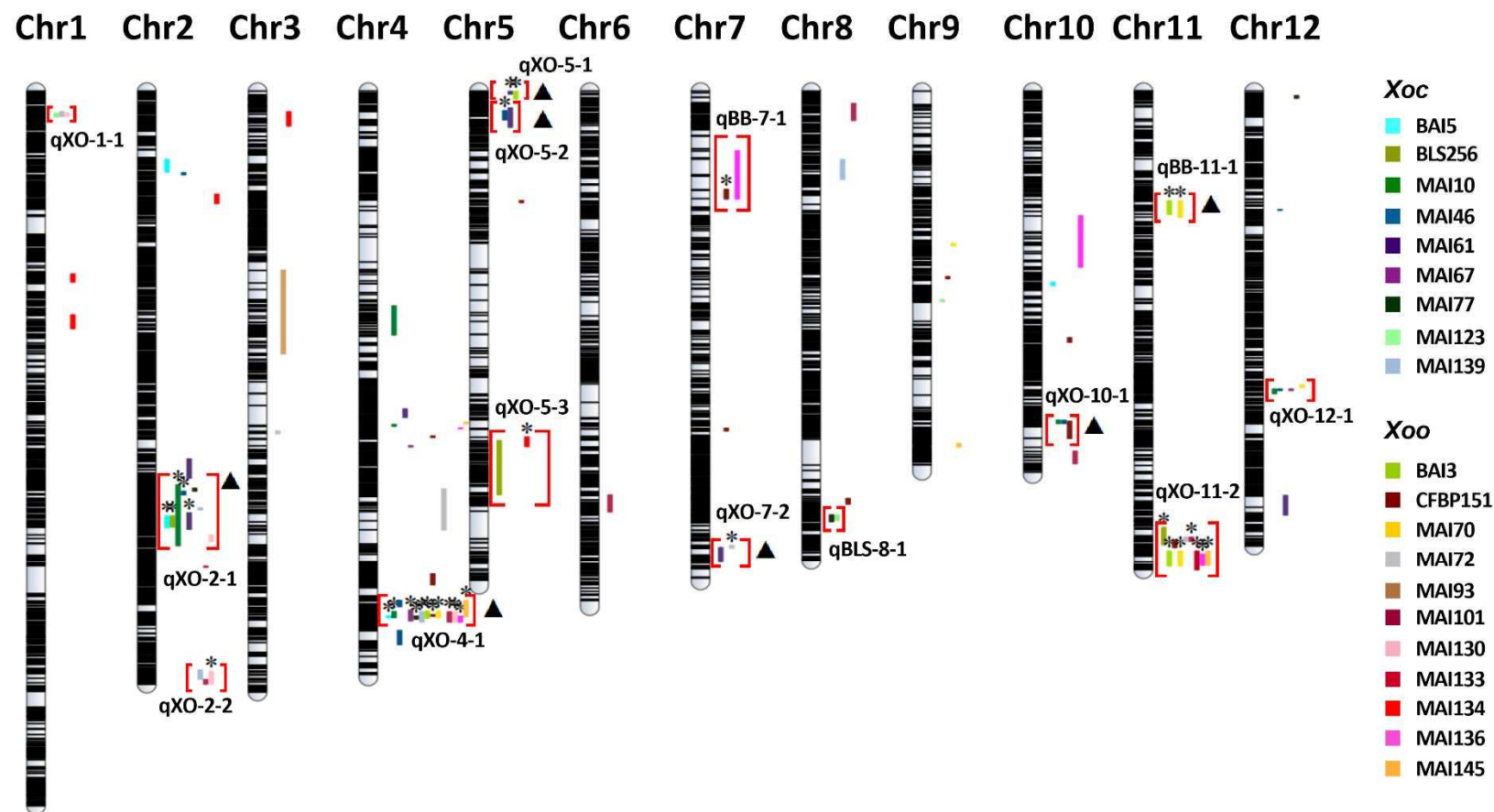


Figure 2.3. Integrative map showing resistance QTL to African and Asian *Xoc* and *Xoo* found in this study. Horizontal black lines represent the physical map using 14,475 SNP markers. Solid colored lines next to chromosomes indicate supporting interval sizes for each strain-specific QTL detected (Appendix B1, Table S2.7). *Xoc* and *Xoo* strains are differentiated by colors, as listed on the right. Red brackets highlight the 14 QTL that confer resistance to multiple *X. oryzae* strains. QTL names indicate whether it confers BSR, named qXO, or pathovar-specific resistance, named qBLS and qBB, for *Xoc* and *Xoo*, respectively. Stars (*) above supporting intervals indicate QTL corroboration by GWAS; triangles (▲) indicate GWAS corroboration of the QTL by strains other than those in the IM.

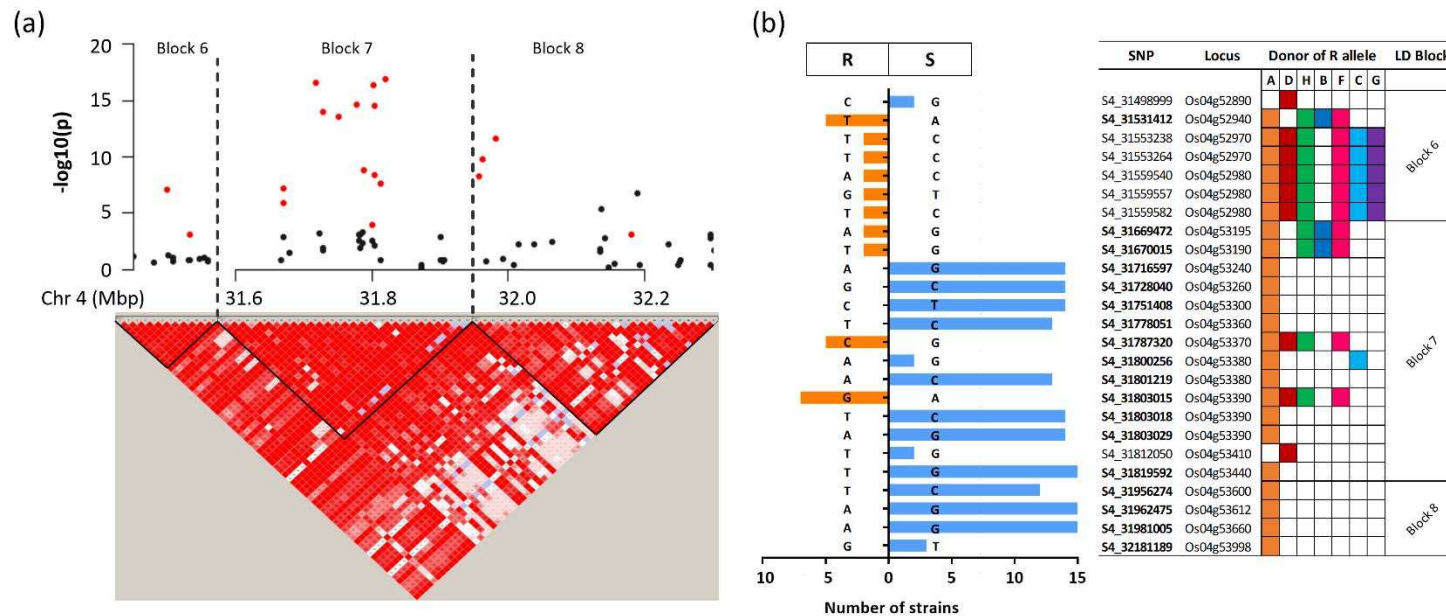


Figure 2.4. Haplotype block analyses and SNP effects in a hotspot region for *X. oryzae* resistance within qXO-4-1. (a) Local Manhattan plot of *Xoc* BAI5 (top) and linkage disequilibrium (LD) with haplotype block analysis (bottom) of the 31.49 – 32.29 Mbp region on chromosome 4. Red filled circles indicate SNPs that are significant to multiple *X. oryzae* strains. LD heatmap shows the standard Haploview color scheme to display LD with bright red for strong LD (LOD = 2 $D' = 1$), pink (LOD = 2 $D' < 1$), and blue (LOD < 2 $D' = 1$) for intermediate LD, and white for no LD (LOD < 2, $D' < 1$). (b) Summary of SNP effects to *X. oryzae* strains within haplotype blocks 6, 7 and 8 on chromosome 4. Size of the bars on the left denotes the number of strains for which a SNP was significant (P -value < 0.001); color and direction of the bars indicate the estimated effect, either negative (left, orange) or positive (right, blue). A negative effect is associated with a more resistant phenotype (R), and a positive effect with a more susceptible phenotype (S). For each SNP, the correspondent allele for the estimated effect is shown. SNPs in bold denote the SNP was significant in both pathovars (*Xoc* and *Xoo*), otherwise the SNP was significant only for *Xoc* strains. The locus ID for each SNP (prefix “LOC_” is omitted), was predicted from the MSU7 rice reference annotation. Founders are indicated with letters (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1). A colored box on the donor column indicates that the founder carries the R allele.

2.6. TABLES

Table 2.1. QTL effective against multiple *X. oryzae* strains identified in this study. Individual IM results (Appendix B1, Table S2.7) were combined using the widest supporting interval shared by the different *X. oryzae* strains in overlapping genetic regions. Detailed information is shown in Appendix B1, Table S2.9. Number of strains combines the total number of strains associated with each QTL by GWAS and IM analyses. Known resistance loci to African or Asian *X. oryzae* refers to previously identified QTL and single resistance genes (denoted by the prefix *Xa* or *Xo*).

QTL	Chr	QTL position			Pathovar	No. strains	Known resistance loci to	
		(cM)	Left Mrk	Right Mrk			African <i>X. oryzae</i>	Asian <i>X. oryzae</i>
qXO-1-1	1	5.2-5.9	S1_1335951	S1_1500023	both	3		
qXO-2-1	2	96.3-107.8	S2_24122049	S2_26993900	both	12		Qbr2a
qXO-2-2	2	141.1-142.9	S2_35289602	S2_35781025	both	3		AQBT001, qBbr2b, <i>Xa24(t)</i>
qXO-4-1	4	125.8-127.7	S4_31553264	S4_32064419	both	16	<i>Xo1</i>	AQBT008, <i>Xa1</i> , <i>Xa2</i> , <i>Xa31(t)</i> , <i>Xa38</i>
qXO-5-1	5	0.1-1.3	S5_69530	S5_353165	both	3		qBLSr5a, qBbr5, <i>xa5</i>
qXO-5-2	5	5.9-8.0	S5_1494420	S5_2046183	both	4		
qXO-5-3	5	84.9-90.7	S5_21255253	S5_22750867	both	2		qBB-5-2, qBB5, qBB-5-2, AQW004, qBBR5
qBB-7-1	7	20.1-23.6	S7_5097414	S7_5993972	<i>Xoo</i>	2	qABB-7	<i>xa8</i>
qXO-7-2	7	109.9-112.3	S7_27578266	S7_28179129	both	3		
qBLS-8-1	8	102.6-102.7	S8_25638183	S8_25729831	<i>Xoc</i>	2		
qXO-10-1	10	79.6-80.8	S10_19975243	S10_20983368	both	5	qABB-10	
qBB-11-1	11	28.0-28.9	S11_7012013	S11_7244498	<i>Xoo</i>	5		
qXO-11-2	11	107.5-114.6	S11_26879946	S11_28697227	both	9	qABB-11	QBbr11, AQBT023, <i>Xa3/Xa26</i> , <i>Xa4</i> , <i>Xa22</i> , <i>Xa32(t)</i> , <i>Xa35(t)</i> , <i>Xa36(t)</i> , <i>Xa40</i>
qXO-12-1	12	70.7-71.8	S12_17786177	S12_18084420	both	4		AQBT029

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CHAPTER 3

FROM QTL TO GENES: A NOVEL APPROACH FOR CANDIDATE GENE SELECTION²

OVERVIEW

PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI) are two components of plant immunity. Both comprise a coordinated modulation of host defense responses to hinder pathogen survival, including a network of signaling pathways and activation of defense response (DR) genes. Promoters are central processors of gene regulation and are important players in rice immune responses. On one hand, they contain *cis*-acting elements that determine gene transcription, such as *cis*-regulatory modules (CRMs). CRMs are structural organizations of motifs involved in DR, which can be used to predict broad-spectrum resistance (BSR) in rice. On the other hand, rice promoters can be hijacked by specialized bacterial effectors, transcription activator-like (TAL) effectors, to favor pathogen fitness. *Xanthomonas oryzae* pvs. *oryzicola* and *oryzae* are distinct pathogens of rice that are equipped with these type of bacterial proteins. In this study, loci within 14 disease resistance QTL were evaluated for promoters with multiple CRMs, promoters with putative targets for TAL effectors from multiple *X. oryzae* strains, and SNP markers associated with resistance to *X. oryzae* strains. A total of 104 candidate genes

² This chapter contains preliminary data for a future publication and is a collaborative effort with these authors: Ana M. Bossa-Castro, Bradley Tonnessen, Álvaro Pérez-Quintero, Jan E. Leach. Author contributions: A.M.B.-C., and J.E.L. designed research; A.M.B.-C., B.T. and A.P-Q. performed research; A.M.B.-C., and J.E.L. analyzed data.

for which at least two of these criteria were met were selected in an effort to identify potential convergence points of PTI and ETI. Two of these loci contained CRM polymorphisms between the MAGIC founders and were putative targets of at least ten different *X. oryzae* strains. The identification of genes implicated in both PTI and ETI responses is a powerful resource to understand plant immunity and to aid the development of improved elite varieties with durable resistance to *X. oryzae*.

3.1 INTRODUCTION

Plant immune responses have been shaped by interactions with diverse pathogens and consist of two layers, basal or non-host resistance and race-specific resistance. Basal resistance enables plants to recognize conserved structures of pathogens, so called microbial or pathogen-associated molecular patterns (MAMPs or PAMPs), through plant transmembrane pattern recognition receptors (PRRs). This type of response has been named PAMP-triggered immunity (PTI). In the arms race between plants and pathogens, pathogens have evolved specialized proteins, or effectors, that are injected to the plant cell, suppressing PTI and causing disease, or effector triggered susceptibility (ETS). Plants, in turn, have developed cytoplasmic localized host nucleotide-binding leucine-rich repeat (NLR) proteins that recognize the presence or activity of these effectors and trigger resistance, the effector-triggered immunity (ETI) (Chisholm et al., 2006, Jones & Dangl, 2006). While PTI confers a quantitative resistance, effective against a wide range of pathogens, ETI elicits a stronger, qualitative response that is effective against a narrow range of pathogens (Boyd et al., 2013). Both types of resistance involve activation and repression of a large array of genes, such as defense response (DR) genes, and share signaling components with distinctive activation dynamics and amplitudes aimed at preventing the spread of the

pathogen in the plant (Ke et al., 2017, Li et al., 2016). Although the transcriptional regulation is largely controlled by promoters and their *cis*-acting elements, most research has focused on the study of genetic variants in coding regions between resistant and susceptible varieties. However, in many cases, the functional difference is due to polymorphisms in promoter regions (Manosalva et al., 2009, Carrillo et al., 2009, Davidson et al., 2010).

In an effort to understand broad-spectrum disease resistance (BSR) on a genome-wide level in rice, groups of DR-related motifs were identified in promoters of co-expressed genes to three major pathogens of rice, *Magnaporthe oryzae*, *Rhizoctonia solani*, and *Xanthomonas oryzae* pv. *oryzae*, and several biotic PAMP-type elicitors, such as chitin, cellulose, jasmonic acid, and benzothiadiazole (BTH) (Tonnessen *et al.*, unpublished). These features were termed *cis*-regulatory modules (CRMs) and were classified in five different groupings, CRM1-5, each composed of different arrays of motifs (Tonnessen *et al.*, unpublished). CRM1 and CRM3 contain motifs putatively involved in epigenetic regulation, CRM2 motifs are related to ethylene and light responsive genes, while CRM4 and CRM5 contain motifs encompassing the W-box, a WRKY transcription factor binding site. CRM1 and CRM3 align with segments of miRNAs as well as MITEs, and they are likely transposon-derived repeat elements. Moreover, methylation patterns at CRM1 and CRM3 sites is highly variable across DR-gene promoters, suggesting an active role in methylation and de-methylation processes (Tonnessen *et al.*, unpublished). CRMs are overrepresented in DR-gene promoters of two rice varieties, Nipponbare and IR64, suggesting their association with BSR. Moreover, resistant and susceptible haplotypes are polymorphic in CRMs of DR-gene promoters, including mutations and/or structural changes of CRMs, thus it has been proposed that CRMs can be used to predict BSR in rice (Tonnessen *et al.*, unpublished).

Promoters not only harbor *cis*-elements that are important for gene expression, but also are targets of specialized bacterial effectors, such as transcription activator-like (TAL) effectors from *Xanthomonas oryzae* species. These proteins bind host promoters to activate gene transcription in a sequence-specific manner. This is mediated by a highly conserved central repeat region (CRR). Each repeat is nearly identical to the others, except at positions 12 and 13, called the repeat variable di-residues (RVDs). RVDs determine the precise DNA sequence that is recognized by a specific TAL, the effector binding element (EBE) (Moscou & Bogdanove, 2009, Boch et al., 2009).

Multiparent populations, such as MAGIC populations, offer a unique opportunity for the study of resistance to diverse plant diseases in a single population. Recently, 14 disease resistance QTL effective against bacterial leaf streak (BLS) and bacterial blight (BB) of rice were identified in an indica MAGIC population (Bossa-Castro et al., 2018). Of these, 11 are effective against multiple *Xoc* and *Xoo* isolates (BSR), and three are pathovar-specific. We hypothesize that convergence points of PTI and ETI can be identified within these QTL. Thus, through a diverse and new approach to refine selection of candidate causal genes in each QTL, we seek to pinpoint loci that are components of both PTI and ETI defense responses. To this aim, we selected a group of loci which had two of the following: (1) promoters with multiple CRMs in IR64, Nipponbare or both, (2) promoters with putative targets for TAL effectors from multiple *X. oryzae* strains in Nipponbare, (3) significant SNP markers for resistance to BLS and BB, located in coding or promoter regions. Overall, 104 candidate genes were obtained within 12 QTL. Among the selected loci, eight promoters had CRM polymorphisms between the MAGIC founders, consistent with the corresponding donor of resistant and susceptible alleles in each QTL. The identification

of BSR DR-genes and their downstream incorporation in elite varieties will provide a more durable and sustainable host resistance in rice producing regions.

3.2. RESULTS

Gene promoters within disease resistance QTL have multiple CRM

As DR-gene promoters were recently found to be enriched in CRMs compared to those of non DR-genes, we analyzed the promoteromes of genes within 14 disease resistance QTL for presence of CRMs (Figure 3.1, Table 3.1). Although these QTL were identified in an indica MAGIC population, both the Nipponbare and IR64 genome sequences were used for the initial screening. A total of 1,163 loci contained CRMs in Nipponbare, IR64, or both promoteromes (Tables 3.2 and S.3.1 -in supplementary folder-). CRM1 and CRM3 were present in 45 and 80 loci, respectively; CRM2 in 86 loci; CRM4 and CRM5 in 1,084 and 365 loci, respectively. A high number of promoters had CRM4 and CRM5, an expected result since both these CRM contain WRKY transcription factor binding sites that are known to modulate a great number of defense responses (Table 3.2). To select the most promising candidate genes, we selected those whose promoters contained multiple CRMs in either variety, obtaining a set of 432 loci (Table 3.3).

Multiple TAL effectors from diverse *X. oryzae* strains have predicted EBE targets in promoters of genes within disease resistance QTL

Nipponbare promoter sequences from the genes within the selected QTL were used to screen the available *X. oryzae* TALomes, i.e. repertoires of TAL effector genes, from 35 *X. oryzae* sequenced strains (14 *Xoc* and 21 *Xoo*). Additionally, we included the TALomes of two strains of *Xanthomonas campestris* pv. *lensiae* (*Xcl*), a weak pathogen of rice (Lang *et al.*, unpublished)

(Table 3.4). Recent work proposed the inclusion of *Xcl* into the genus *oryzae* due to phylogenetic similarities with *Xoc* and *Xoo*, thus we treated them as *X. oryzae* strains (Lang *et al.*, unpublished). A total of 1,979 promoters were predicted targets of at least one *X. oryzae* TAL effector (Table S.3.2 – in supplementary folder). Different combinations of targets were found: 334 unique *Xoc* targets, 361 unique *Xoo* targets, and 32 common targets of African and Asian strains of both *Xoc* and *Xoo*. Interestingly, some loci contained a high number of predicted EBE. For instance, LOC_Os02g43100 is the predicted target of 43 TAL from 33 *X. oryzae* strains with 11 different EBE, and LOC_Os07g09620 is the predicted target of 34 TAL from 19 *X. oryzae* strains with nine different EBE. To narrow the most promising genes for broad-spectrum resistance, we selected those promoters putatively targeted by more than 10 different *X. oryzae* strains, obtaining a set of 536 loci (Table S.3.2 – in supplementary folder). Genes whose promoters are targets of various strains are possibly functioning as *S* genes. Conversely, if the target EBE in that promoter has been altered in one rice variety, it can function as a loss of susceptibility resistance gene.

Loci within selected QTL harbor SNPs significantly associated with BLS and BB resistance

In the Bossa-Castro *et al.* study, 369 SNP markers were significantly associated with resistance to at least one *X. oryzae* strain (P -value > 0.001) (Bossa-Castro *et al.*, 2018). Of these, 153 SNPs present only in coding or promoter regions were selected, and these were distributed in 104 loci that encompassed most of the identified QTL, except qXO-1-1, qXO-5-3, qBLS-8-1, and qXO-12-1 (Tables 3.5 and 3.6). A total of 81 loci had more than one significant SNP. Among these, LOC_Os11g47870 and LOC_Os04g52590 had four and seven SNP, respectively, located in exons. LOC_Os11g47870 belongs to the GRAS transcription factor family and was associated with resistance to both *Xoc* and *Xoo*, while LOC_Os04g52590 is a kinase associated only with

resistance to *Xoc*. LOC_Os07g46039, an unknown function protein, contained four SNP in the 5' UTR and promoter region and was associated only with resistance to *Xoo*.

qXO-4-1 and qXO-11-2 had numerous individual loci explaining resistance to multiple *X. oryzae* strains. For instance, LOC_Os04g53440, a putative RNA recognition motif containing protein, is associated with resistance to 15 *X. oryzae* strains; whereas LOC_Os11g47650, a putative tryptophan repressor/replication initiator, is associated with resistance to seven *X. oryzae* strains.

Putative convergence points of PTI and ETI identified in disease resistance QTL

The three data sets of (1) 432 loci with multiple CRM, (2) 536 loci with multiple predicted EBE, and (3) 104 loci with significant SNPs were combined, obtaining a set of 977 loci (Table 3.7 and 3.8). Only four loci shared the three parameters, an AP2 domain containing protein (LOC_Os02g42585), a zinc finger C3HC4 type domain containing protein (LOC_Os02g42690), a putative kinase (LOC_Os11g44430), and a putative thaumatin (LOC_Os11g47944). Thus, we selected loci for which at least two of the above criteria were met, with a final group of 104 loci. Of those, 11 loci had significant SNP and multiple EBE, while 24 loci had significant SNP and multiple CRM. A total of 77 loci had multiple EBE and multiple CRM, suggesting potential convergence points of PTI and ETI. Among these genes, several loci with immunity related roles were found, such as AP2 domain containing proteins, putative disease resistance protein RPM1, glutathione S-transferases, glycosyl hydrolases, NLR proteins, PINHEAD proteins, polyphenol oxidases, kinases and serine/threonine-protein kinases.

A subset of 35 of these loci, present in BSR QTL qXO-2-1, qXO-4-1, qXO-5-1 and qXO-11-2, was selected to specifically evaluate their motif and CRM composition in the eight indica MAGIC founders. The previously identified donors of the resistant alleles on these QTL were IR77298-14-1-2-10 (IR77) and Shan-Huang Zhan-2 (SHZ-2) for qXO-2-1, IR4630-22-2-5-1-3 (IR46) for qXO-4-1, and PSBRc82 for qXO-5-1. For qXO-11-2, the donors of the susceptible alleles are Sambha Mahsuri+Sub1 (Sambha) and PSBRc82, while the rest of the founders are predicted to contribute the resistant alleles (Bossa-Castro et al., 2018). Polymorphisms in CRMs between resistant and susceptible donors were identified in eight loci (Table 3.9), LOC_Os02g42620, LOC_Os02g42890 and LOC_Os02g43000 on chromosome 2, LOC_Os04g53430 on chromosome 4, LOC_Os05g01040, LOC_Os05g01380 and LOC_Os05g01580 on chromosome 5, and LOC_Os11g47550 on chromosome 11.

LOC_Os02g42620 is a putative protein kinase with presence of CRM4 and CRM5 near the transcription start site (TSS) in all MAGIC founders (Figure 3.2.A.). However, IR77 and SHZ-2 (resistant donors) and PSBRc82 have an additional CRM4 at approximately 1.4 Kb from the TSS, which was absent in the susceptible donor founders. LOC_Os02g42890 is a putative cytochrome b561 with CRM4 and CRM5 at approximately 900 bp from the TSS (Figure 3.2.B.). In these promoters, the resistant donors IR77 and SHZ-2 have different SNPs at the third B-motif (containing the W-box), consequently the CRM5 is absent. LOC_Os02g43000 codes for a predicted cysteine-rich repeat secretory protein precursor. In the promoter regions of the MAGIC founders, CRM3 and CRM4 were detected in an interesting pattern (Figure 3.2.C.). CRM3 is present in IR46 and SHZ-2 at approximately 1.6 Kb from the TSS, and CRM4 is nested within CRM3. Founders IR77 and PSBRc82 have only CRM4.

On chromosome 4, the only locus with CRM polymorphism was LOC_Os04g53430. This gene codes a MATH-BTB containing protein, OsMBTB8 (Figure 3.3). In all MAGIC founders, a CRM4 was detected near the TSS. At approximately 1.6 Kb from the TSS, CRM4 and CRM5 were present in five founders, including the resistant donor IR46, whereas the other three founders have only CRM4. However, a 36 bp deletion in IR46 causes CRM4 and CRM5 to be located 500 bp downstream with respect to the other founders, with possible consequences on W-box regulation.

LOC_Os05g01380 codes for a predicted serine/threonine kinase with a CRM1 at approximately 250 bp from the TSS in Sambha, SHZ-2 and IR45427-2B-2-2B-1-1 (IR45). CRM1 was absent in the resistant donor PSRBc82 due to two SNPs in Motif D (Figure 3.4.A.). LOC_Os05g01580 is a putative polygalacturonase inhibitor with multiple CRM in the MAGIC founder promoters (Figure 3.4.B.). Overall, CRM3, CRM4 and CRM5 were detected in the eight promoters, however PSRBc82 shows a unique combination of CRM, compared to the other founders. It has a CRM4 and CRM5 approximately at 100bp from the TSS, another CRM4 at 350 bp and a CRM3 at 1.5 Kb from the TSS. LOC_Os05g01580 is a predicted integral membrane protein DUF6 containing protein with presence of CRM3 and CRM4 in all founders (Figure 3.4.C.). CRM4 is located at approximately 350 bp from the TSS in all of them, whereas the CRM3 position differs among them. In seven founders, CRM3 is located at 1.7 Kb from the TSS, whereas in the resistant donor PSRBc82 is located at 1.6 Kb from the TSS, due to a 108 bp deletion in this founder. In addition, CRM3 of PSRBc82 has an extra W-box (B motif).

The locus LOC_Os11g47550, a putative glycosyl hydrolase on chromosome 11, had a surprising combination of CRM1 and CRM3, both associated with epigenetic regulation (Figure

3.5). The resistant donors contained both CRM, whereas CRM3 was absent in the susceptible haplotypes.

3.3. DISCUSSION

In this study, we used a diverse approach to narrow down the candidate genes in 11 BSR and three pathovar-specific rice QTL effective against multiple *X. oryzae* strains. Traditionally, candidate gene searches have been focused on protein-coding sequences, however, due to the importance of promoters in the regulation of transcription and the novel prediction resources, a new methodology was pursued towards this aim. Recent evidence shows rice DR-gene promoters are enriched in CRMs. Moreover, these organizations of motifs are polymorphic between resistant and susceptible genotypes and can be used as predictors of genes involved in PTI and ETI (Tonnessen *et al.*, unpublished). Additionally, the deciphered TAL effector code can be employed to predict ETI or ETS related genes, and their involvement in resistance or susceptibility, respectively (Moscou & Bogdanove, 2009, Boch et al., 2009).

Based on our three parameters for the search, only four loci located in the BSR QTL qXO-2-1 and qXO-11-2 met all the criteria examined (Tables 3.7 and 3.8). These genes code for DR-proteins, an AP2 and a zinc finger domain containing proteins, a putative kinase, and a putative thaumatin, and thus are promising candidates for future validation. However, none of these loci had CRM polymorphisms in the indica MAGIC founders. Besides these genes, 100 more were pinpointed as possible candidates (Tables 3.7 and 3.8). Among these, eight loci had CRM polymorphisms in the MAGIC founders between resistant and susceptible haplotypes, suggesting possible differences in the transcription regulation among these varieties (Figures 3.2, 3.3, 3.4,

and 3.5). Three of these loci, a putative cytochrome b561 (LOC_Os02g42890), a MATH-BTB (LOC_Os04g53430) and a putative glycosyl hydrolase (LOC_Os11g47550) were predicted targets of ten or more TAL effectors from *X. oryzae* strains. However, LOC_Os11g47550 is a putative target only of African *Xoo* strains, whereas LOC_Os02g42890 and LOC_Os04g53430 are targeted by both *Xoc* and *Xoo* from different geographical origins (Table S.3.2 – in supplementary folder). Although our CRM search in the MAGIC founders pinpointed promising loci for validation, a refined search needs to be conducted in the MAGIC progeny. As the advanced lines of multiparent populations have increased recombination, the evaluation of CRM structure in the MAGIC lines is the next step.

So far, the validated targets of *Xoc* and *Xoo* TAL effectors are sulfate and sucrose transporters, respectively (Chen et al., 2010, Cernadas et al., 2014). The only suggested common target of these two pathogens is OsHEN1, a methyl transferase (Moscou & Bogdanove, 2009, Hutin et al., 2015). In this study, 32 putative common targets of African and Asian strains of both *Xoc* and *Xoo* were identified. Among these, no transporters were found, but instead DR-genes such as glycosyltransferase, kinase, ethylene-responsive element-binding protein, glutathione S-transferase, and glycosyl hydrolase were detected. Further functional validation is required to confirm these targets.

BSR is usually conferred by a quantitative type of resistance that does not impose an intense selection pressure on pathogens and, consequently, achieves a more durable resistance in the host. However, the study of the causal genes underlying BSR QTL is challenging (Kou & Wang, 2010). By combining the advantage of MAGIC populations to study diverse plant diseases,

coupled with recent prediction methodologies for BSR and bacterial effector targets, putative convergence points of PTI and ETI in rice were identified.

3.4. MATERIALS AND METHODS

Mining of Nipponbare, IR64 and indica MAGIC founders' promoteromes for presence of CRMs

Coding and promoter regions of genes within the 14 selected QTL (Table 3.1) from the rice variety Nipponbare were extracted from the MSU7 rice reference annotation (Kawahara et al., 2013). Promoter regions for the rice variety IR64 were constructed from the recent annotation developed by Schatz *et al.* 2017 (unpublished). Gene orthologs in the mentioned regions were identified between IR64 and Nipponbare based on 90% similarity in full gene sequence. IR64 orthologs were aligned to Nipponbare to obtain accurate TSS positions. Promoter sequences from the eight indica MAGIC founders were extracted from the 3,000 genomes database (3K.R.G.P., 2014) using the variant calls generated from alignment of MAGIC founder sequence reads to the IR64 scaffolds.

CRMs were identified using a window-based, pairwise alignment approach of motifs in the selected promoters with the Regulatory region Local Alignment tool (ReLA). Each CRM has a specific window size, as follows: CRM1 is 153 bp long, with one G motif and two D motifs, the full palindromic version has an additional G motif. CRM2 is 199 bp long, with one P motif and two O motifs. CRM3 is 245 bp long, with two K motifs and one B motif, the full palindromic version has an additional B motif. CRM4 is 95 bp long contains two B motifs (W-box). CRM5 is 136 bp long with three B motifs (W-box). Visualizations of CRMs and motifs in promoters of selected genes were performed using a python script, and the PyX package (pyx.sourceforge.net).

TAL effector EBE prediction in Nipponbare promoterome

Promoter sequences from the rice variety Nipponbare were extracted from the MSU7 rice reference annotation (Kawahara et al., 2013). Promoter regions were defined as the 1 Kb region upstream of the transcription start site. TALomes, i.e. repertoires of TAL effector genes, from 37 *X. oryzae* sequenced strains (14 *Xoc*, 21 *Xoo*, and 2 *Xol*) were used to extract the TAL effector sequences for each *X. oryzae* strain (Table 3.4). EBE prediction in the rice variety Nipponbare (MSU7 reference annotation) was conducted using Talvez 3.2 (Perez-Quintero et al., 2013), defining QTL limits as the target region (Table 3.1); qXO-5-3 was not included. Predictions were conducted against both strands, with no position correction, using minimum score 8, keeping the top 500 targets per TAL, and using the RVD-DNA matrix published in Perez-Quintero et al. (2015).

3.5 FIGURES

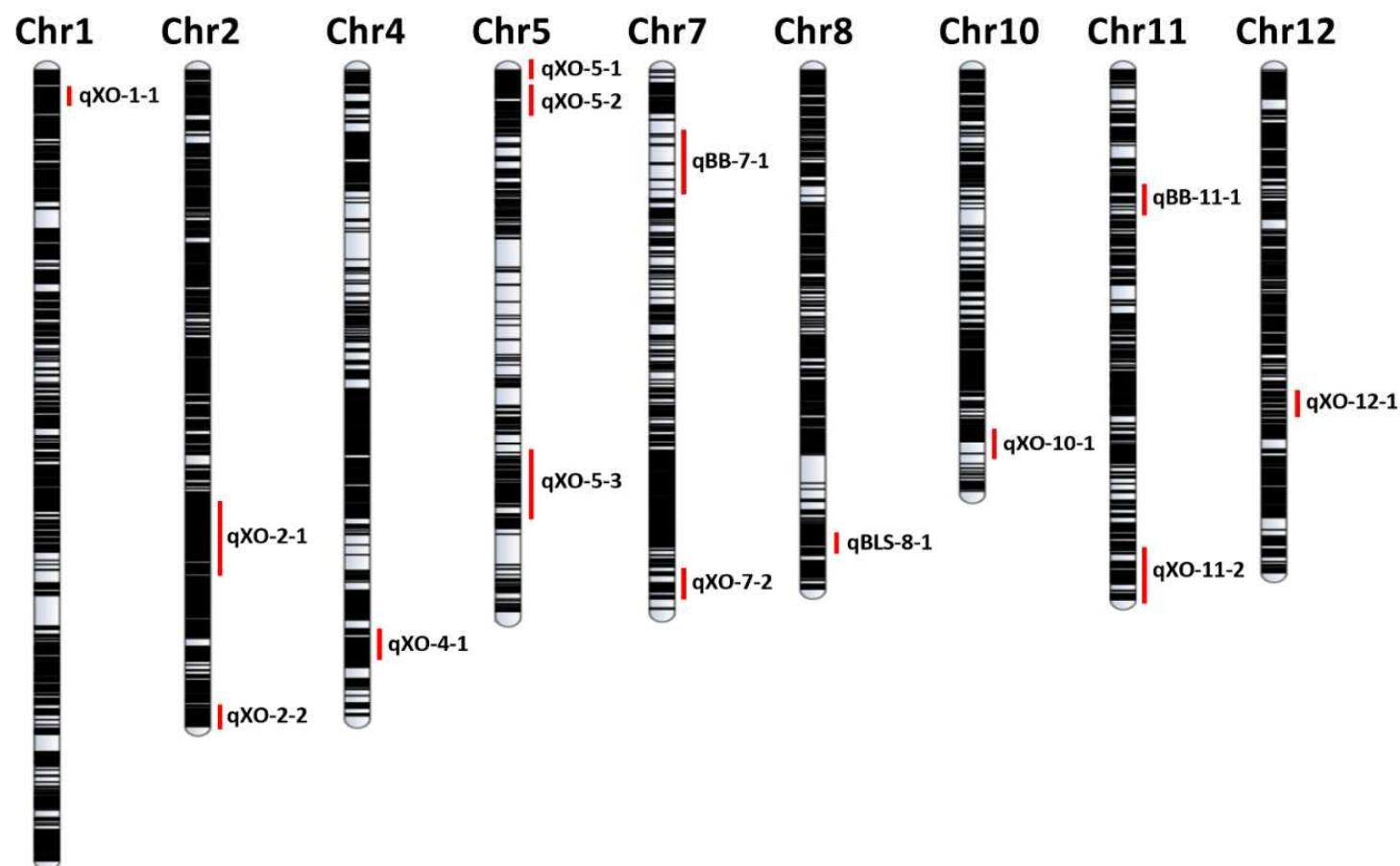


Figure 3.1. Disease resistance QTL to multiple *X. oryzae* strains identified in an indica MAGIC population. Horizontal black lines represent the physical map using 14,475 SNP markers. Solid red lines next to chromosomes represent supporting intervals for each QTL. QTL names indicate whether it confers BSR, named qXO, or pathovar-specific resistance, named qBLS and qBB, for *Xoc* and *Xoo*, respectively (Bossa-Castro et al., 2018).

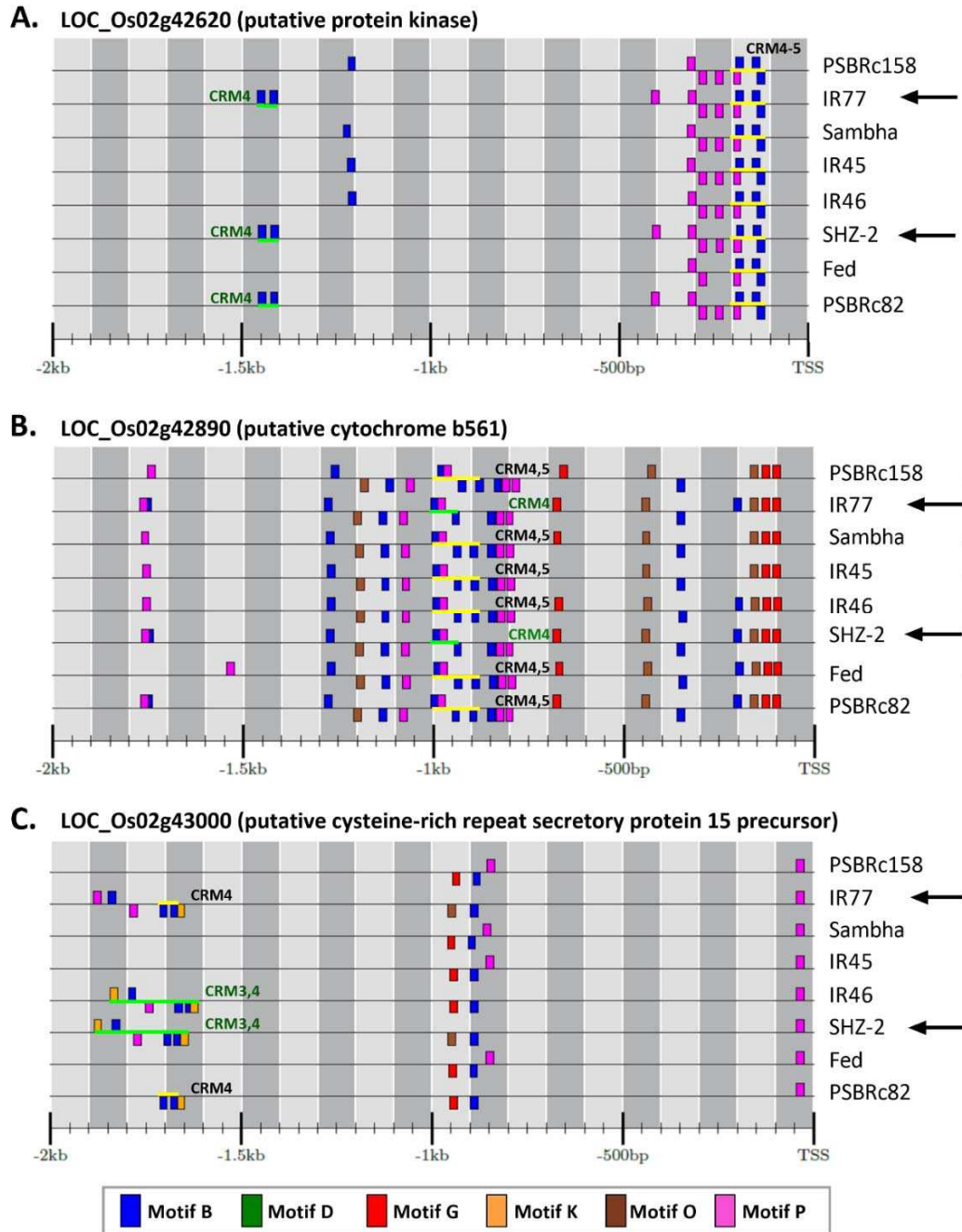


Figure 3.2. CRM and motif differences in promoter regions of eight indica MAGIC founders in qXO-2-1. Horizontal black lines represent the promoter region of each gene, starting at -2 Kb, ending at -1 bp from the transcription start site (TSS). Each motif is represented by a colored box either above the line (+ strand) or below the line (- strand) in each promoter. Donors of the resistant alleles in this QTL are founders IR77298-14-1-2-10 (IR77) and Shan-Huang Zhan-2 (SHZ-2), indicated with black arrows. CRMs are represented by colored horizontal lines and different colors are used to show differences between founders. **A.** Promoter region of LOC_Os02g42620. **B.** Promoter region of LOC_Os02g42890. **C.** Promoter region of LOC_Os02g43000.

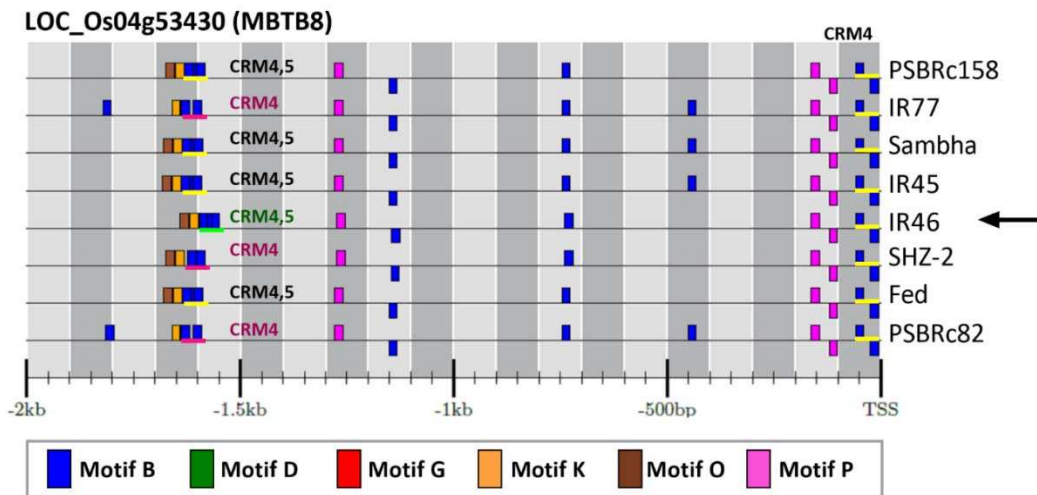


Figure 3.3. CRMs and motifs differences in LOC_Os04g53430 promoter regions of eight indica MAGIC founders in qXO-4-1. Horizontal black lines represent the promoter regions, starting at -2 Kb, ending at -1 bp from the TSS. Each motif is represented by a colored box either above the line (+ strand) or below the line (- strand) in each promoter. The predicted donor of the resistant alleles in this region of qXO-4-1 is founder IR4630-22-2-5-1-3 (IR46), indicated with a black arrow. CRMs are represented by colored horizontal lines and different colors are used to show differences between founders.

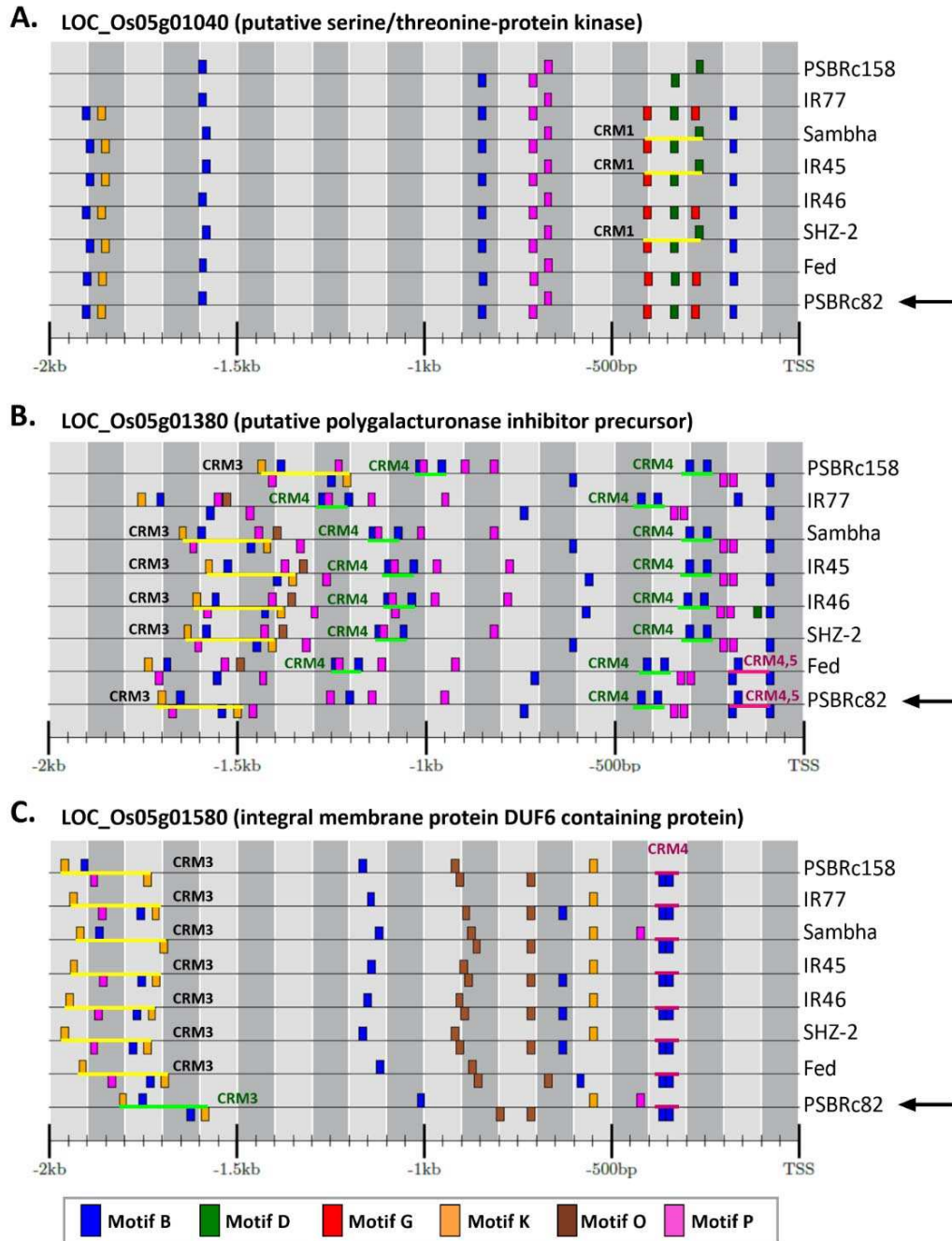


Figure 3.4. CRM and motif differences in promoter regions of eight indica MAGIC founders in qXO-5-1. Horizontal black lines represent the promoter region of each gene, starting at -2 Kb, ending at -1 bp from the transcription start site (TSS). Each motif is represented by a colored box either above the line (+ strand) or below the line (- strand) in each promoter. The resistance alleles in this QTL are donated by founder PSBRc82, indicated with a black arrow. CRMs are represented by colored horizontal lines and different colors are used to show differences between founders. **A.** Promoter region of LOC_Os05g01040. **B.** Promoter region of LOC_Os05g01380. **C.** Promoter region of LOC_Os05g01580.

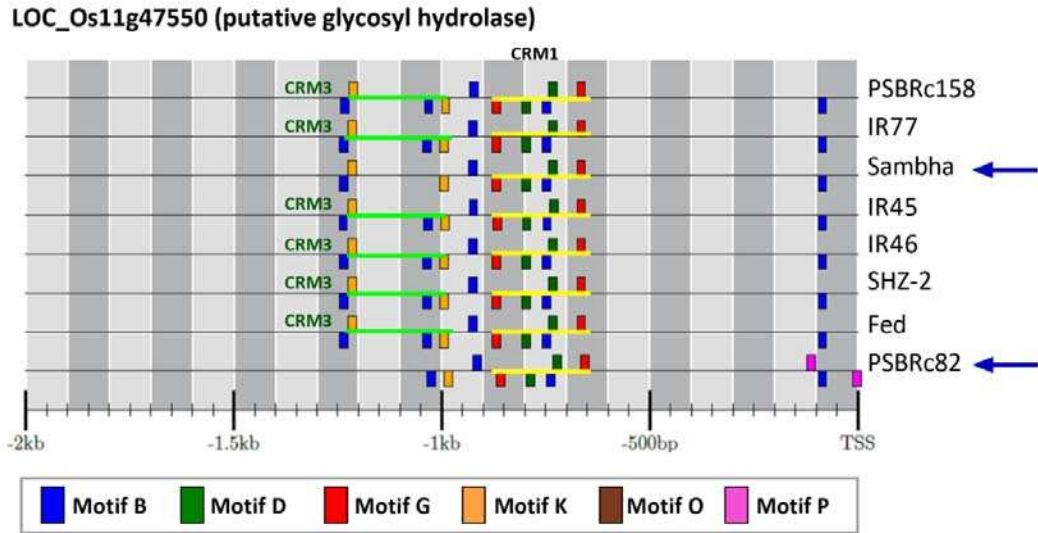


Figure 3.5. CRM and motif differences in LOC_Os11g47550 promoter regions of eight indica MAGIC founders in qXO-11-2. Horizontal black lines represent the promoter regions, starting at -2 Kb, ending at -1 bp from the TSS. Each motif is represented by a colored box either above the line (+ strand) or below the line (- strand) in each promoter. The predicted donors of the susceptible alleles in this region of qXO-11-2 are Sambha Mahsuri+Sub1 (Sambha) and PSBRc82, indicated with blue arrows, while the rest of the founders are predicted to contribute the resistant alleles. CRMs are represented by colored horizontal lines and different colors are used to show differences between founders.

3.6 TABLES

Table 3.1. Summary of disease resistance QTL to multiple *X. oryzae* strains identified in an indica MAGIC population (Bossa-Castro et al., 2018).

QTL	Chr	Pathovar	Supporting interval		Interval size (Kb)	No. <i>X. oryzae</i> strains
			Left Mrk	Right Mrk		
qXO-1-1	1	both	S1_1264553	S1_1550887	286	3
qXO-2-1	2	both	S2_23819009	S2_27466604	3,648	12
qXO-2-2	2	both	S2_35068072	S2_35891364	823	3
qXO-4-1	4	both	S4_30862506	S4_32134600	1,272	17
qXO-5-1	5	both	S5_37878	S5_453169	415	3
qXO-5-2	5	both	S5_1027632	S5_2167880	1,140	4
qXO-5-3	5	both	S5_20924798	S5_24383716	3,459	2
qBB-7-1	7	<i>Xoo</i>	S7_3622979	S7_6502570	2,880	2
qXO-7-2	7	both	S7_27479742	S7_28469553	990	3
qBLS-8-1	8	<i>Xoc</i>	S8_25638183	S8_26014015	376	2
qXO-10-1	10	both	S10_19903199	S10_20983368	1,080	5
qBB-11-1	11	<i>Xoo</i>	S11_6647060	S11_7616946	970	5
qXO-11-2	11	both	S11_26393474	S11_28977691	2,584	9
qXO-12-1	12	both	S12_17780296	S12_18274373	494	4

Table 3.2. Summary of CRMs in IR64 and Nipponbare promoters within selected QTL.

QTL	CRM1			CRM2			CRM3			CRM4			CRM5			No. unique loci	No. loci with multiple CRM	Total No. of CRM
	IR64	Both	Nipp	IR64	Both	Nipp	IR64	Both	Nipp	IR64	Both	Nipp	IR64	Both	Nipp			
qXO-1-1										2	14	1		3		17	3	20
qXO-2-1	1	6		2	8	4	2	6	5	22	139	28	11	43	17	204	78	294
qXO-2-2	1	2	1	2	5	2			4	9	36	10	2	11	3	60	23	88
qXO-4-1		2			3	2	2	1	2	6	57	10	3	19	11	76	37	118
qXO-5-1		2	1		1			3	1	2	23	2		5	3	30	10	43
qXO-5-2				1	2	1	3	3	1	1	38	14	1	10	5	57	19	80
qXO-5-3		5	1	5	16	2	5	11	6	16	155	29	5	33	16	222	72	305
qBB-7-1	1	4	2	2	8	1		8	1	18	120	26	9	38	8	168	69	246
qXO-7-2	2	1	1		2	2	1	2		15	43	12	10	9	8	71	30	108
qBLS-8-1		1								5	12	3	2	4		21	6	27
qXO-10-1		2		2	2			1	4	9	46	14	4	15	7	73	30	106
qBB-11-1		2	1					1		3	21	7	3	8	2	34	13	50
qXO-11-2	1	1	4	2	2	7	3		3	11	39	59	5	12	19	123	41	168
qXO-12-1							1			7			1			7	1	9
Tot. No. Loci	45			86			80			1,084			365			1,163	432	1,662

Table 3.3. Loci within selected QTL with multiple CRMs in IR64 and Nipponbare.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-1-1	LOC_Os01g03310	uti_cns_0001010_LOC_Os01g03310				Both	Both	BBT11 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
qXO-1-1	LOC_Os01g03380	uti_cns_0001010_LOC_Os01g03380				Both	Both	BBT16 - Bowman-Birk type bran trypsin inhibitor precursor, putative, expressed
qXO-1-1	LOC_Os01g03520	uti_cns_0001010_LOC_Os01g03520				Both	Both	ubiquitin conjugating enzyme protein, putative, expressed
qXO-2-1	LOC_Os02g39470	uti_cns_0000030_LOC_Os02g39470			Both	Both	Both	cyclin, N-terminal domain containing protein, expressed
qXO-2-1	LOC_Os02g39600	None				Nippon	Nippon	outer envelope protein, putative, expressed
qXO-2-1	LOC_Os02g39650	uti_cns_0000030_LOC_Os02g39650	Both			IR64		expressed protein
qXO-2-1	LOC_Os02g39700	uti_cns_0000030_LOC_Os02g39700				Nippon	Nippon	RNA binding protein, putative, expressed
qXO-2-1	LOC_Os02g39840	uti_cns_0000030_LOC_Os02g39840				IR64	IR64	eukaryotic initiation factor iso-4F subunit p82-34, putative, expressed
qXO-2-1	LOC_Os02g39880	uti_cns_0000030_LOC_Os02g39880				Both	IR64	expressed protein
qXO-2-1	LOC_Os02g39960	uti_cns_0000030_LOC_Os02g39960				Both	Both	exostosin family protein, putative, expressed
qXO-2-1	LOC_Os02g40270	None		Nippon	Nippon	Nippon	Nippon	expressed protein
qXO-2-1	LOC_Os02g40320	uti_cns_0000030_LOC_Os02g40320	IR64			Both	Both	PINHEAD, putative, expressed
qXO-2-1	LOC_Os02g40420	uti_cns_0000030_LOC_Os02g40420				Both	Both	expressed protein
qXO-2-1	LOC_Os02g40500	uti_cns_0000030_LOC_Os02g40500			IR64	Both		OsGrx_C2.1 - glutaredoxin subgroup I, expressed
qXO-2-1	LOC_Os02g40640	uti_cns_0000030_LOC_Os02g40640				Both	IR64	expressed protein
qXO-2-1	LOC_Os02g41490	uti_cns_0000030_LOC_Os02g41490				Both	Both	expressed protein
qXO-2-1	LOC_Os02g41520	uti_cns_0000055_LOC_Os02g41520				Both	Both	glycosyl transferase 8 domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g41560	uti_cns_0000055_LOC_Os02g41560		Both		Both		pentatricopeptide, putative, expressed
qXO-2-1	LOC_Os02g41570	uti_cns_0000055_LOC_Os02g41570				Nippon	Nippon	expressed protein
qXO-2-1	LOC_Os02g41680	uti_cns_0000055_LOC_Os02g41680		Both		Both		phenylalanine ammonia-lyase, putative, expressed
qXO-2-1	LOC_Os02g41710	uti_cns_0000055_LOC_Os02g41710				Both	Both	cyclic nucleotide-gated ion channel, putative, expressed
qXO-2-1	LOC_Os02g41810	None				Nippon	Nippon	expressed protein
qXO-2-1	LOC_Os02g41840	uti_cns_0000055_LOC_Os02g41840				Nippon	Nippon	DUF584 domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g41850	None				Nippon	Nippon	expressed protein

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-2-1	LOC_Os02g41890	uti_cns_0000055_LOC_Os02g41890				Both	Both	phytosulfokine receptor precursor, putative, expressed
qXO-2-1	LOC_Os02g41900	uti_cns_0000055_LOC_Os02g41900				Both	Both	expressed protein
qXO-2-1	LOC_Os02g41990	uti_cns_0001009_LOC_Os02g41990				Both	Both	expressed protein
qXO-2-1	LOC_Os02g42040	uti_cns_0001009_LOC_Os02g42040				IR64	IR64	MIF4G domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g42120	uti_cns_0001009_LOC_Os02g42120				Both	Both	expressed protein
qXO-2-1	LOC_Os02g42160	None				Nippon	Nippon	OsWAK15 - OsWAK receptor-like protein kinase, expressed
qXO-2-1	LOC_Os02g42170	None				Nippon	Nippon	phospholipase, putative, expressed
qXO-2-1	LOC_Os02g42280	uti_cns_0001009_LOC_Os02g42280				Both	Both	UDP-glucuronosyl/UDP-glucosyl transferase family protein, putative, expressed
qXO-2-1	LOC_Os02g42290	uti_cns_0001009_LOC_Os02g42290				Both	Both	OsClp3 - Putative Clp protease homologue, expressed
qXO-2-1	LOC_Os02g42330	uti_cns_0001009_LOC_Os02g42330			Nippon	IR64		nitrilase, putative, expressed
qXO-2-1	LOC_Os02g42360	uti_cns_0001009_LOC_Os02g42360				Both	Both	expressed protein
qXO-2-1	LOC_Os02g42390	uti_cns_0001009_LOC_Os02g42390			Both	Both	Both	expressed protein
qXO-2-1	LOC_Os02g42400	uti_cns_0001009_LOC_Os02g42400			Both	Both	Both	bolA-like family protein, putative, expressed
qXO-2-1	LOC_Os02g42585	uti_cns_0001009_LOC_Os02g42585				Both	IR64	AP2 domain containing protein, expressed
qXO-2-1	LOC_Os02g42590	uti_cns_0001009_LOC_Os02g42590				Both	Both	WD-40 repeat family protein, putative, expressed
qXO-2-1	LOC_Os02g42620	uti_cns_0001009_LOC_Os02g42620				Both	Both	protein kinase, putative, expressed
qXO-2-1	LOC_Os02g42690	uti_cns_0001009_LOC_Os02g42690			IR64	IR64	IR64	zinc finger, C3HC4 type domain containing protein, expressed
qXO-2-1	LOC_Os02g42780	uti_cns_0001009_LOC_Os02g42780				Both	Both	lectin receptor-type protein kinase, putative, expressed
qXO-2-1	LOC_Os02g42790	uti_cns_0001009_LOC_Os02g42790				Both	Both	short-chain dehydrogenase/reductase, putative, expressed
qXO-2-1	LOC_Os02g42890	uti_cns_0001009_LOC_Os02g42890				Both	Both	cytochrome b561, putative, expressed
qXO-2-1	LOC_Os02g42900	uti_cns_0001009_LOC_Os02g42900				Both	Both	expressed protein
qXO-2-1	LOC_Os02g42910	uti_cns_0001009_LOC_Os02g42910				Both	Nippon	expressed protein
qXO-2-1	LOC_Os02g42920	None				Nippon	Nippon	DTA2, putative, expressed
qXO-2-1	LOC_Os02g42950	uti_cns_0001009_LOC_Os02g42950				Both	Both	YABBY domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g43000	uti_cns_0001009_LOC_Os02g43000			Both	Both	Nippon	cysteine-rich repeat secretory protein 15 precursor, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-2-1	LOC_Os02g43040	uti_cns_0001009_LOC_Os02g43040				Both	Both	expressed protein
qXO-2-1	LOC_Os02g43080	uti_cns_0001009_LOC_Os02g43080				IR64	IR64	PPR repeat domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g43120	uti_cns_0001009_LOC_Os02g43120			Nippon	IR64		zinc finger, C3HC4 type domain containing protein, expressed
qXO-2-1	LOC_Os02g43150	uti_cns_0001009_LOC_Os02g43150				Nippon	Nippon	GATA zinc finger domain containing protein, expressed
qXO-2-1	LOC_Os02g43220	uti_cns_0001009_LOC_Os02g43220				Both	Both	polyamine oxidase, putative, expressed
qXO-2-1	LOC_Os02g43380	uti_cns_0001009_LOC_Os02g43380				Both	Both	expressed protein
qXO-2-1	LOC_Os02g43440	uti_cns_0001009_LOC_Os02g43440				Both	Both	expressed protein
qXO-2-1	LOC_Os02g43470	uti_cns_0001009_LOC_Os02g43470				Both	Both	glutamate dehydrogenase protein, putative, expressed
qXO-2-1	LOC_Os02g43480	uti_cns_0001009_LOC_Os02g43480				Both	Nippon	expressed protein
qXO-2-1	LOC_Os02g43490	None				Nippon	Nippon	expressed protein
qXO-2-1	LOC_Os02g43660	uti_cns_0001009_LOC_Os02g43660			Nippon	Both	Both	plastocyanin-like domain containing protein, putative, expressed
qXO-2-1	LOC_Os02g43710	uti_cns_0001009_LOC_Os02g43710				Both	IR64	enoyl-CoA hydratase/isomerase family protein, putative, expressed
qXO-2-1	LOC_Os02g43740	uti_cns_0001009_LOC_Os02g43740				Both	Both	AGC_PVPK_like_kin82y.6 - ACG kinases include homologs to PKA, PKG and PKC, expressed
qXO-2-1	LOC_Os02g43860	uti_cns_0001009_LOC_Os02g43860				Both	Both	amino acid permease, putative, expressed
qXO-2-1	LOC_Os02g43880	uti_cns_0001009_LOC_Os02g43880				Both	IR64	expressed protein
qXO-2-1	LOC_Os02g43930	uti_cns_0001009_LOC_Os02g43930				Both	Both	chaperone protein dnaJ, putative, expressed
qXO-2-1	LOC_Os02g44090	uti_cns_0001009_LOC_Os02g44090				Both	IR64	zinc finger protein, putative, expressed
qXO-2-1	LOC_Os02g44132	uti_cns_0001009_LOC_Os02g44132				Both	IR64	expressed protein
qXO-2-1	LOC_Os02g44134	uti_cns_0001009_LOC_Os02g44134	Both			Both	Both	thioesterase family protein, putative, expressed
qXO-2-1	LOC_Os02g44230	None		Nippon		Nippon		CPuORF22 - conserved peptide uORF-containing transcript, expressed
qXO-2-1	LOC_Os02g44310	uti_cns_0001009_LOC_Os02g44310				Both	Both	LTPL112 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
qXO-2-1	LOC_Os02g44330	uti_cns_0001009_LOC_Os02g44330				Both	Both	rho guanine nucleotide exchange factor, putative, expressed
qXO-2-1	LOC_Os02g44340	uti_cns_0001009_LOC_Os02g44340				Both	Both	expressed protein
qXO-2-1	LOC_Os02g44360	uti_cns_0001009_LOC_Os02g44360				Both	Both	scarecrow transcription factor family protein, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-2-1	LOC_Os02g44370	uti_cns_0001009_LOC_Os02g44370				Both	Nippon	scarecrow, putative, expressed
qXO-2-1	LOC_Os02g44630	uti_cns_0001009_LOC_Os02g44630				Both	Both	aquaporin protein, putative, expressed
qXO-2-1	LOC_Os02g44654	uti_cns_0001009_LOC_Os02g44654				Both	Nippon	cytochrome P450, putative, expressed
qXO-2-1	LOC_Os02g44670	uti_cns_0001009_LOC_Os02g44670				Both	Both	harpin-induced protein 1 domain containing protein, expressed
qXO-2-1	LOC_Os02g44810	uti_cns_0001009_LOC_Os02g44810				Both	Both	tRNA pseudouridine synthase family protein, putative, expressed
qXO-2-1	LOC_Os02g44910	uti_cns_0001009_LOC_Os02g44910			Both	Both	Both	transmembrane protein, putative, expressed
qXO-2-1	LOC_Os02g45070	uti_cns_0001009_LOC_Os02g45070				Both	Both	PINHEAD, putative, expressed
qXO-2-1	LOC_Os02g45180	uti_cns_0001009_LOC_Os02g45180		IR64		Both	Both	ORM1, putative, expressed
qXO-2-2	LOC_Os02g57290	uti_cns_0001017_LOC_Os02g57290			Nippon	Both	Both	cytochrome P450, putative, expressed
qXO-2-2	LOC_Os02g57350	None	Nippon	Nippon		Nippon		expressed protein
qXO-2-2	LOC_Os02g57400	uti_cns_0001017_LOC_Os02g57400				Both	Both	2-phosphoglycerate kinase-related, putative, expressed
qXO-2-2	LOC_Os02g57420	uti_cns_0001017_LOC_Os02g57420		Both		IR64		protein kinase APK1A, chloroplast precursor, putative, expressed
qXO-2-2	LOC_Os02g57450	uti_cns_0001017_LOC_Os02g57450				Both	Both	Ser/Thr protein phosphatase family protein, putative, expressed
qXO-2-2	LOC_Os02g57480	uti_cns_0001017_LOC_Os02g57480				Both	Both	transferase family protein, putative, expressed
qXO-2-2	LOC_Os02g57490	uti_cns_0001017_LOC_Os02g57490		IR64		Both		DUF260 domain containing protein, putative, expressed
qXO-2-2	LOC_Os02g57560	uti_cns_0001017_LOC_Os02g57560			Nippon	Nippon	Nippon	tyrosine protein kinase domain containing protein, putative, expressed
qXO-2-2	LOC_Os02g57570	uti_cns_0001017_LOC_Os02g57570			Nippon	Nippon	Nippon	MATE efflux family protein, putative, expressed
qXO-2-2	LOC_Os02g57590	uti_cns_0001017_LOC_Os02g57590	Both			IR64	IR64	rRNA 2-O-methyltransferase fibrillarin 2, putative, expressed
qXO-2-2	LOC_Os02g57620	uti_cns_0001017_LOC_Os02g57620				Both	Both	Citrate transporter protein, putative, expressed
qXO-2-2	LOC_Os02g57660	uti_cns_0001017_LOC_Os02g57660				Both	Both	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed
qXO-2-2	LOC_Os02g57760	uti_cns_0001017_LOC_Os02g57760				Both	Both	O-methyltransferase, putative, expressed
qXO-2-2	LOC_Os02g58000	uti_cns_0001017_LOC_Os02g58000				Both	Both	expressed protein
qXO-2-2	LOC_Os02g58100	uti_cns_0001017_LOC_Os02g58100				Both	Both	expressed protein
qXO-2-2	LOC_Os02g58280	uti_cns_0001017_LOC_Os02g58280		Both		Nippon		expressed protein
qXO-2-2	LOC_Os02g58290	uti_cns_0001017_LOC_Os02g58290		Both		Nippon		expressed protein
qXO-2-2	LOC_Os02g58350	uti_cns_0001017_LOC_Os02g58350				Both	Both	OsRR3 type-A response regulator, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-2-2	LOC_Os02g58440	uti_cns_0001017_LOC_Os02g58440	IR64			Both		zinc finger C-x8-C-x5-C-x3-H type family protein, expressed
qXO-2-2	LOC_Os02g58600	uti_cns_0001017_LOC_Os02g58600				IR64	IR64	expressed protein
qXO-2-2	LOC_Os02g58670	uti_cns_0001017_LOC_Os02g58670		Nippon		Both		bZIP transcription factor domain containing protein, expressed
qXO-2-2	LOC_Os02g58720	uti_cns_0001017_LOC_Os02g58720				Both	Both	peroxidase precursor, putative, expressed
qXO-2-2	LOC_Os02g58740	uti_cns_0001012_LOC_Os02g58740				Both	Nippon	expressed protein
qXO-4-1	LOC_Os04g51980	uti_cns_0001005_LOC_Os04g51980				Both	Both	transferase family domain containing protein, expressed
qXO-4-1	LOC_Os04g52130	uti_cns_0001005_LOC_Os04g52130				Both	Both	coproporphyrinogen III oxidase, chloroplast precursor, putative, expressed
qXO-4-1	LOC_Os04g52164	uti_cns_0001005_LOC_Os04g52164		Both	Both	Both		transferase family protein, putative, expressed
qXO-4-1	LOC_Os04g52200	uti_cns_0001005_LOC_Os04g52200				Both	Both	RNA recognition motif containing protein, putative, expressed
qXO-4-1	LOC_Os04g52210	uti_cns_0001005_LOC_Os04g52210				Both	Both	terpene synthase, putative, expressed
qXO-4-1	LOC_Os04g52260	uti_cns_0001003_LOC_Os04g52260				Nippon	Nippon	LTPL124 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
qXO-4-1	LOC_Os04g52310	uti_cns_0001003_LOC_Os04g52310				Both	Nippon	metal cation transporter, putative, expressed
qXO-4-1	LOC_Os04g52370	uti_cns_0001003_LOC_Os04g52370				Both	Both	UTP--glucose-1-phosphate uridylyltransferase, putative, expressed
qXO-4-1	LOC_Os04g52600	uti_cns_0001003_LOC_Os04g52600				Both	Nippon	SHR5-receptor-like kinase, putative, expressed
qXO-4-1	LOC_Os04g52606	None				Nippon	Nippon	SHR5-receptor-like kinase, putative, expressed
qXO-4-1	LOC_Os04g52684	uti_cns_0001003_LOC_Os04g52684				Both	Both	expressed protein
qXO-4-1	LOC_Os04g52730	uti_cns_0001003_LOC_Os04g52730		Both		Both		NAD dependent epimerase/dehydratase family domain containing protein, expressed
qXO-4-1	LOC_Os04g52740	uti_cns_0001003_LOC_Os04g52740				Both	Nippon	expressed protein
qXO-4-1	LOC_Os04g52780	uti_cns_0001003_LOC_Os04g52780				Both	Both	leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed
qXO-4-1	LOC_Os04g52810	None			Nippon	Nippon	Nippon	no apical meristem protein, putative, expressed
qXO-4-1	LOC_Os04g52830	uti_cns_0001003_LOC_Os04g52830				Both	Both	OsFBK15 - F-box domain and kelch repeat containing protein, expressed
qXO-4-1	LOC_Os04g52850	uti_cns_0001003_LOC_Os04g52850	Both			Both		OTU-like cysteine protease family protein, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-4-1	LOC_Os04g52870	uti_cns_0001003_LOC_Os04g52870			IR64	Both	IR64	OsFBW1 - F-box domain and WD40 repeat containing protein, expressed
qXO-4-1	LOC_Os04g52880	uti_cns_0001003_LOC_Os04g52880			IR64	Nippon		expressed protein
qXO-4-1	LOC_Os04g52920	uti_cns_0001003_LOC_Os04g52920				Both	Both	remorin family protein, putative, expressed
qXO-4-1	LOC_Os04g52990	None				Nippon	Nippon	expressed protein
qXO-4-1	LOC_Os04g53000	None			Nippon	Nippon	Nippon	NBS-LRR disease resistance protein, putative, expressed
qXO-4-1	LOC_Os04g53030	uti_cns_0001003_LOC_Os04g53030				Nippon	Nippon	NBS-LRR disease resistance protein, putative, expressed
qXO-4-1	LOC_Os04g53060	uti_cns_0001003_LOC_Os04g53060				Both	Both	NBS-LRR disease resistance protein, putative, expressed
qXO-4-1	LOC_Os04g53220	uti_cns_0001003_LOC_Os04g53220				Both	IR64	signal recognition particle 14 kDa protein, putative, expressed
qXO-4-1	LOC_Os04g53240	uti_cns_0001003_LOC_Os04g53240				Both	Nippon	autophagy-related protein, putative, expressed
qXO-4-1	LOC_Os04g53260	uti_cns_0001003_LOC_Os04g53260		Nippon		Both	Both	polyphenol oxidase, putative, expressed
qXO-4-1	LOC_Os04g53300	uti_cns_0001003_LOC_Os04g53300				Both	Both	polyphenol oxidase, putative, expressed
qXO-4-1	LOC_Os04g53380	uti_cns_0001003_LOC_Os04g53380				Both	Both	expressed protein
qXO-4-1	LOC_Os04g53390	uti_cns_0001003_LOC_Os04g53390				Both	Both	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
qXO-4-1	LOC_Os04g53460	uti_cns_0001003_LOC_Os04g53460				Both	Both	AT hook motif family protein, expressed
qXO-4-1	LOC_Os04g53470	uti_cns_0001003_LOC_Os04g53470				IR64	IR64	expressed protein
qXO-4-1	LOC_Os04g53540	uti_cns_0001003_LOC_Os04g53540				Both	Both	homeobox and START domains containing protein, putative, expressed
qXO-4-1	LOC_Os04g53550	uti_cns_0001003_LOC_Os04g53550				Both	Both	ABC transporter, ATP-binding protein, putative, expressed
qXO-4-1	LOC_Os04g53580	uti_cns_0001003_LOC_Os04g53580				Both	Both	P21-Rho-binding domain containing protein, putative, expressed
qXO-4-1	LOC_Os04g53640	uti_cns_0001003_LOC_Os04g53640				Both	Both	peroxidase precursor, putative, expressed
qXO-4-1	LOC_Os04g53770	uti_cns_0001003_LOC_Os04g53770				Both	Nippon	SDA1, putative, expressed
qXO-5-1	LOC_Os05g01090	uti_cns_0000467_LOC_Os05g01090			Nippon	Both		pex14, putative, expressed
qXO-5-1	LOC_Os05g01180	uti_cns_0000467_LOC_Os05g01180				Both	Nippon	zinc knuckle family protein, expressed
qXO-5-1	LOC_Os05g01230	uti_cns_0000467_LOC_Os05g01230				Both	Both	zinc finger, C3HC4 type domain containing protein, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-5-1	LOC_Os05g01330	uti_cns_0000467_LOC_Os05g01330	Both			Both		expressed protein
qXO-5-1	LOC_Os05g01380	uti_cns_0000467_LOC_Os05g01380			Both	Both	Both	polygalacturonase inhibitor precursor, putative, expressed
qXO-5-1	LOC_Os05g01490	uti_cns_0000467_LOC_Os05g01490				Both	Both	ras-related protein, putative, expressed
qXO-5-1	LOC_Os05g01500	uti_cns_0000467_LOC_Os05g01500				Both	Both	tubulin-specific chaperone E, putative, expressed
qXO-5-1	LOC_Os05g01550	uti_cns_0000467_LOC_Os05g01550			Both	Both	Both	ZOS5-01 - C2H2 zinc finger protein, expressed
qXO-5-1	LOC_Os05g01580	uti_cns_0000467_LOC_Os05g01580			Both	Both	Nippon	integral membrane protein DUF6 containing protein, expressed
qXO-5-1	LOC_Os05g01700	uti_cns_0000467_LOC_Os05g01700				Both	Nippon	ABC transporter, ATP-binding protein, putative, expressed
qXO-5-2	LOC_Os05g02920	None				Nippon	Nippon	expressed protein
qXO-5-2	LOC_Os05g02970	uti_cns_0000467_LOC_Os05g02970				Both	Both	expressed protein
qXO-5-2	LOC_Os05g03040	uti_cns_0000467_LOC_Os05g03040		Both	Both	Both	Both	AP2 domain containing protein, expressed
qXO-5-2	LOC_Os05g03200	uti_cns_0000467_LOC_Os05g03200				Both	Nippon	expressed protein
qXO-5-2	LOC_Os05g03390	uti_cns_0000463_LOC_Os05g03390				Both	Both	expressed protein
qXO-5-2	LOC_Os05g03410	uti_cns_0000463_LOC_Os05g03410				Both	Both	expressed protein
qXO-5-2	LOC_Os05g03420	uti_cns_0000463_LOC_Os05g03420				Both	Both	expressed protein
qXO-5-2	LOC_Os05g03574	uti_cns_0000463_LOC_Os05g03574		Both		Both		expressed protein
qXO-5-2	LOC_Os05g03590	uti_cns_0000463_LOC_Os05g03590				Both	Both	expressed protein
qXO-5-2	LOC_Os05g03740	uti_cns_0000463_LOC_Os05g03740		Nippon		Both		transcription factor TF2, putative, expressed
qXO-5-2	LOC_Os05g03920	uti_cns_0000463_LOC_Os05g03920		IR64	Nippon	Nippon		TKL_IRAK_DUF26-lf.3 - DUF26 kinases have homology to DUF26 containing loci, expressed
qXO-5-2	LOC_Os05g04020	uti_cns_0000463_LOC_Os05g04020			Both	Both	IR64	plant protein of unknown function domain containing protein, expressed
qXO-5-2	LOC_Os05g04150	uti_cns_0000463_LOC_Os05g04150				Nippon	Nippon	expressed protein
qXO-5-2	LOC_Os05g04170	uti_cns_0000463_LOC_Os05g04170				Both	Both	AMP-binding enzyme, putative, expressed
qXO-5-2	LOC_Os05g04240	uti_cns_0000463_LOC_Os05g04240				Both	Both	GDSL-like lipase/acylhydrolase, putative, expressed
qXO-5-2	LOC_Os05g04310	None				Nippon	Nippon	expressed protein
qXO-5-2	LOC_Os05g04370	uti_cns_0000463_LOC_Os05g04370				Both	Both	expressed protein
qXO-5-2	LOC_Os05g04520	uti_cns_0000463_LOC_Os05g04520				Both	Both	protein kinase, putative, expressed
qXO-5-2	LOC_Os05g04584	uti_cns_0000153_LOC_Os05g04584				Both	Nippon	transferase family protein, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-5-3	LOC_Os05g35240	uti_cns_0000050_LOC_Os05g35240				Both	Both	expressed protein
qXO-5-3	LOC_Os05g35300	uti_cns_0000050_LOC_Os05g35300				Both	Both	expressed protein
qXO-5-3	LOC_Os05g35310	uti_cns_0000850_LOC_Os05g35310				Nippon	Nippon	ankyrin repeat family protein, putative, expressed
qXO-5-3	LOC_Os05g35400	uti_cns_0000850_LOC_Os05g35400				Both	Both	DnaK family protein, putative, expressed
qXO-5-3	LOC_Os05g35510	uti_cns_0000850_LOC_Os05g35510				Nippon	Nippon	expressed protein
qXO-5-3	LOC_Os05g35520	uti_cns_0000850_LOC_Os05g35520	Both			Both		deoxynucleoside kinase family, putative, expressed
qXO-5-3	LOC_Os05g35690	uti_cns_0000850_LOC_Os05g35690				Both	Both	GASR6 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed
qXO-5-3	LOC_Os05g35820	uti_cns_0000850_LOC_Os05g35820				Both	Nippon	expressed protein
qXO-5-3	LOC_Os05g35910	uti_cns_0000850_LOC_Os05g35910		Both		Both		expressed protein
qXO-5-3	LOC_Os05g35950	uti_cns_0000850_LOC_Os05g35950				Both	Both	expressed protein
qXO-5-3	LOC_Os05g36240	uti_cns_0000850_LOC_Os05g36240				Both	Both	expressed protein
qXO-5-3	LOC_Os05g36360	uti_cns_0000850_LOC_Os05g36360				Both	Both	U-box domain containing protein, expressed
qXO-5-3	LOC_Os05g36900	uti_cns_0000850_LOC_Os05g36900		Both	IR64	Both		dof zinc finger domain containing protein, putative, expressed
qXO-5-3	LOC_Os05g36920	uti_cns_0000850_LOC_Os05g36920			IR64	Both		histone deacetylase, putative, expressed
qXO-5-3	LOC_Os05g36970	uti_cns_0000850_LOC_Os05g36970				Both	Both	DUF623 domain containing protein, expressed
qXO-5-3	LOC_Os05g37130	uti_cns_0000850_LOC_Os05g37130			Both	Both	Nippon	glycosyl hydrolases family 17, putative, expressed
qXO-5-3	LOC_Os05g37170	uti_cns_0000850_LOC_Os05g37170				Nippon	Nippon	transcription factor, putative, expressed
qXO-5-3	LOC_Os05g37200	uti_cns_0000850_LOC_Os05g37200				Both	Both	solute carrier family 35 member F2, putative, expressed
qXO-5-3	LOC_Os05g37210	uti_cns_0000850_LOC_Os05g37210				Nippon	Nippon	eukaryotic protein of unknown function DUF914 domain containing protein, expressed
qXO-5-3	LOC_Os05g37340	uti_cns_0000850_LOC_Os05g37340				Both	IR64	expressed protein
qXO-5-3	LOC_Os05g37350	uti_cns_0000850_LOC_Os05g37350				Both	Both	hhH-GPD superfamily base excision DNA repair protein, expressed
qXO-5-3	LOC_Os05g37600	uti_cns_0000850_LOC_Os05g37600				Both	Both	glycerol-3-phosphate acyltransferase, putative, expressed
qXO-5-3	LOC_Os05g37830	uti_cns_0000850_LOC_Os05g37830				Both	Both	expressed protein
qXO-5-3	LOC_Os05g37840	uti_cns_0000850_LOC_Os05g37840				Both	Both	expressed protein
qXO-5-3	LOC_Os05g38140	uti_cns_0000850_LOC_Os05g38140			Nippon	Both	Both	basic helix-loop-helix DND-binding domain containing protein, expressed
qXO-5-3	LOC_Os05g38170	uti_cns_0000850_LOC_Os05g38170			Both	Both		phosphoribosyl transferase, putative, expressed
qXO-5-3	LOC_Os05g38180	uti_cns_0000850_LOC_Os05g38180			Both	Both		Yip1 domain containing protein, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-5-3	LOC_Os05g38210	uti_cns_0000850_LOC_Os05g38210				IR64	IR64	mitochondrial glycoprotein, putative, expressed
qXO-5-3	LOC_Os05g38264	uti_cns_0000850_LOC_Os05g38264			Both	Nippon	Nippon	expressed protein
qXO-5-3	LOC_Os05g38310	uti_cns_0000850_LOC_Os05g38310				Both	Nippon	ubiquitin family protein, putative, expressed
qXO-5-3	LOC_Os05g38350	uti_cns_0000850_LOC_Os05g38350			Both	Both	Both	glycerol-3-phosphate acyltransferase 8, putative, expressed
qXO-5-3	LOC_Os05g38400	uti_cns_0000850_LOC_Os05g38400				Both	Both	OsFtsH8 FtsH protease, homologue of AtFtsH3/10, expressed
qXO-5-3	LOC_Os05g38590	uti_cns_0000850_LOC_Os05g38590				Both	IR64	expressed protein
qXO-5-3	LOC_Os05g38600	uti_cns_0000850_LOC_Os05g38600	Both			Both		ZOS5-09 - C2H2 zinc finger protein, expressed
qXO-5-3	LOC_Os05g38630	uti_cns_0000850_LOC_Os05g38630				IR64	IR64	ras-related protein, putative, expressed
qXO-5-3	LOC_Os05g38660	uti_cns_0000850_LOC_Os05g38660				Both	Both	expressed protein
qXO-5-3	LOC_Os05g38680	uti_cns_0000850_LOC_Os05g38680				Both	Both	plant-specific domain TIGR01589 family protein, expressed
qXO-5-3	LOC_Os05g38730	uti_cns_0000850_LOC_Os05g38730				Both	Both	SAC3/GANP family protein, putative, expressed
qXO-5-3	LOC_Os05g38980	uti_cns_0000850_LOC_Os05g38980				Nippon	Nippon	respiratory burst oxidase, putative, expressed
qXO-5-3	LOC_Os05g38984	uti_cns_0000850_LOC_Os05g38984			IR64	Both		expressed protein
qXO-5-3	LOC_Os05g39000	uti_cns_0000850_LOC_Os05g39000				Both	IR64	KIP1, putative, expressed
qXO-5-3	LOC_Os05g39080	uti_cns_0000850_LOC_Os05g39080			Nippon	Both		protein kinase family protein, putative, expressed
qXO-5-3	LOC_Os05g39180	uti_cns_0000850_LOC_Os05g39180				Both	Nippon	expressed protein
qXO-5-3	LOC_Os05g39380	uti_cns_0000850_LOC_Os05g39380	Both			Both	Both	zinc finger, C3HC4 type domain containing protein, expressed
qXO-5-3	LOC_Os05g39530	uti_cns_0000850_LOC_Os05g39530			Nippon	Both	Both	ribonuclease P family protein, putative, expressed
qXO-5-3	LOC_Os05g39540	uti_cns_0000850_LOC_Os05g39540			Nippon	Both	Nippon	metal cation transporter, putative, expressed
qXO-5-3	LOC_Os05g39590	uti_cns_0000850_LOC_Os05g39590				Both	Both	AP2 domain containing protein, expressed
qXO-5-3	LOC_Os05g39670	uti_cns_0000850_LOC_Os05g39670				Nippon	Nippon	prenylated rab acceptor, putative, expressed
qXO-5-3	LOC_Os05g39720	uti_cns_0000850_LOC_Os05g39720				Both	Both	WRKY70, expressed
qXO-5-3	LOC_Os05g39840	uti_cns_0000850_LOC_Os05g39840			Both	Both		expressed protein
qXO-5-3	LOC_Os05g39930	uti_cns_0000850_LOC_Os05g39930				Both	Both	spotted leaf 11, putative, expressed
qXO-5-3	LOC_Os05g40070	uti_cns_0000850_LOC_Os05g40070			Both	Both		WRKY84, expressed
qXO-5-3	LOC_Os05g40080	uti_cns_0000850_LOC_Os05g40080				Both	Nippon	WRKY54, expressed
qXO-5-3	LOC_Os05g40130	None				Nippon	Nippon	expressed protein
qXO-5-3	LOC_Os05g40170	uti_cns_0000850_LOC_Os05g40170	Both			Nippon	Nippon	expressed protein

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-5-3	LOC_Os05g40180	uti_cns_0000850_LOC_Os05g40180		Both		Both	Both	serine/threonine-protein kinase stt7, chloroplast precursor, putative, expressed
qXO-5-3	LOC_Os05g40200	uti_cns_0000850_LOC_Os05g40200			Both	Both		inactive receptor kinase At2g26730 precursor, putative, expressed
qXO-5-3	LOC_Os05g40700	uti_cns_0000850_LOC_Os05g40700				Both	Both	transmembrane protein 56, putative, expressed
qXO-5-3	LOC_Os05g40710	uti_cns_0000850_LOC_Os05g40710				Both	Both	DELLA protein GAI, putative, expressed
qXO-5-3	LOC_Os05g40770	uti_cns_0000850_LOC_Os05g40770	IR64			Both		leucine-rich repeat family protein, putative, expressed
qXO-5-3	LOC_Os05g40820	uti_cns_0000850_LOC_Os05g40820				Both	Both	ribosomal protein L24, putative, expressed
qXO-5-3	LOC_Os05g40980	uti_cns_0000850_LOC_Os05g40980	IR64			Both		zinc finger, C3HC4 type domain containing protein, expressed
qXO-5-3	LOC_Os05g40990	uti_cns_0000850_LOC_Os05g40990	IR64			Both		NADH-cytochrome b5 reductase, putative, expressed
qXO-5-3	LOC_Os05g41050	uti_cns_0000184_LOC_Os05g41050			Nippon	IR64		expressed protein
qXO-5-3	LOC_Os05g41080	uti_cns_0000850_LOC_Os05g41080				Both	Both	histone H3, putative, expressed
qXO-5-3	LOC_Os05g41120	uti_cns_0000850_LOC_Os05g41120				Both	Nippon	endoplasmic reticulum-Golgi intermediate compartment protein 3, putative, expressed
qXO-5-3	LOC_Os05g41200	uti_cns_0000850_LOC_Os05g41200			Both	Both		OsCML9 - Calmodulin-related calcium sensor protein, expressed
qXO-5-3	LOC_Os05g41240	uti_cns_0000850_LOC_Os05g41240			Both	Both	Both	Myb-like DNA-binding domain containing protein, putative, expressed
qXO-5-3	LOC_Os05g41310	uti_cns_0000850_LOC_Os05g41310				Both	Both	disease resistance protein RGA2, putative, expressed
qXO-5-3	LOC_Os05g41370	uti_cns_0000850_LOC_Os05g41370	Nippon		Both			TKL_IRAK_DUF26-la.1 - DUF26 kinases have homology to DUF26 containing loci, expressed
qXO-5-3	LOC_Os05g41540	uti_cns_0000848_LOC_Os05g41540				Both	Both	bZIP transcription factor domain containing protein, expressed
qXO-5-3	LOC_Os05g41610	uti_cns_0000848_LOC_Os05g41610				Both	Both	glycosyl hydrolases family 17, putative, expressed
qBB-7-1	LOC_Os07g07440	uti_cns_0000850_LOC_Os07g07440				Both	Both	versicolorin reductase, putative, expressed
qBB-7-1	LOC_Os07g07450	uti_cns_0000850_LOC_Os07g07450				Both	Both	versicolorin reductase, putative, expressed
qBB-7-1	LOC_Os07g07530	uti_cns_0000850_LOC_Os07g07530	Both			Both		expressed protein
qBB-7-1	LOC_Os07g07560	uti_cns_0000850_LOC_Os07g07560			Both	Both	Both	CK1-CaseinKinase_1a.6 - CK1 includes the casein kinase 1 kinases, expressed
qBB-7-1	LOC_Os07g07590	uti_cns_0000850_LOC_Os07g07590				Both	IR64	expressed protein
qBB-7-1	LOC_Os07g07630	uti_cns_0000850_LOC_Os07g07630	Both			Both		expressed protein
qBB-7-1	LOC_Os07g07670	uti_cns_0000850_LOC_Os07g07670				Both	Both	expressed protein
qBB-7-1	LOC_Os07g07760	None				Nippon	Nippon	expressed protein

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qBB-7-1	LOC_Os07g07780	None				Nippon	Nippon	expressed protein
qBB-7-1	LOC_Os07g07790	uti_cns_0000850_LOC_Os07g07790				Both	Nippon	LTPL75 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
qBB-7-1	LOC_Os07g07910	uti_cns_0000850_LOC_Os07g07910		IR64		Both		potassium channel AKT1, putative, expressed
qBB-7-1	LOC_Os07g07930	uti_cns_0000850_LOC_Os07g07930				Both	Both	LTPL78 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
qBB-7-1	LOC_Os07g08040	uti_cns_0000850_LOC_Os07g08040				Both	Both	expressed protein
qBB-7-1	LOC_Os07g08050	uti_cns_0000850_LOC_Os07g08050				Both	Both	expressed protein
qBB-7-1	LOC_Os07g08120	uti_cns_0000850_LOC_Os07g08120				Both	IR64	BTBT2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with tetratricopeptide repeats, expressed
qBB-7-1	LOC_Os07g08140	uti_cns_0000850_LOC_Os07g08140				Both	Both	heat stress transcription factor, putative, expressed
qBB-7-1	LOC_Os07g08190	uti_cns_0000850_LOC_Os07g08190				Both	Both	cyclophilin, putative, expressed
qBB-7-1	LOC_Os07g08210	uti_cns_0000850_LOC_Os07g08210				Both	Both	cytidyltransferase domain containing protein, expressed
qBB-7-1	LOC_Os07g08260	uti_cns_0000850_LOC_Os07g08260				Both	Both	expressed protein
qBB-7-1	LOC_Os07g08300	None	Nippon			Nippon		major facilitator superfamily antiporter, putative, expressed
qBB-7-1	LOC_Os07g08350	uti_cns_0000030_LOC_Os07g08350				Both	Both	C4-dicarboxylate transporter/malic acid transport protein, expressed
qBB-7-1	LOC_Os07g08380	uti_cns_0000030_LOC_Os07g08380				Both	Both	expressed protein
qBB-7-1	LOC_Os07g08390	uti_cns_0000030_LOC_Os07g08390				IR64	IR64	plant-specific domain TIGR01615 family protein, expressed
qBB-7-1	LOC_Os07g08400	uti_cns_0000030_LOC_Os07g08400	Both			Both		GTP binding protein, putative, expressed
qBB-7-1	LOC_Os07g08680	uti_cns_0000030_LOC_Os07g08680			Both	Both	Both	expressed protein
qBB-7-1	LOC_Os07g08760	uti_cns_0000030_LOC_Os07g08760			Both	Both	Both	START domain containing protein, putative, expressed
qBB-7-1	LOC_Os07g08820	uti_cns_0000030_LOC_Os07g08820			Both	Nippon		C-Myc-binding protein, putative, expressed
qBB-7-1	LOC_Os07g08840	uti_cns_0000030_LOC_Os07g08840		Both		IR64		thioredoxin, putative, expressed
qBB-7-1	LOC_Os07g09000	uti_cns_0000030_LOC_Os07g09000				Both	Both	WD domain, G-beta repeat domain containing protein, expressed
qBB-7-1	LOC_Os07g09010	uti_cns_0000030_LOC_Os07g09010				Both	Both	nodulin, putative, expressed
qBB-7-1	LOC_Os07g09020	uti_cns_0000030_LOC_Os07g09020				Both	Both	argonaute, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qBB-7-1	LOC_Os07g09050	uti_cns_0000030_LOC_Os07g09050		Nippon		Nippon		exostosin family protein, putative, expressed
qBB-7-1	LOC_Os07g09060	uti_cns_0000030_LOC_Os07g09060				Both	Both	aldehyde dehydrogenase, putative, expressed
qBB-7-1	LOC_Os07g09200	uti_cns_0000030_LOC_Os07g09200				Both	Both	expressed protein
qBB-7-1	LOC_Os07g09330	uti_cns_0000030_LOC_Os07g09330				IR64	IR64	inositol-1-monophosphatase, putative, expressed
qBB-7-1	LOC_Os07g09480	uti_cns_0000030_LOC_Os07g09480		Both		Both		ATPase, putative, expressed
qBB-7-1	LOC_Os07g09500	uti_cns_0000030_LOC_Os07g09500				Both	Both	expressed protein
qBB-7-1	LOC_Os07g09580	uti_cns_0000030_LOC_Os07g09580				Both	Both	aminoacyl-tRNA synthetase, putative, expressed
qBB-7-1	LOC_Os07g09590	uti_cns_0000030_LOC_Os07g09590				Both	Both	bHLH transcription factor, putative, expressed
qBB-7-1	LOC_Os07g09675	uti_cns_0000030_LOC_Os07g09675			Both	Both	Both	expressed protein
qBB-7-1	LOC_Os07g09830	None				Nippon	Nippon	no apical meristem protein, expressed
qBB-7-1	LOC_Os07g09840	None				Nippon	Nippon	expressed protein
qBB-7-1	LOC_Os07g09880	uti_cns_0000030_LOC_Os07g09880				Both	Both	expressed protein
qBB-7-1	LOC_Os07g09890	uti_cns_0000030_LOC_Os07g09890				Both	Both	hexokinase, putative, expressed
qBB-7-1	LOC_Os07g09900	None				Nippon	Nippon	disease resistance protein RPM1, putative, expressed
qBB-7-1	LOC_Os07g10110	uti_cns_0000030_LOC_Os07g10110	Both			Both	Both	expressed protein
qBB-7-1	LOC_Os07g10120	None	Nippon			Nippon		expressed protein
qBB-7-1	LOC_Os07g10160	uti_cns_0000030_LOC_Os07g10160				Both	Both	glucosyltransferase, putative, expressed
qBB-7-1	LOC_Os07g10240	uti_cns_0000030_LOC_Os07g10240				Nippon	Nippon	anthocyanidin 3-O-glucosyltransferase, putative, expressed
qBB-7-1	LOC_Os07g10520	uti_cns_0000030_LOC_Os07g10520				IR64	IR64	nucleotide binding protein, putative, expressed
qBB-7-1	LOC_Os07g10560	uti_cns_0000030_LOC_Os07g10560				Both	Both	expressed protein
qBB-7-1	LOC_Os07g10680	uti_cns_0000030_LOC_Os07g10680		Both		Both		polygalacturonase, putative, expressed
qBB-7-1	LOC_Os07g10700	uti_cns_0000030_LOC_Os07g10700		Both		Both	Both	polygalacturonase, putative, expressed
qBB-7-1	LOC_Os07g10710	uti_cns_0000030_LOC_Os07g10710				Both	IR64	OsFBX223 - F-box domain containing protein, expressed
qBB-7-1	LOC_Os07g10780	uti_cns_0000030_LOC_Os07g10780			Nippon	Nippon	Nippon	remorin, putative, expressed
qBB-7-1	LOC_Os07g10830	uti_cns_0000030_LOC_Os07g10830				Both	Both	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor, putative, expressed
qBB-7-1	LOC_Os07g10840	uti_cns_0000030_LOC_Os07g10840				Both	Both	uncharacterized glycosyltransferase, putative, expressed
qBB-7-1	LOC_Os07g10860	uti_cns_0000030_LOC_Os07g10860				Both	Both	expressed protein
qBB-7-1	LOC_Os07g10880	uti_cns_0000030_LOC_Os07g10880				IR64	IR64	expressed protein

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qBB-7-1	LOC_Os07g10910	uti_cns_0000030_LOC_Os07g10910	IR64			Both	Both	ATEXO70F1, putative, expressed
qBB-7-1	LOC_Os07g10920	uti_cns_0000030_LOC_Os07g10920				Both		expressed protein
qBB-7-1	LOC_Os07g10960	uti_cns_0000030_LOC_Os07g10960				IR64	IR64	expressed protein
qBB-7-1	LOC_Os07g10970	uti_cns_0000030_LOC_Os07g10970				Both	IR64	leucine zipper protein-like, putative, expressed
qBB-7-1	LOC_Os07g11010	uti_cns_0000030_LOC_Os07g11010				Both	Both	protein Kinase-associated protein phosphatase, putative, expressed
qBB-7-1	LOC_Os07g11020	uti_cns_0000030_LOC_Os07g11020	Both		Both	Both		rc - bHLH transcription factor regulating proanthocyanidin production in seeds, expressed
qBB-7-1	LOC_Os07g11060	uti_cns_0000030_LOC_Os07g11060						expressed protein
qBB-7-1	LOC_Os07g11070	uti_cns_0000030_LOC_Os07g11070						DUF630/DUF632 domains containing protein, putative, expressed
qBB-7-1	LOC_Os07g11110	uti_cns_0000030_LOC_Os07g11110		Both		Both	Both	NAD dependent epimerase/dehydratase family protein, putative, expressed
qBB-7-1	LOC_Os07g11120	uti_cns_0000030_LOC_Os07g11120						hydrolase, NUDIX family, domain containing protein, expressed
qXO-7-2	LOC_Os07g46070	None	Nippon			Nippon	Nippon	expressed protein
qXO-7-2	LOC_Os07g46080	None				Nippon	Nippon	expressed protein
qXO-7-2	LOC_Os07g46170	uti_cns_0000030_LOC_Os07g46170				IR64	IR64	OsRhmbd13 - Putative Rhomboid homologue, expressed
qXO-7-2	LOC_Os07g46180	uti_cns_0000030_LOC_Os07g46180	IR64			IR64	IR64	PWWP domain containing protein, expressed
qXO-7-2	LOC_Os07g46315	uti_cns_0000030_LOC_Os07g46315				IR64	IR64	expressed protein
qXO-7-2	LOC_Os07g46350	uti_cns_0000030_LOC_Os07g46350				Both		OsSCP40 - Putative Serine Carboxypeptidase homologue, expressed
qXO-7-2	LOC_Os07g46420	uti_cns_0000030_LOC_Os07g46420				IR64	IR64	expressed protein
qXO-7-2	LOC_Os07g46450	uti_cns_0000030_LOC_Os07g46450			Both	Both	Nippon	pleckstrin homology domain-containing protein, putative, expressed
qXO-7-2	LOC_Os07g46460	uti_cns_0000030_LOC_Os07g46460				Both		ferredoxin-dependent glutamate synthase, chloroplast precursor, putative, expressed
qXO-7-2	LOC_Os07g46490	uti_cns_0000030_LOC_Os07g46490				IR64	IR64	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed
qXO-7-2	LOC_Os07g46510	uti_cns_0000030_LOC_Os07g46510	Both			Both	Both	expressed protein
qXO-7-2	LOC_Os07g46610	uti_cns_0000030_LOC_Os07g46610				Both	IR64	cis-zeatin O-glucosyltransferase, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-7-2	LOC_Os07g46620	uti_cns_0000030_LOC_Os07g46620				Both	IR64	WD repeat-containing protein 55, putative, expressed
qXO-7-2	LOC_Os07g46700	uti_cns_0000030_LOC_Os07g46700				Both	Both	zinc finger, RING-type, putative, expressed
qXO-7-2	LOC_Os07g46770	uti_cns_0000030_LOC_Os07g46770				Both	Nippon	expressed protein
qXO-7-2	LOC_Os07g46780	uti_cns_0000030_LOC_Os07g46780				Both	Nippon	tyrosine-specific transport protein, putative, expressed
qXO-7-2	LOC_Os07g46790	uti_cns_0000030_LOC_Os07g46790	IR64	Both	Both	IR64		4-alpha-glucanotransferase, putative, expressed
qXO-7-2	LOC_Os07g46840	uti_cns_0000030_LOC_Os07g46840				IR64	IR64	oxidoreductase, short chain dehydrogenase/reductase family domain containing protein, expressed
qXO-7-2	LOC_Os07g46846	uti_cns_0000030_LOC_Os07g46846		Nippon		Both	Nippon	sex determination protein tasselseed-2, putative, expressed
qXO-7-2	LOC_Os07g46930	uti_cns_0000030_LOC_Os07g46930				IR64	IR64	sex determination protein tasselseed-2, putative, expressed
qXO-7-2	LOC_Os07g46950	uti_cns_0000030_LOC_Os07g46950				Both	Both	ligA, putative, expressed
qXO-7-2	LOC_Os07g47000	uti_cns_0000030_LOC_Os07g47000				Both	IR64	expressed protein
qXO-7-2	LOC_Os07g47040	uti_cns_0000030_LOC_Os07g47040		Both		Both	Both	expressed protein
qXO-7-2	LOC_Os07g47120	None				Nippon	Nippon	beta-amylase, putative, expressed
qXO-7-2	LOC_Os07g47130	None				Nippon	Nippon	OCL5 protein, putative, expressed
qXO-7-2	LOC_Os07g47280	uti_cns_0000030_LOC_Os07g47280				Both	Both	DNA polymerase zeta catalytic subunit, putative, expressed
qXO-7-2	LOC_Os07g47310	uti_cns_0000030_LOC_Os07g47310				Both	Both	expressed protein
qXO-7-2	LOC_Os07g47320	uti_cns_0000030_LOC_Os07g47320				Both	Both	expressed protein
qXO-7-2	LOC_Os07g47520	uti_cns_0000030_LOC_Os07g47520				Both	Both	expressed protein
qXO-7-2	LOC_Os07g47590	uti_cns_0000030_LOC_Os07g47590				Both	Both	expressed protein
qBLS-8-1	LOC_Os08g40520	uti_cns_0000970_LOC_Os08g40520				Both	IR64	expressed protein
qBLS-8-1	LOC_Os08g40680	uti_cns_0000970_LOC_Os08g40680				Both	Both	glycosyl hydrolase, putative, expressed
qBLS-8-1	LOC_Os08g40690	uti_cns_0000970_LOC_Os08g40690				Both	IR64	glycosyl hydrolase, putative, expressed
qBLS-8-1	LOC_Os08g40740	uti_cns_0000970_LOC_Os08g40740				Both	Both	glycosyl hydrolase, putative, expressed
qBLS-8-1	LOC_Os08g40930	uti_cns_0000970_LOC_Os08g40930				Both	Both	Alpha amylase, catalytic domain containing protein, expressed
qBLS-8-1	LOC_Os08g41120	uti_cns_0000970_LOC_Os08g41120				Both	Both	MBTB29 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-10-1	LOC_Os10g37210	uti_cns_0000851_LOC_Os10g37210			Both	Both		FAD dependent oxidoreductase domain containing protein, expressed
qXO-10-1	LOC_Os10g37340	uti_cns_0000851_LOC_Os10g37340				Both	Both	cystathionine gamma-synthase, putative, expressed
qXO-10-1	LOC_Os10g37450	uti_cns_0000851_LOC_Os10g37450				Both	Both	expressed protein
qXO-10-1	LOC_Os10g37510	uti_cns_0000851_LOC_Os10g37510				Both	Both	expressed protein
qXO-10-1	LOC_Os10g37520	uti_cns_0000851_LOC_Os10g37520				Both	Both	major facilitator superfamily domain-containing protein 5, putative, expressed
qXO-10-1	LOC_Os10g37600	uti_cns_0000851_LOC_Os10g37600		IR64		IR64		expressed protein
qXO-10-1	LOC_Os10g37630	uti_cns_0000851_LOC_Os10g37630				Both	Both	UBX domain-containing protein, putative, expressed
qXO-10-1	LOC_Os10g37640	uti_cns_0000851_LOC_Os10g37640				Both	Both	HIT zinc finger domain containing protein, expressed
qXO-10-1	LOC_Os10g37650	uti_cns_0000851_LOC_Os10g37650				Both	Both	impaired sucrose induction 1, putative, expressed
qXO-10-1	LOC_Os10g37660	uti_cns_0000851_LOC_Os10g37660				Both	Both	trehalase precursor, putative, expressed
qXO-10-1	LOC_Os10g37700	uti_cns_0000851_LOC_Os10g37700				Both	Both	hydrolase protein, putative, expressed
qXO-10-1	LOC_Os10g38070	uti_cns_0000851_LOC_Os10g38070				IR64	IR64	expressed protein
qXO-10-1	LOC_Os10g38080	uti_cns_0000851_LOC_Os10g38080				Both	Both	OsSub61 - Putative Subtilisin homologue, expressed
qXO-10-1	LOC_Os10g38110	None				Nippon	Nippon	cytochrome P450, putative, expressed
qXO-10-1	LOC_Os10g38140	uti_cns_0000851_LOC_Os10g38140				Both	IR64	glutathione S-transferase, putative, expressed
qXO-10-1	LOC_Os10g38150	None				Nippon	Nippon	glutathione S-transferase, N-terminal domain containing protein, expressed
qXO-10-1	LOC_Os10g38160	None				Nippon	Nippon	glutathione S-transferase, putative, expressed
qXO-10-1	LOC_Os10g38170	None				Nippon	Nippon	expressed protein
qXO-10-1	LOC_Os10g38189	uti_cns_0000851_LOC_Os10g38189				Nippon	Nippon	glutathione S-transferase, putative, expressed
qXO-10-1	LOC_Os10g38314	None				Nippon	Nippon	glutathione S-transferase, N-terminal domain containing protein, expressed
qXO-10-1	LOC_Os10g38360	uti_cns_0000851_LOC_Os10g38360				Both	Both	glutathione S-transferase, putative, expressed
qXO-10-1	LOC_Os10g38640	uti_cns_0000851_LOC_Os10g38640				Both	IR64	glutathione S-transferase, putative, expressed
qXO-10-1	LOC_Os10g38800	uti_cns_0000851_LOC_Os10g38800				Both	IR64	leucine-rich repeat transmembrane protein kinase, putative, expressed
qXO-10-1	LOC_Os10g38820	uti_cns_0000851_LOC_Os10g38820		Both		Both	Both	bZIP family transcription factor, putative, expressed
qXO-10-1	LOC_Os10g38860	uti_cns_0000851_LOC_Os10g38860			Nippon	Both	Both	hydrolase, alpha/beta fold family domain containing protein, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-10-1	LOC_Os10g38930	uti_cns_0000851_LOC_Os10g38930				Both	Both	shikimate/quinate 5-dehydrogenase, putative, expressed
qXO-10-1	LOC_Os10g39010	uti_cns_0000851_LOC_Os10g39010				Nippon	Nippon	TKL_IRAK_CrRLK1L-1.16 - The CrRLK1L-1 subfamily has homology to the CrRLK1L homolog, expressed
qXO-10-1	LOC_Os10g39020	uti_cns_0000851_LOC_Os10g39020			Nippon	Both	Both	fringe-related protein, putative, expressed
qXO-10-1	LOC_Os10g39060	uti_cns_0000851_LOC_Os10g39060	IR64			Both		expressed protein
qXO-10-1	LOC_Os10g39320	uti_cns_0000851_LOC_Os10g39320			Nippon	Both		aspartic proteinase nepenthesin precursor, putative, expressed
qBB-11-1	LOC_Os11g11980	uti_cns_0001072_LOC_Os11g11980				Both	Both	expressed protein
qBB-11-1	LOC_Os11g12000	None				Nippon	Nippon	NBS-LRR disease resistance protein, putative, expressed
qBB-11-1	LOC_Os11g12050	None				Nippon	Nippon	NBS-LRR type disease resistance protein, putative, expressed
qBB-11-1	LOC_Os11g12320	uti_cns_0001072_LOC_Os11g12320				Both	IR64	disease resistance protein RPM1, putative, expressed
qBB-11-1	LOC_Os11g12330	uti_cns_0001072_LOC_Os11g12330				Both	Both	disease resistance protein RPM1, putative, expressed
qBB-11-1	LOC_Os11g12420	uti_cns_0001072_LOC_Os11g12420				Both	Both	serpin domain containing protein, putative, expressed
qBB-11-1	LOC_Os11g12460	uti_cns_0001072_LOC_Os11g12460				Both	IR64	serpin domain containing protein, putative, expressed
qBB-11-1	LOC_Os11g12480	uti_cns_0001072_LOC_Os11g12480				Both	Both	OsFBL54 - F-box domain and LRR containing protein, expressed
qBB-11-1	LOC_Os11g13390	uti_cns_0001072_LOC_Os11g13390			Both	Both	Both	expressed protein
qBB-11-1	LOC_Os11g13720	uti_cns_0001072_LOC_Os11g13720				Both	Both	expressed protein
qBB-11-1	LOC_Os11g13770	uti_cns_0001072_LOC_Os11g13770				Both	Both	expressed protein
qBB-11-1	LOC_Os11g13800	uti_cns_0001072_LOC_Os11g13800				IR64	IR64	expressed protein
qBB-11-1	LOC_Os11g13810	uti_cns_0001072_LOC_Os11g13810				Both	Both	non-lysosomal glucosylceramidase, putative, expressed
qXO-11-2	LOC_Os11g43750	uti_cns_0000957_LOC_Os11g43750		Both		Both	Both	polygalacturonase, putative, expressed
qXO-11-2	LOC_Os11g43860	uti_cns_0000957_LOC_Os11g43860				Both	IR64	sodium/calcium exchanger protein, putative, expressed
qXO-11-2	LOC_Os11g43950	uti_cns_0000957_LOC_Os11g43950				Both	IR64	dnaJ domain containing protein, expressed
qXO-11-2	LOC_Os11g44230	None				Nippon	Nippon	expressed protein
qXO-11-2	LOC_Os11g44300	uti_cns_0000957_LOC_Os11g44300	IR64			Both		expressed protein
qXO-11-2	LOC_Os11g44415	None				Nippon	Nippon	expressed protein
qXO-11-2	LOC_Os11g44430	None				Nippon	Nippon	protein kinase, putative, expressed
qXO-11-2	LOC_Os11g44570	uti_cns_0000957_LOC_Os11g44570				Both	Both	expressed protein
qXO-11-2	LOC_Os11g44660	uti_cns_0000957_LOC_Os11g44660				Both	Both	protein kinase, putative, expressed
qXO-11-2	LOC_Os11g44680	None				Nippon	Nippon	calmodulin binding protein, putative, expressed

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation	
qXO-11-2	LOC_Os11g44800	uti_cns_0000957_LOC_Os11g44800	Nippon		IR64	Both	Nippon	expressed protein	
qXO-11-2	LOC_Os11g45270	uti_cns_0000957_LOC_Os11g45270				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g45280	uti_cns_0000957_LOC_Os11g45280						protein kinase family protein, putative, expressed	
qXO-11-2	LOC_Os11g45320	None				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g45330	None						disease resistance protein RPM1, putative, expressed	
qXO-11-2	LOC_Os11g45570	None				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g45780	uti_cns_0000957_LOC_Os11g45780				Both	Nippon	RGH2B, putative, expressed	
qXO-11-2	LOC_Os11g45840	uti_cns_0000957_LOC_Os11g45840				Both	Both	expressed protein	
qXO-11-2	LOC_Os11g45940	uti_cns_0000957_LOC_Os11g45940				Nippon	Both	Nippon	expressed protein
qXO-11-2	LOC_Os11g45970	None				Nippon	Nippon	NBS-LRR disease resistance protein, putative, expressed	
qXO-11-2	LOC_Os11g45980	uti_cns_0000957_LOC_Os11g45980	Nippon	Nippon	NBS-LRR type disease resistance protein, putative, expressed				
qXO-11-2	LOC_Os11g46080	None	Nippon		IR64	Nippon	Nippon	NB-ARC domain containing protein, expressed	
qXO-11-2	LOC_Os11g46150	None				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g46850	uti_cns_0000957_LOC_Os11g46850				Both	IR64	wall-associated kinase, putative, expressed	
qXO-11-2	LOC_Os11g46980	uti_cns_0000957_LOC_Os11g46980				Both	Both	receptor-like protein kinase 2 precursor, putative, expressed	
qXO-11-2	LOC_Os11g47110	None				Nippon	Nippon	OsWAK121 - OsWAK receptor-like protein kinase, expressed	
qXO-11-2	LOC_Os11g47140	None						OsWAK123 - OsWAK receptor-like protein kinase, expressed	
qXO-11-2	LOC_Os11g47160	uti_cns_0000957_LOC_Os11g47160				Both	Both	receptor kinase 1, putative, expressed	
qXO-11-2	LOC_Os11g47370	None				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g47453	None				Nippon	Nippon	expressed protein	
qXO-11-2	LOC_Os11g47460	uti_cns_0000957_LOC_Os11g47460				IR64	IR64	MYB family transcription factor, putative, expressed	
qXO-11-2	LOC_Os11g47500	uti_cns_0000957_LOC_Os11g47500	Nippon	Nippon	glycosyl hydrolase, putative, expressed				
qXO-11-2	LOC_Os11g47550	uti_cns_0000957_LOC_Os11g47550	IR64		IR64	glycosyl hydrolase, putative, expressed			
qXO-11-2	LOC_Os11g47580	uti_cns_0000957_LOC_Os11g47580		Both	Both	glycosyl hydrolase, putative, expressed			
qXO-11-2	LOC_Os11g47600	uti_cns_0000957_LOC_Os11g47600		Both	Both	glycosyl hydrolase, putative, expressed			
qXO-11-2	LOC_Os11g47630	uti_cns_0000957_LOC_Os11g47630		Both	Both	ZOS11-10 - C2H2 zinc finger protein, expressed			
qXO-11-2	LOC_Os11g47840	uti_cns_0000957_LOC_Os11g47840		IR64	IR64	OsRhmbd18 - Putative Rhomboid homologue, expressed			
qXO-11-2	LOC_Os11g47860	uti_cns_0000957_LOC_Os11g47860		Both	Both	expressed protein			
qXO-11-2	LOC_Os11g47920	uti_cns_0000957_LOC_Os11g47920		Both	Both	SCARECROW, putative, expressed			

Continuation Table 3.3.

QTL	Nipponbare locus	IR64 locus	CRM1	CRM2	CRM3	CRM4	CRM5	Annotation
qXO-11-2	LOC_Os11g47930	uti_cns_0000957_LOC_Os11g47930				Both	Both	alpha-hemolysin, putative, expressed
qXO-11-2	LOC_Os11g47944	uti_cns_0001072_LOC_Os11g47944			Nippon	Nippon	Nippon	thaumatin, putative, expressed
qXO-12-1	LOC_Os12g30320	uti_cns_0000955_LOC_Os12g30320			Both	IR64	IR64	expressed protein

Table 3.4. *X. oryzae* strains used to screen the putative TAL targets. African strains are shaded.

Pathovar	Strain	Origin	Country	No. TAL
<i>Xoc</i>	BAI5	African	Burkina Faso	22
<i>Xoc</i>	BAI11	African	Burkina Faso	24
<i>Xoc</i>	MAI10	African	Mali	22
<i>Xoc</i>	B8-12	Asian	China	28
<i>Xoc</i>	BLS256	Asian	Philippines	28
<i>Xoc</i>	BLS279	Asian	Philippines	26
<i>Xoc</i>	BLS303	Asian	Philippines	27
<i>Xoc</i>	BXORI	Asian	India	27
<i>Xoc</i>	CFBP2286	Asian	Malaysia	28
<i>Xoc</i>	L8	Asian	China	29
<i>Xoc</i>	RS105	Asian	China	24
<i>Xoo</i>	BAI3	African	Burkina Faso	9
<i>Xoo</i>	CFBP1947	African	Cameroon	9
<i>Xoo</i>	MAI1	African	Mali	9
<i>Xoo</i>	MAI68	African	Mali	9
<i>Xoo</i>	MAI73	African	Mali	9
<i>Xoo</i>	MAI95	African	Mali	9
<i>Xoo</i>	MAI99	African	Mali	9
<i>Xoo</i>	MAI106	African	Mali	9
<i>Xoo</i>	MAI129	African	Mali	9
<i>Xoo</i>	MAI134	African	Mali	9
<i>Xoo</i>	MAI145	African	Mali	9
<i>Xoo</i>	KACC10331	Asian	Korea	13
<i>Xoo</i>	MAFF311018	Asian	Japan	17
<i>Xoo</i>	PXO71	Asian	Philippines	19
<i>Xoo</i>	PXO83	Asian	Philippines	18
<i>Xoo</i>	PXO86	Asian	Philippines	18
<i>Xoo</i>	PXO99 ^A	Asian	Philippines	19
<i>Xoo</i>	PXO145	Asian	Philippines	17
<i>Xoo</i>	PXO211	Asian	Philippines	17
<i>Xoo</i>	PXO236	Asian	Philippines	16
<i>Xoo</i>	PXO282	Asian	Philippines	17
<i>Xoo</i>	PXO524	Asian	Philippines	17
<i>Xoo</i>	PXO563	Asian	Philippines	18
<i>Xoo</i>	PXO602	Asian	Philippines	19
<i>Xcl</i>	BAI23	African	Burkina Faso	13
<i>Xcl</i>	NCPP4346	Asian	China	12
Total No. TAL				634

Table 3.5. Summary of loci within selected QTL containing SNPs significantly associated with BLS and BB resistance. Stars in significance correspondence panel indicate level of significance of GWAS markers as follows: (*) P -value < 0.001 and q -value > 0.05; (***) P -value < 0.0001 and q -value < 0.05 (Bossa-Castro et al., 2018). Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes.

QTL	No. Loci with significant SNPs	Significance correspondence
qXO-1-1	none	
qXO-2-1	28	* / ***
qXO-2-2	1	*
qXO-4-1	25	* / ***
qXO-5-1	10	* / ***
qXO-5-2	4	* / ***
qXO-5-3	intergenic	
qBB-7-1	1	* / ***
qXO-7-2	6	*
qBLS-8-1	none	
qXO-10-1	1	*
qBB-11-1	3	* / ***
qXO-11-2	25	* / ***
qXO-12-1	none	
Total	104	

Table 3.6. Loci within selected QTL containing SNPs significantly associated with BLS and BB resistance. Stars in significance correspondence panel indicate level of significance of GWAS markers as follows: (*) P -value < 0.001 and q -value > 0.05; (**) P -value < 0.001 and q -value < 0.05; (***) P -value < 0.0001 and q -value < 0.05 (Bossa-Castro et al., 2018).

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-2-1	<i>Xoc</i>	1	S2_23819009	***	LOC_Os02g39470	1	Intron		cyclin, N-terminal domain containing protein, expressed
qXO-2-1	<i>Xoc</i>	1	S2_23826988	*	LOC_Os02g39480	2	Promoter		protein phosphatase 2C, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_23827020	*			Promoter		
qXO-2-1	<i>Xoc</i>	1	S2_23874924	*	LOC_Os02g39550	1	Promoter		calcium-binding mitochondrial protein anon-60Da, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24006214	***	LOC_Os02g39750	1	Intron		inorganic phosphate transporter, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24135986	*	LOC_Os02g39910	1	Exon	Non synonymous variant	B4-BTB1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with B4 subfamily conserved sequence, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24273471	*	LOC_Os02g40090	1	Intron		transporter-related, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24278919	*	LOC_Os02g40100	1	Exon	Synonymous variant	plant protein of unknown function DUF869 domain containing protein, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24405470	*	LOC_Os02g40320	1	Intron		PINHEAD, putative, expressed
qXO-2-1	<i>Xoc</i>	2	S2_24527947	*	LOC_Os02g40454	1	3' UTR		serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24575274	*	LOC_Os02g40514	1	5' UTR		h/ACA ribonucleoprotein complex subunit 3, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24688545	*	LOC_Os02g40720	1	Promoter		expressed protein
qXO-2-1	<i>Xoc</i>	2	S2_24691050	*	LOC_Os02g40730	2	Exon	Synonymous variant	ammonium transporter protein, putative, expressed
qXO-2-1	<i>Xoc</i>	2	S2_24692377	*			Exon	Non synonymous variant	
qXO-2-1	<i>Xoc</i>	1	S2_24754613	*	LOC_Os02g40840	1	5' UTR		alcohol oxidase, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24786166	*	LOC_Os02g40900	2	Exon	Non synonymous variant	RNA recognition motif containing protein, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_24786718	*			Promoter		
qXO-2-1	<i>Xoc</i>	1	S2_24874086	*	LOC_Os02g41500	1	Exon	Synonymous variant	OsWAK13 - OsWAK receptor-like protein kinase, expressed

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-2-1	<i>Xoc</i>	1	S2_25075755	***	LOC_Os02g41720	1	Exon	Stop gained	transposon protein, putative, unclassified, expressed
qXO-2-1	<i>Xoc</i>	1	S2_25400243	*	LOC_Os02g42220	1	Exon	Synonymous variant	transposon protein, putative, unclassified, expressed
qXO-2-1	<i>Xoc</i>	1	S2_25596670	*	LOC_Os02g42585	1	Exon	Synonymous variant	AP2 domain containing protein, expressed
qXO-2-1	<i>Xoc</i>	2	S2_25618890	*	LOC_Os02g42590	1	Promoter		WD-40 repeat family protein, putative, expressed
qXO-2-1	<i>Xoc</i>	2	S2_25639335	*** / *	LOC_Os02g42620	3	Exon	Synonymous variant	protein kinase, putative, expressed
qXO-2-1	<i>Xoc</i>	2	S2_25639338	*** / *			Exon	Synonymous variant	
qXO-2-1	<i>Xoc</i>	2	S2_25639568	*** / *			Exon	Non synonymous variant	
qXO-2-1	<i>Xoc</i>	1	S2_25654974	*	LOC_Os02g42650	1	Intron		expansin precursor, putative, expressed
qXO-2-1	<i>Xoc</i>	1	S2_25672672	*	LOC_Os02g42690	1	Exon	Synonymous variant	zinc finger, C3HC4 type domain containing protein, expressed
qXO-2-1	<i>Xoc</i>	3	S2_25803692	*** / *	LOC_Os02g42900	1	Exon	Synonymous variant	expressed protein
qXO-2-1	<i>Xoc</i>	1	S2_25885474	*	LOC_Os02g43000	1	Exon	Synonymous variant	cysteine-rich repeat secretory protein 15 precursor, putative, expressed
qXO-2-1	<i>Xoc</i>	4	S2_26126554	*	LOC_Os02g43314	1	Exon	Synonymous variant	expressed protein
qXO-2-1	<i>Xoc</i>	1	S2_26329353	*	LOC_Os02g43630	1	Exon	Non synonymous variant	hypothetical protein
qXO-2-1	<i>Xoc</i>	1	S2_26349262	*	LOC_Os02g43670	1	3' UTR		transferase family protein, putative, expressed
qXO-2-1	both	2	S2_27203917	*	LOC_Os02g44900	2	Promoter		expressed protein
qXO-2-1	<i>Xoc</i>	1	S2_27204005	*			Promoter		
qXO-2-2	<i>Xoo</i>	1	S2_35216593	*	LOC_Os02g57460	2	5' UTR		RING-H2 finger protein ATL5G, putative, expressed
qXO-2-2	<i>Xoo</i>	1	S2_35217191	*			Exon	Synonymous variant	
qXO-4-1	<i>Xoc</i>	1	S4_31263800	***	LOC_Os04g52590	7	Exon	Non synonymous variant	protein kinase domain containing
qXO-4-1	<i>Xoc</i>	1	S4_31263806	***			Exon	Non synonymous variant	protein, expressed
qXO-4-1	<i>Xoc</i>	1	S4_31263820	***			Exon	Synonymous variant	
qXO-4-1	<i>Xoc</i>	1	S4_31263829	***			Exon	Synonymous variant	
qXO-4-1	<i>Xoc</i>	1	S4_31264880	***			Exon	Non synonymous variant	
qXO-4-1	<i>Xoc</i>	1	S4_31264887	***			Exon	Synonymous variant	
qXO-4-1	<i>Xoc</i>	1	S4_31264905	***			Exon	Synonymous variant	

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-4-1	<i>Xoc</i>	1	S4_31316473	***	LOC_Os04g52630	1	Promoter		leucine-rich repeat-containing protein kinase family protein, putative, expressed
qXO-4-1	both	2	S4_31420093	***/**	LOC_Os04g52770	1	3' UTR		helix-loop-helix DNA-binding domain containing protein, expressed
qXO-4-1	<i>Xoc</i>	2	S4_31498999	*** / *	LOC_Os04g52890	1	Intron		ATBAG1, putative, expressed
qXO-4-1	both	5	S4_31531412	*** / *	LOC_Os04g52940	1	Promoter		SIT4 phosphatase-associated protein domain containing protein, expressed
qXO-4-1	<i>Xoc</i>	2	S4_31553238	*	LOC_Os04g52970	2	Exon	Synonymous variant	NBS-LRR disease resistance protein, putative, expressed
qXO-4-1	<i>Xoc</i>	2	S4_31553264	*			Exon	Non synonymous variant	expressed protein
qXO-4-1	<i>Xoc</i>	2	S4_31559540	*	LOC_Os04g52980	3	Promoter		
qXO-4-1	<i>Xoc</i>	2	S4_31559557	*			Promoter		
qXO-4-1	<i>Xoc</i>	2	S4_31559582	*			Promoter		
qXO-4-1	both	2	S4_31669472	***	LOC_Os04g53195	1	3' UTR		expressed protein
qXO-4-1	both	2	S4_31670015	***	LOC_Os04g53190	1	Exon	Non synonymous variant	CPuORF12 - conserved peptide uORF-containing transcript, expressed
qXO-4-1	both	14	S4_31716597	*** / *	LOC_Os04g53240	1	Exon	Synonymous variant	autophagy-related protein, putative, expressed
qXO-4-1	<i>Xoc</i>	1	S4_31721763	*	LOC_Os04g53250	1	Exon	Synonymous variant	polyphenol oxidase protein, putative, expressed
qXO-4-1	both	14	S4_31728040	*** / *	LOC_Os04g53260	1	Exon	Non synonymous variant	polyphenol oxidase, putative, expressed
qXO-4-1	both	14	S4_31751408	*** / *	LOC_Os04g53300	1	Exon	Synonymous variant	polyphenol oxidase, putative, expressed
qXO-4-1	both	13	S4_31778051	*** / *	LOC_Os04g53360	1	Exon	Non synonymous variant	expressed protein
qXO-4-1	<i>Xoc</i>	1	S4_31786637	*	LOC_Os04g53370	2	5' UTR		acyltransferase, putative, expressed
qXO-4-1	both	5	S4_31787320	*** / *			Exon	Non synonymous variant	
qXO-4-1	both	2	S4_31800256	***/**	LOC_Os04g53380	2	Exon	Non synonymous variant	expressed protein
qXO-4-1	both	13	S4_31801219	*** / *			Promoter		
qXO-4-1	both	7	S4_31803015	*** / *	LOC_Os04g53390	3	Exon	Non synonymous variant	MrBTB2 - Bric-a-Brac, Tramtrack, Broad
qXO-4-1	both	14	S4_31803018	*** / *			Exon	Non synonymous variant	Complex BTB domain with Meprin and
qXO-4-1	both	14	S4_31803029	*** / *			Exon	Non synonymous variant	TRAF Homology MATH-related domain,
qXO-4-1	<i>Xoc</i>	2	S4_31812050	*** / *	LOC_Os04g53410	1	Exon	Synonymous variant	MBTB7 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain, expressed

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-4-1	both	15	S4_31819592	*** / *	LOC_Os04g53440	1	Exon	Synonymous variant	RNA recognition motif containing protein, putative, expressed
qXO-4-1	both	12	S4_31956274	*** / *	LOC_Os04g53600	1	Exon	Synonymous variant	expressed protein
qXO-4-1	both	15	S4_31962475	*** / *	LOC_Os04g53612	1	Promoter		APO, putative, expressed
qXO-4-1	both	15	S4_31981005	*** / *	LOC_Os04g53660	1	5' UTR		transposon protein, putative, unclassified, expressed
qXO-4-1	<i>Xoc</i>	1	S4_31992079	*	LOC_Os04g53670	1	Intron		expressed protein
qXO-4-1	<i>Xoo</i>	1	S4_32007187	*	LOC_Os04g53700	1	Exon	Synonymous variant	zinc finger protein, putative, expressed
qXO-4-1	<i>Xoo</i>	1	S4_32134600	*	LOC_Os04g53920	1	Exon	Non synonymous variant	leucoanthocyanidin reductase, putative, expressed
qXO-5-1	<i>Xoc</i>	1	S5_69377	*	LOC_Os05g01040	1	Exon	Synonymous variant	serine/threonine-protein kinase, putative, expressed
qXO-5-1	both	2	S5_103237	*** / *	LOC_Os05g01120	1	Exon	Synonymous variant	cytochrome P450, putative, expressed
qXO-5-1	<i>Xoo</i>	1	S5_227187	***	LOC_Os05g01370	1	Exon	Synonymous variant	polygalacturonase inhibitor precursor, putative, expressed
qXO-5-1	<i>Xoc</i>	1	S5_231622	*	LOC_Os05g01380	1	Exon	Non synonymous variant	polygalacturonase inhibitor precursor, putative, expressed
qXO-5-1	<i>Xoc</i>	1	S5_251710	*	LOC_Os05g01440	1	Exon	Non synonymous variant	phosphoribosylformylglycinamide synthase, putative, expressed
qXO-5-1	<i>Xoo</i>	1	S5_285834	***	LOC_Os05g01480	1	Intron		ras-related protein, putative, expressed
qXO-5-1	<i>Xoo</i>	1	S5_347328	**	LOC_Os05g01580	1	Exon	Non synonymous variant	integral membrane protein DUF6 containing protein, expressed
qXO-5-1	<i>Xoo</i>	2	S5_353165	*** / *	LOC_Os05g01590	1	Exon	Non synonymous variant	heat shock protein DnaJ, putative, expressed
qXO-5-1	<i>Xoo</i>	1	S5_440644	***	LOC_Os05g01710	1	Intron		transcription initiation factor IIA gamma chain, putative, expressed
qXO-5-1	<i>Xoo</i>	1	S5_453169	***	LOC_Os05g01750	1	5' UTR		TruB family pseudouridylylase synthase, putative, expressed
qXO-5-2	<i>Xoo</i>	1	S5_1200961	***	LOC_Os05g03070	3	Exon	Synonymous variant	transporter, putative, expressed
qXO-5-2	<i>Xoo</i>	1	S5_1200964	***			Exon	Non synonymous variant	
qXO-5-2	<i>Xoo</i>	1	S5_1200971	***			Exon	Non synonymous variant	

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-5-2	<i>Xoo</i>	1	S5_1224178	***	LOC_Os05g03100	1	Intron		HECT-domain domain containing protein, expressed
qXO-5-2	<i>Xoo</i>	1	S5_1258051	*	LOC_Os05g03140	1	Exon	Synonymous variant	tetraspanin family protein, putative, expressed
qXO-5-2	<i>Xoc</i>	1	S5_1475022	*	LOC_Os05g03480	2	Promoter		acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed
qXO-5-2	<i>Xoc</i>	1	S5_1475065	*			Promoter		
qBB-7-1	<i>Xoo</i>	1	S7_5993972	***	LOC_Os07g10940	2	Intron		exo70 exocyst complex subunit family protein, expressed
qBB-7-1	<i>Xoo</i>	1	S7_5994097	***			Intron		
qXO-7-2	<i>Xoo</i>	1	S7_27479752	*	LOC_Os07g46039	4	5' UTR		expressed protein
qXO-7-2	<i>Xoo</i>	1	S7_27480009	*			Promoter		
qXO-7-2	<i>Xoo</i>	1	S7_27480033	*			Promoter		
qXO-7-2	<i>Xoo</i>	1	S7_27480041	*			Promoter		
qXO-7-2	<i>Xoo</i>	1	S7_27590866	*	LOC_Os07g46240	1	3' UTR		choline transporter-related, putative, expressed
qXO-7-2	<i>Xoo</i>	1	S7_27619799	*	LOC_Os07g46300	1	Promoter		expressed protein
qXO-7-2	<i>Xoo</i>	1	S7_28070395	*	LOC_Os07g46970	1	Intron		sex determination protein tasselseed-2, putative, expressed
qXO-7-2	<i>Xoo</i>	1	S7_28165250	*	LOC_Os07g47100	2	Intron		transporter, monovalent cation:proton
qXO-7-2	<i>Xoo</i>	1	S7_28165258	*			Intron		antiporter-2 family, putative, expressed
qXO-7-2	<i>Xoo</i>	1	S7_28445131	*	LOC_Os07g47560	1	Promoter		expressed protein
qXO-10-1	<i>Xoo</i>	1	S10_20158998	*	LOC_Os10g37660	1	Exon	Non synonymous variant	trehalase precursor, putative, expressed
qBB-11-1	<i>Xoo</i>	1	S11_6940850	*	LOC_Os11g12420	1	Exon	Non synonymous variant	serpin domain containing protein, putative, expressed
qBB-11-1	<i>Xoo</i>	2	S11_6970503	*** / *	LOC_Os11g12470	2	Exon	Start gained	expressed protein
qBB-11-1	<i>Xoo</i>	3	S11_6970755	*			5' UTR		
qBB-11-1	<i>Xoo</i>	1	S11_7104422	*	LOC_Os11g12620	3	Exon	Non synonymous variant	receptor protein kinase CLAVATA1
qBB-11-1	<i>Xoo</i>	2	S11_7104857	*			Exon	Non synonymous variant	precursor, putative, expressed
qBB-11-1	<i>Xoo</i>	1	S11_7107785	*			Intron		
qXO-11-2	<i>Xoc</i>	1	S11_26879946	*	LOC_Os11g44430	1	Exon	Synonymous variant	protein kinase, putative, expressed
qXO-11-2	both	4	S11_26950888	***/**/*	LOC_Os11g44570	1	Exon	Non synonymous variant	expressed protein
qXO-11-2	both	3	S11_27033636	***/**/*	LOC_Os11g44700	2	Exon	Non synonymous variant	calmodulin binding protein, putative, expressed
qXO-11-2	both	3	S11_27033687	*** / *			Exon	Non synonymous variant	
qXO-11-2	both	5	S11_27181429	*** / *	LOC_Os11g44910	3	Exon	Non synonymous variant	DEAD-box ATP-dependent RNA
qXO-11-2	both	5	S11_27181436	*** / *			Exon	Synonymous variant	helicase, putative, expressed
qXO-11-2	<i>Xoo</i>	1	S11_27183806	***			Intron		

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-11-2	<i>Xoo</i>	4	S11_27192125	*** / *	LOC_Os11g44920	1	Exon	Synonymous variant	expressed protein
qXO-11-2	both	4	S11_27205864	*** / *	LOC_Os11g44950	1	Exon	Synonymous variant	glycosyl hydrolase family 3 protein, putative, expressed
qXO-11-2	<i>Xoo</i>	1	S11_27412501	**	LOC_Os11g45295	2	Exon	Non synonymous variant	retrotransposon protein, putative, expressed
qXO-11-2	<i>Xoo</i>	1	S11_27412530	**			Exon	Non synonymous variant	unclassified, expressed
qXO-11-2	both	5	S11_27451641	*** / *	LOC_Os11g45380	1	Exon	Synonymous variant	zinc finger family protein, putative, expressed
qXO-11-2	both	4	S11_27468322	*** / *	LOC_Os11g45390	1	Exon	Non synonymous variant	von Willebrand factor type A domain containing protein, putative, expressed
qXO-11-2	<i>Xoc</i>	2	S11_27496126	** / *	LOC_Os11g45410	2	Exon	Non synonymous variant	expressed protein
qXO-11-2	both	5	S11_27496991	*** / *			Exon	Non synonymous variant	
qXO-11-2	<i>Xoc</i>	1	S11_27574157	*	LOC_Os11g45540	1	Promoter		TKL_IRAK_DUF26-lh.11 - DUF26 kinases have homology to DUF26 containing loci, expressed
qXO-11-2	both	4	S11_27603799	*** / *	LOC_Os11g45620	1	Exon	Non synonymous variant	rust-resistance protein Lr21, putative, expressed
qXO-11-2	both	5	S11_27672705	*** / *	LOC_Os11g45740	3	Intron		MYB family transcription factor, putative, expressed
qXO-11-2	both	5	S11_27672709	*** / *			Intron		
qXO-11-2	both	5	S11_27672719	*** / *			Intron		
qXO-11-2	<i>Xoo</i>	5	S11_28483934	*** / *	LOC_Os11g47350	2	Exon	Synonymous variant	beta-D-xylosidase, putative, expressed
qXO-11-2	<i>Xoo</i>	5	S11_28483987	*** / *			Exon	Synonymous variant	
qXO-11-2	both	7	S11_28775260	*** / *	LOC_Os11g47650	2	Intron		trp repressor/replication initiator, putative, expressed
qXO-11-2	<i>Xoo</i>	1	S11_28777668	***			3' UTR		
qXO-11-2	<i>Xoo</i>	1	S11_28784287	**	LOC_Os11g47690	2	Exon	Synonymous variant	zinc finger, C3HC4 type domain
qXO-11-2	<i>Xoo</i>	1	S11_28784296	**			Exon	Synonymous variant	containing protein, expressed
qXO-11-2	<i>Xoo</i>	2	S11_28794135	*	LOC_Os11g47730	1	Exon	Synonymous variant	expressed protein
qXO-11-2	<i>Xoo</i>	3	S11_28815283	*** / *	LOC_Os11g47780	2	Exon	Synonymous variant	pollen signalling protein with adenylyl cyclase activity, putative, expressed
qXO-11-2	both	3	S11_28815394	*** / *			Exon	Synonymous variant	
qXO-11-2	<i>Xoo</i>	3	S11_28852557	*** / *	LOC_Os11g47830	1	Exon	Non synonymous variant	RNA recognition motif containing protein, expressed
qXO-11-2	<i>Xoo</i>	1	S11_28865011	*	LOC_Os11g47860	2	Exon	Non synonymous variant	expressed protein
qXO-11-2	both	5	S11_28865030	*** / *			Promoter		
qXO-11-2	<i>Xoo</i>	2	S11_28870403	** / *	LOC_Os11g47870	4	Exon	Synonymous variant	GRAS family transcription factor domain
qXO-11-2	<i>Xoo</i>	3	S11_28870482	*** / *			Exon	Non synonymous variant	containing protein, expressed
qXO-11-2	<i>Xoo</i>	2	S11_28870897	*** / *			Exon	Non synonymous variant	
qXO-11-2	both	5	S11_28870941	*** / *			Exon	Non synonymous variant	

Continuation Table 3.6.

QTL	Pathovar	No. strains	SNP	Significance	Locus	No. SNPs/Locus	Feature	Effect	Annotation
qXO-11-2	<i>Xoo</i>	2	S11_28895438	**/*	LOC_Os11g47910	2	Exon	Non synonymous variant	SCARECROW, putative, expressed
qXO-11-2	<i>Xoo</i>	1	S11_28896289	*			Exon	Non synonymous variant	
qXO-11-2	<i>Xoo</i>	1	S11_28904361	*	LOC_Os11g47930	1	Intron		alpha-hemolysin, putative, expressed
qXO-11-2	both	5	S11_28920280	*	LOC_Os11g47944	3	Promoter		thaumatin, putative, expressed
qXO-11-2	<i>Xoo</i>	2	S11_28920303	*			Promoter		
qXO-11-2	<i>Xoo</i>	2	S11_28920325	*			Promoter		
qXO-11-2	<i>Xoo</i>	1	S11_28938622	*	LOC_Os11g47980	1	Exon	Synonymous variant	expressed protein

Table 3.7. Summary of candidate loci according to different criteria. SNP: loci within selected QTL containing significantly associated SNPs with BLS and BB resistance. EBE: loci with putative targets for TAL effectors from multiple *X. oryzae* strains in Nipponbare. CRM: loci with multiple CRMs in IR64, Nipponbare or both.

QTL	One parameter	Two parameters				Three parameters
		SNP+EBE	SNP+CRM	EBE+CRM	Total	
qXO-1-1	18					
qXO-2-1	194	4	8	12	20	2
qXO-2-2	48			7	7	
qXO-4-1	85		5	5	10	
qXO-5-1	31		3	2	5	
qXO-5-2	63	2		5	7	
qXO-5-3	74					
qBB-7-1	139			16	16	
qXO-7-2	65	1		10	11	
qBLS-8-1	21			5	5	
qXO-10-1	62		1	4	5	
qBB-11-1	35	1	1	3	5	
qXO-11-2	127	3	6	8	13	2
qXO-12-1	15					
Total No. loci	977	11	24	77	104	4

Table 3.8. Candidate loci selected. Loci that meet the three criteria are in bold. The locus ID for each SNP was predicted from the MSU7 rice reference annotation.

Locus	QTL	SNPs		EBE \geq 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os02g39470	qXO-2-1	Intron	1				Both	Both	Both	cyclin, N-terminal domain containing protein, expressed
LOC_Os02g40320	qXO-2-1	Intron	1		IR64			Both	Both	PINHEAD, putative, expressed
LOC_Os02g41500	qXO-2-1	Exon	1	X						OsWAK13 - OsWAK receptor-like protein kinase, expressed
LOC_Os02g42220	qXO-2-1	Exon	1	X						transposon protein, putative, unclassified, expressed
LOC_Os02g42585	qXO-2-1	Exon	1	X				Both	IR64	AP2 domain containing protein, expressed
LOC_Os02g42590	qXO-2-1	Promoter	1					Both	Both	WD-40 repeat family protein, putative, expressed
LOC_Os02g42620	qXO-2-1	Exon	3					Both	Both	protein kinase, putative, expressed
LOC_Os02g42690	qXO-2-1	Exon	1	X			IR64	IR64	IR64	zinc finger, C3HC4 type domain containing protein, expressed
LOC_Os02g42890	qXO-2-1			X				Both	Both	cytochrome b561, putative, expressed
LOC_Os02g42900	qXO-2-1	Exon	1					Both	Both	expressed protein
LOC_Os02g43000	qXO-2-1	Exon	1				Both	Both	Nippon	cysteine-rich repeat secretory protein 15 precursor, putative, expressed
LOC_Os02g43150	qXO-2-1			X				Nippon	Nippon	GATA zinc finger domain containing protein, expressed
LOC_Os02g43490	qXO-2-1			X				Nippon	Nippon	expressed protein
LOC_Os02g43820	qXO-2-1			X	Both					AP2 domain containing protein, expressed
LOC_Os02g44330	qXO-2-1			X				Both	Both	rho guanine nucleotide exchange factor, putative, expressed
LOC_Os02g44370	qXO-2-1			X				Both	Nippon	scarecrow, putative, expressed
LOC_Os02g44630	qXO-2-1			X				Both	Both	aquaporin protein, putative, expressed
LOC_Os02g44654	qXO-2-1			X				Both	Nippon	cytochrome P450, putative, expressed

Continuation Table 3.8.

Locus	QTL	SNPs		EBE ≥ 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os02g44910	qXO-2-1			X			Both	Both	Both	transmembrane protein, putative, expressed
LOC_Os02g45070	qXO-2-1			X				Both	Both	PINHEAD, putative, expressed
LOC_Os02g57480	qXO-2-2			X				Both	Both	transferase family protein, putative, expressed
LOC_Os02g57570	qXO-2-2			X			Nippon	Nippon	Nippon	MATE efflux family protein, putative, expressed
LOC_Os02g57590	qXO-2-2			X	Both			IR64	IR64	rRNA 2-O-methyltransferase fibrillarin 2, putative, expressed
LOC_Os02g57620	qXO-2-2			X				Both	Both	Citrate transporter protein, putative, expressed
LOC_Os02g58000	qXO-2-2			X				Both	Both	expressed protein
LOC_Os02g58280	qXO-2-2			X		Both		Nippon		expressed protein
LOC_Os02g58290	qXO-2-2			X		Both		Nippon		expressed protein
LOC_Os04g52606	qXO-4-1			X				Nippon	Nippon	SHR5-receptor-like kinase, putative, expressed
LOC_Os04g52730	qXO-4-1			X		Both		Both		NAD dependent epimerase/dehydratase family domain containing protein, expressed
LOC_Os04g52810	qXO-4-1			X			Nippon	Nippon	Nippon	no apical meristem protein, putative, expressed
LOC_Os04g52850	qXO-4-1			X	Both			Both		OTU-like cysteine protease family protein, putative, expressed
LOC_Os04g53240	qXO-4-1	Exon	1					Both	Nippon	autophagy-related protein, putative, expressed
LOC_Os04g53260	qXO-4-1	Exon	1			Nippon		Both	Both	polyphenol oxidase, putative, expressed
LOC_Os04g53300	qXO-4-1	Exon	1					Both	Both	polyphenol oxidase, putative, expressed
LOC_Os04g53380	qXO-4-1	Exon	2					Both	Both	expressed protein

Continuation Table 3.8.

Locus	QTL	SNPs		EBE ≥ 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os04g53390	qXO-4-1	Exon	3					Both	Both	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed homeobox and START domains containing protein, putative, expressed
LOC_Os04g53540	qXO-4-1			X				Both	Both	
LOC_Os05g01040	qXO-5-1	Exon	1		Nippon					serine/threonine-protein kinase, putative, expressed
LOC_Os05g01230	qXO-5-1			X				Both	Both	zinc finger, C3HC4 type domain containing protein, expressed
LOC_Os05g01320	qXO-5-1			X	Both					expressed protein
LOC_Os05g01380	qXO-5-1	Exon	1				Both	Both	Both	polygalacturonase inhibitor precursor, putative, expressed
LOC_Os05g01580	qXO-5-1	Exon	1				Both	Both	Nippon	integral membrane protein DUF6 containing protein, expressed
LOC_Os05g02920	qXO-5-2			X				Nippon	Nippon	expressed protein
LOC_Os05g03100	qXO-5-2	Intron	1	X						HECT-domain domain containing protein, expressed
LOC_Os05g03480	qXO-5-2	Promoter	2	X						acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed
LOC_Os05g04020	qXO-5-2			X			Both	Both	IR64	plant protein of unknown function domain containing protein, expressed
LOC_Os05g04240	qXO-5-2			X				Both	Both	GDSL-like lipase/acylhydrolase, putative, expressed
LOC_Os05g04520	qXO-5-2			X				Both	Both	protein kinase, putative, expressed
LOC_Os05g04584	qXO-5-2			X				Both	Nippon	transferase family protein, putative, expressed

Continuation Table 3.8.

Locus	QTL	SNPs		EBE ≥ 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os07g08210	qBB-7-1			X				Both	Both	cytidyltransferase domain containing
LOC_Os07g08350	qBB-7-1			X				Both	Both	C4-dicarboxylate transporter/malic acid transport protein, expressed
LOC_Os07g08390	qBB-7-1			X				IR64	IR64	plant-specific domain TIGR01615 family protein, expressed
LOC_Os07g08510	qBB-7-1			X	Both					expressed protein
LOC_Os07g09000	qBB-7-1			X				Both	Both	WD domain, G-beta repeat domain containing protein, expressed
LOC_Os07g09580	qBB-7-1			X				Both	Both	aminoacyl-tRNA synthetase, putative, expressed
LOC_Os07g09620	qBB-7-1			X			Both			acanthoscurrin-1 precursor, putative, expressed
LOC_Os07g09675	qBB-7-1			X			Both	Both	Both	expressed protein
LOC_Os07g09900	qBB-7-1			X				Nippon	Nippon	disease resistance protein RPM1, putative, expressed
LOC_Os07g10560	qBB-7-1			X				Both	Both	expressed protein
LOC_Os07g10880	qBB-7-1			X				IR64	IR64	expressed protein
LOC_Os07g10920	qBB-7-1			X	IR64			Both		expressed protein
LOC_Os07g10960	qBB-7-1			X				IR64	IR64	expressed protein
LOC_Os07g10970	qBB-7-1			X				Both	IR64	leucine zipper protein-like, putative, expressed
LOC_Os07g11110	qBB-7-1			X		Both		Both	Both	NAD dependent epimerase/dehydratase family protein, putative, expressed
LOC_Os07g11120	qBB-7-1			X		Both		Both		hydrolase, NUDIX family, domain containing protein, expressed
LOC_Os07g46070	qXO-7-2			X				Nippon	Nippon	expressed protein
LOC_Os07g46170	qXO-7-2			X				IR64	IR64	OsRhmbd13 - Putative Rhomboid homologue, expressed

Continuation Table 3.8.

Locus	QTL	SNPs		EBE ≥ 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os07g46240	qXO-7-2	3' UTR	1	X						choline transporter-related, putative, expressed
LOC_Os07g46490	qXO-7-2			X				IR64	IR64	phosphatidylinositol-4-phosphate 5-kinase, putative, expressed
LOC_Os07g46510	qXO-7-2			X	Both			Both	Both	expressed protein
LOC_Os07g46700	qXO-7-2			X				Both	Both	zinc finger, RING-type, putative, expressed
LOC_Os07g46790	qXO-7-2			X	IR64	Both	Both	IR64		4-alpha-glucanotransferase, putative, expressed
LOC_Os07g46930	qXO-7-2			X				IR64	IR64	sex determination protein tasselseed-2, putative, expressed
LOC_Os07g47130	qXO-7-2			X				Nippon	Nippon	OCL5 protein, putative, expressed
LOC_Os07g47520	qXO-7-2			X				Both	Both	expressed protein
LOC_Os07g47590	qXO-7-2			X				Both	Both	expressed protein
LOC_Os08g40520	qBLS-8-1			X				Both	IR64	expressed protein
LOC_Os08g40680	qBLS-8-1			X				Both	Both	glycosyl hydrolase, putative, expressed
LOC_Os08g40690	qBLS-8-1			X				Both	IR64	glycosyl hydrolase, putative, expressed
LOC_Os08g40740	qBLS-8-1			X				Both	Both	glycosyl hydrolase, putative, expressed
LOC_Os08g40880	qBLS-8-1			X	Both					RNA recognition motif containing protein, putative, expressed
LOC_Os10g37660	qXO-10-1	Exon	1					Both	Both	trehalase precursor, putative, expressed
LOC_Os10g38160	qXO-10-1			X				Nippon	Nippon	glutathione S-transferase, putative, expressed
LOC_Os10g38189	qXO-10-1			X				Nippon	Nippon	glutathione S-transferase, putative, expressed
LOC_Os10g39010	qXO-10-1			X				Nippon	Nippon	TKL_IRAK_CrRLK1L-1.16 - The CrRLK1L-1 subfamily has homology to the CrRLK1L homolog, expressed
LOC_Os10g39020	qXO-10-1			X			Nippon	Both	Both	fringe-related protein, putative, expressed

Continuation Table 3.8.

Locus	QTL	SNPs		EBE ≥ 10 strains	CRM					Annotation
		Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os11g12000	qBB-11-1			X				Nippon	Nippon	NBS-LRR disease resistance protein, putative, expressed
LOC_Os11g12050	qBB-11-1			X				Nippon	Nippon	NBS-LRR type disease resistance protein, putative, expressed
LOC_Os11g12420	qBB-11-1	Exon	1					Both	Both	serpin domain containing protein, putative, expressed
LOC_Os11g12620	qBB-11-1	Exon	3	X						receptor protein kinase CLAVATA1 precursor, putative, expressed
LOC_Os11g13390	qBB-11-1			X			Both	Both	Both	expressed protein
LOC_Os11g44430	qXO-11-2	Exon	1	X				Nippon	Nippon	protein kinase, putative, expressed
LOC_Os11g44570	qXO-11-2	Exon	1					Both	Both	expressed protein
LOC_Os11g44920	qXO-11-2	Exon	1				Nippon			expressed protein
LOC_Os11g45320	qXO-11-2			X				Nippon	Nippon	expressed protein
LOC_Os11g45570	qXO-11-2			X				Nippon	Nippon	expressed protein
LOC_Os11g47140	qXO-11-2			X		Nippon		Nippon		OsWAK123 - OsWAK receptor-like protein kinase, expressed
LOC_Os11g47350	qXO-11-2	Exon	2	X						beta-D-xylosidase, putative, expressed
LOC_Os11g47550	qXO-11-2			X	IR64		IR64			glycosyl hydrolase, putative, expressed
LOC_Os11g47600	qXO-11-2			X				Both	Both	glycosyl hydrolase, putative, expressed
LOC_Os11g47860	qXO-11-2	Exon	2					Both	Both	expressed protein
LOC_Os11g47920	qXO-11-2			X				Both	Both	SCARECROW, putative, expressed
LOC_Os11g47930	qXO-11-2	Intron	1					Both	Both	alpha-hemolysin, putative, expressed
LOC_Os11g47944	qXO-11-2	Promoter	3	X			Nippon	Nippon	Nippon	thaumatin, putative, expressed

Table 3.9. CRMs present in MAGIC founders. Loci with CRM polymorphisms among MAGIC founders are in bold. Presence of SNPs or EBE are denoted with an X. Founders are indicated with letters (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1).

Locus	QTL	SNP	SNPs		EBE ≥ 10 strains	CRM					Annotation
			Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os02g39470	qXO-2-1	X	Intron	1				C, D, E, G, H	All	All	cyclin, N-terminal domain containing protein, expressed
LOC_Os02g40320	qXO-2-1	X	Intron	1		A, B, C, D, E, G			All	All	PINHEAD, putative, expressed
LOC_Os02g42585	qXO-2-1	X	Exon	1	X				All	All	AP2 domain containing protein, expressed
LOC_Os02g42590	qXO-2-1	X	Promoter	1					All	All	WD-40 repeat family protein, putative, expressed
LOC_Os02g42620	qXO-2-1	X	Exon	3					All	All	protein kinase, putative, expressed
LOC_Os02g42690	qXO-2-1	X	Exon	1	X			All	All	C, D, E, F, G, H	zinc finger, C3HC4 type domain containing protein, expressed
LOC_Os02g42890	qXO-2-1				X				All	A, B, E, F, G, H	cytochrome b561, putative, expressed
LOC_Os02g43000	qXO-2-1	X	Exon	1				A, D	A, C, D, E		cysteine-rich repeat secretory protein 15 precursor, putative, expressed
LOC_Os02g43150	qXO-2-1				X						GATA zinc finger domain containing protein, expressed
LOC_Os02g43820	qXO-2-1				X	All					AP2 domain containing protein, expressed
LOC_Os02g44330	qXO-2-1				X				All	All	rho guanine nucleotide exchange factor, putative, expressed
LOC_Os02g44370	qXO-2-1				X				All	H	scarecrow, putative, expressed
LOC_Os02g44630	qXO-2-1				X				All	All	aquaporin protein, putative, expressed
LOC_Os02g44654	qXO-2-1				X				All	H	cytochrome P450, putative, expressed
LOC_Os02g44910	qXO-2-1				X			A, C, D, F, H	All except E	A, C, D, F, H	transmembrane protein, putative, expressed
LOC_Os02g45070	qXO-2-1				X				All	All	PINHEAD, putative, expressed

Continuation Table 3.9.

Locus	QTL	SNP	SNPs		EBE ≥ 10 strains	CRM					Annotation
			Feature	No. SNPs/ Locus		CRM1	CRM2	CRM3	CRM4	CRM5	
LOC_Os04g52730	qXO-4-1				X				All		NAD dependent epimerase/dehydratase family domain containing protein, expressed
LOC_Os04g52850	qXO-4-1				X				All except G		OTU-like cysteine protease family protein, putative, expressed
LOC_Os04g53240	qXO-4-1	X	Exon	1					All	A, B, F, G, H	autophagy-related protein, putative, expressed
LOC_Os04g53260	qXO-4-1	X	Exon	1					All except D	All except D	polyphenol oxidase, putative, expressed
LOC_Os04g53300	qXO-4-1	X	Exon	1					All	All	polyphenol oxidase, putative, expressed
LOC_Os04g53390	qXO-4-1	X	Exon	3					All	All	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
LOC_Os04g53430	qXO-4-1				X				All	A, B, F, G, H	MBTB8 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain, expressed
LOC_Os04g53496	qXO-4-1				X				All		NBS-LRR disease resistance protein, putative, expressed
LOC_Os04g53540	qXO-4-1				X		D, H		All	All	homeobox and START domains containing protein, putative, expressed
LOC_Os05g01040	qXO-5-1	X	Exon	1		D, F, H					serine/threonine-protein kinase, putative, expressed
LOC_Os05g01230	qXO-5-1				X				All	All	zinc finger, C3HC4 type domain containing protein, expressed
LOC_Os05g01380	qXO-5-1	X	Exon	1				A, D, E, F, G, H	All	A, E	polygalacturonase inhibitor precursor, putative, expressed
LOC_Os05g01580	qXO-5-1	X	Exon	1				All	All		integral membrane protein DUF6 containing protein, expressed
LOC_Os11g47350	qXO-11-2		Exon	2	X		All except H				beta-D-xylosidase, putative, expressed
LOC_Os11g47550	qXO-11-2				X	All		All			glycosyl hydrolase, putative, expressed
LOC_Os11g47600	qXO-11-2				X				All	All	glycosyl hydrolase, putative, expressed
LOC_Os11g47920	qXO-11-2				X				All	All	SCARECROW, putative, expressed
LOC_Os11g47930	qXO-11-2	X	Intron	1					All	All except H	alpha-hemolysin, putative, expressed
LOC_Os11g47944	qXO-11-2	X	Promoter	3	X						thaumatin, putative, expressed

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CHAPTER 4

UNDERSTANDING THE ROLE OF THE MATH-BTB GENE FAMILY IN A RICE

BROAD-SPECTRUM QTL³

OVERVIEW

MATH-BTB proteins are involved in a wide range of cellular processes and have been associated with immunity in plants. These proteins are substrate-binding adaptors for the CULLIN3 (CUL3)-based RING E3 ligases (CRL3), an important protein complex that mediates protein ubiquitination and degradation. A cluster of four *MATH-BTB* genes is present in qXO-4-1, a rice broad-spectrum disease resistance (BSR) QTL identified on chromosome 4. This QTL confers resistance to multiple isolates of the causal agents of bacterial leaf streak (BLS) and bacterial blight (BB). BLS and BB are major threats in rice production worldwide and are caused by different pathovars of the *Xanthomonas oryzae* species. Transcription activator-like (TAL) are major virulence factors employed by *X. oryzae* species to manipulate host gene expression and facilitate bacterial colonization. This is achieved through the binding of TAL effectors to specific sequence of host promoters, the effector binding elements (EBEs). Coding and promoter sequences of the

³ This chapter contains preliminary data for a future publication and is a collaborative effort with these authors: Ana M. Bossa-Castro, Álvaro Pérez-Quintero, Bradley Tonnessen, Jan E. Leach. Author contributions: A.M.B.-C., and J.E.L. designed research; A.M.B.-C., A.P.-Q. and B.T. performed research; A.M.B.-C., and J.E.L. analyzed data.

MATH-BTB genes were compared among resistant and susceptible lines. Structural variations and amino acid changes were identified among all of them. Single residue changes, such as the ones identified in this study, could interfere with the function of MATH and BTB domains, affecting the protein ability to dimerize or to interact with their substrates, thus altering the defense response. Putative EBEs in the *MATH-BTB* promoters were also identified using TAL effector sequences from 35 diverse *X. oryzae* strains. All the promoters are predicted targets of at least three different *X. oryzae* strains. Overall, *OsMrBTB2* and *OsMBTB8* are promising candidates for future validation as important genes in the defense responses of rice to BLS and BB.

4.1 INTRODUCTION

Proteins encompassing a MATH (Meprin and TRAF Homology related) (Chen et al., 2015, Weber & Hellmann, 2009, Chen et al., 2013) and a BTB (Bric-A-Brac, Tramtrack, Broad Complex) domain, are broadly present among eukaryotes, except fungi, and are involved in a wide range of cellular processes to regulate development and cell homeostasis (Zapata et al., 2007, Juranic & Dresselhaus, 2014). Both the MATH and BTB domains mediate protein-protein interactions, moreover, BTB domains can create homodimers, heterodimers and multimers (Weber et al., 2005).

In plants, MATH-BTB proteins act as substrate-binding adaptors for the CULLIN3 (CUL3)-based RING E3 ligases (CRL3). In the CRL3 complex, a MATH-BTB dimerizes with other MATH-BTB proteins through the BTB domain, while a CUL3 protein acts as a scaffolding subunit, interacting at its N-terminal part with the BTB domains and with RBX1 protein at its C-terminal end. Recognition of the substrate is carried out by the MATH domain, which delivers it to the CRL3 core for ubiquitination and consequent degradation via the 26S proteasome (Weber et al., 2005,

Gingerich et al., 2007, Chen et al., 2013). The ubiquitin/proteasome pathway is a vital component of the regulatory networks controlling essential cellular processes, including development and defense responses (Sharma et al., 2016).

Six MATH-BTB genes are present in Arabidopsis, whereas 69 putative genes have been identified in rice (Juranic & Dresselhaus, 2014). In Arabidopsis, substrates of MATH-BTB proteins are predominantly transcription factors, such as AtRAP2.4, AtWRI1, AtHB6 and AtMYB56 (Weber & Hellmann, 2009, Chen et al., 2013, Chen et al., 2015, Lechner et al., 2011). AtRAP2.4 and AtWRI1 are members of the ERF/AP2 transcription factor family (Chen et al., 2013, Weber & Hellmann, 2009); AtRAP2.4 is involved in abiotic stress tolerance, whereas AtWR1 is a key player in fatty acid and carbohydrate metabolism (Chen et al., 2013). AtHB6 is a homeobox-leucine zipper (HD-ZIP) transcription factor that negatively regulates ABA signaling (Lechner et al., 2011), while AtMYB56 belongs to the R2R3-MYB transcription factor family and is a negative regulator of flowering (Chen et al., 2015). One predicted group of substrates for the MATH-BTB proteins are pathogen effectors that are under strong positive selection to avoid detection and inactivation by the host (Thomas, 2006, Gingerich et al., 2007). In rice, MATH-BTB proteins are predicted to be localized mainly in the cytoplasm and the chloroplast (Kushwaha et al., 2016). The rice CRL3 complex was found to mediate ubiquitination of OsNPR1, for subsequent degradation, thus acting as a negative regulator of cell death and immunity (Liu et al., 2017).

Two devastating bacterial diseases of rice are bacterial leaf streak (BLS) and bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzicola* (*Xoc*) and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), respectively. qXO-4-1 is a rice broad-spectrum disease resistance (BSR) QTL, conferring resistance to eight African *Xoc* and eight *Xoo* strains, and was detected using a rice

indica MAGIC population (Bossa-Castro et al., 2018). While the entire QTL is located between 30.8 Mb – 32.1 Mb on chromosome 4, a smaller region at the end of this QTL, encompassing 627 Kb (31.6 – 32.1 Mb) was highlighted as the responsible for the resistance to the 16 *X. oryzae* strains. Genome-wide association studies (GWAS) identified 18 SNPs significantly associated with BLS and BB resistance in this region (P -value < 0.001). From these, 14 SNPs were shown to have positive effects in lesion length, indicating their association with an increase in susceptibility (Bossa-Castro et al., 2018). A cluster of four members of the MATH-BTB gene family is present in this region of qXO-4-1: *OsMrBTB2* (LOC_Os04g53390), *OsMBTB6* (LOC_Os04g53400), *OsMBTB7* (LOC_Os04g53410) and *OsMBTB8* (LOC_Os04g53430). This cluster was targeted as a potential candidate in the rice-*X. oryzae* interaction because four significant SNPs were localized in the coding sequence of two *MATH-BTB* genes (Table 4.1) (Bossa-Castro et al., 2018). Each of them is characterized by an N-terminal MATH domain and a C-terminal BTB domain, as in the vast majority of MATH-BTB proteins (Zapata et al., 2007). In a recent study, *OsMBTB7* (LOC_Os04g53410) was upregulated under biotic (*Xoc*, *Xoo*, *Magnaporthe oryzae*) and abiotic (drought, salinity) stress conditions (Kushwaha et al., 2016, Tripathi et al., 2012). Moreover, *OsMBTB7* interacted strongly *in vitro* with full-length AtCUL3a (Gingerich et al., 2007).

X. oryzae strains deliver transcription activator-like (TAL) effectors to rice cells during infection. These TAL recognize and bind to specific sequences in the plant gene promoters, the effector binding elements (EBEs), activating their transcription and promoting bacterial infection (Bogdanove & Voytas, 2011). Different bioinformatic tools, such as Talvez, allow the prediction of EBEs from the sequence of each TAL effector (Perez-Quintero et al., 2013). The type of resistance achieved when the EBE of a target host gene is mutated, and therefore blocks the

ability for the TAL to recognize and bind to the promoter, is termed the loss of susceptibility (Boch et al., 2014). In the previous chapter, the *MATH-BTB* promoters were found to be predicted targets of multiple *X. oryzae* TAL effectors and two of them to have *cis*-regulatory modules CRM4 and CRM5, which are associated with WRKY transcription factors (Table 4.1).

In this study, we cloned four members of the *MATH-BTB* gene family present in qXO-4-1, from two rice MAGIC advanced intercross lines (one resistant and one susceptible AIL). Structural variations among resistant and susceptible lines were detected at nucleotide and amino acid levels in the coding sequences, leading to possible phenotypic differences among them. Putative EBE on the *MATH-BTB* promoters were also identified, using TAL effector sequences from 35 *X. oryzae* strains from different geographical regions and genetic backgrounds.

4.2. RESULTS

***MATH-BTB* genes display structural variations between MAGIC AILs**

In a recent study, 340 MAGIC AILs were screened with multiple *Xoc* and *Xoo* strains (Bossa-Castro et al., 2018). We selected line 163 as a common resistant variety to most of the strains tested, and line 194 as a common susceptible variety to all strains tested. The putative donor of the resistant alleles in the 627 Kb region at the end of qXO-4-1 is the MAGIC founder IR4630-22-2-5-1-3 (IR46). Fedearroz 50 (Fed), another founder of the MAGIC population, is one of the possible donors of the susceptible alleles in this region (Chapter 2, Table S2.11).

OsMrBTB2 was amplified from MAGIC AILs and founders using gene-specific primers (Figure 4.1, Table 4.2) and size differences were observed between resistant varieties (163 and IR46), susceptible varieties (194, Fed) and Nipponbare. Amplification of gDNA from lines 163 and

IR46 yielded a product of 1,302 bp, while a fragment of 1,056 bp was obtained from lines 194 and Fed. The control variety Nipponbare yielded a product of 1,299 bp (Figure 4.1.A.). In addition, a cDNA amplicon obtained from line 194 was 860 bp (Figure 4.1.B). Structural variations between resistant and susceptible lines were identified by alignment of sequenced products (Figure 4.1.C). *OsMrBTB2* coding sequence contains two exons and an intron in Nipponbare. Clones from susceptible lines comprised a 285 bp deletion between exon 1 and the intron, a 26 bp insertion in the intron, and an extra codon in exon 2. Clones from resistant lines contained a different extra codon in exon 2 (Figure 4.1.C). Resistant lines also contained two non-synonymous SNPs in exon 1, compared to Nipponbare, whereas susceptible lines contained seven non-synonymous SNPs in exon 2.

In contrast to *OsMrBTB2*, *OsMBTB6-8* contain a single exon. These *MATH-BTB* genes were amplified from Nipponbare and the MAGIC AILs 163 and 194 using gene-specific primers, and revealed size differences only in *OsMBTB6* and *OsMBTB8* (Figure 4.2, Table 4.2). For *OsMBTB6*, a 1,128 bp fragment was amplified from Nipponbare and resistant AIL 163, while a 2,040 bp product was amplified from the susceptible AIL 194 (Figure 4.2.A). Three SNPs were found between AILs 163 and 194, but only two of them lead to non-synonymous variants. Although no structural variation was observed in *OsMBTB7*, one synonymous and one non-synonymous SNP distinguished the resistant and susceptible lines. A fragment of 1,192 bp was obtained in all three varieties (Figure 4.2.B). For *OsMBTB8*, a 1,122 bp product was obtained from Nipponbare and susceptible AIL 194, whereas the resistant line 163 had a 9 bp deletion yielding a 1,113 bp fragment (Figure 4.2.C). Two non-synonymous SNP variants were detected between AILs 163 and 194.

Residue variations among MATH-BTB proteins in MAGIC AILs could explain phenotypic differences

Amino acid sequences were predicted from the four *MATH-BTB* nucleotide sequences for MAGIC AILs and founders. Domain prediction indicated an N-terminal MATH domain and a C-terminal BTB domain in all four MATH-BTB proteins. Each protein differed in at least one residue between resistant and susceptible lines. For OsMrBTB2, the 285 bp deletion at the end of exon 1 led to the disruption of the MATH domain, and an extra glycine was present in the BTB domain of the susceptible lines 194 and Fed. An extra aspartic acid residue was detected in the BTB domain of the resistant lines 163 and IR46. Additionally, six different residues were found among resistant and susceptible lines (Figure 4.3). For OsMBTB6, an isoleucine and an arginine were changed for valine and glycine among the resistant and the susceptible lines in the MATH domain (Figure 4.4). For OsMBTB7, a lysine residue was altered for an arginine in the BTB domain, again distinguishing resistant and susceptible lines (Figure 4.5). For OsMBTB8, a tryptophan in the MATH domain and a leucine in the BTB domain in the resistant line were changed from a glycine and a valine, respectively, compared to Nipponbare and the susceptible AIL. Additionally, a deletion of three residues was found near the MATH domain in the resistant line (Figure 4.6).

Multiple TAL effectors from diverse *X. oryzae* strains have predicted EBE targets in the *MATH-BTB* promoters

Nipponbare promoter sequences from the four *MATH-BTB* were used to screen the available TALomes, i.e. repertoires of TAL effector genes, from 35 *X. oryzae* sequenced strains (14 *Xoc* and 21 *Xoo*) (Chapter 3, Table 3.4). Nine different EBEs were predicted targets of 34 TAL

effectors in these promoters (Table 5.1, Table 5.3). Promoter sequences from the eight indica MAGIC founders were extracted from the 3,000 genomes database (3K.R.G.P., 2014) and were aligned with Nipponbare promoters to search for unique features in the IR46 founder, the putative donor of resistant alleles for these loci.

The *OsMrBTB2* promoter has three predicted EBEs to four *Xoo* strains (Figure 4.7.A, Table 4.3). Of these, two EBEs are overlapping and correspond to Asian *Xoo* strains, one of which has two TAL targeting the same region, approximately 600 bp upstream of the transcription start site (TSS). At 700 bp upstream of the TSS, a single EBE for TalB of *Xoo* African strain MAI134 was predicted. Downstream from this EBE a unique SNP in IR46 promoter was found. Closer to the TSS, a possible deletion and two additional unique SNPs in IR46 were detected.

The *OsMBTB6* promoter has the same putative EBE for 11 Asian *Xoo* strains, approximately 400 bp upstream of the TSS (Figure 4.7.B, Table 4.3). Although IR46 has two unique SNP, these are far upstream from the EBE.

The *OsMBTB7* promoter had two predicted EBE for four TAL of two African and two Asian *Xoc* strains (Figure 4.7.C, Table 4.3). The EBEs are located approximately at 700 and 600 bp from the TSS. Additionally, the IR46 founder has two unique SNPs at 400 bp from the TSS and a possible deletion at 200 bp.

Finally, the *OsMBTB8* promoter has three putative EBE for a total of three *Xoc* and seven *Xoo* strains (Figure 4.7.D, Table 4.3). Of these, two EBE overlap and correspond to African and Asian *Xoc* strain targets, located at approximately 600 bp from the TSS. The third EBE is located at 60 bp from the TSS and corresponds to seven Asian *Xoo* TAL targets. However, the EBE present

in Nipponbare was not conserved among the MAGIC founders, consistent with a loss of susceptibility type of resistance in the eight founders. Moreover, the founder IR46 has three unique SNPs compared to Nipponbare and the other founders in the region between the predicted EBEs.

4.3. DISCUSSION

Two approaches were used to study the role of the *MATH-BTB* genes in qXO-4-1, variations at the DNA and protein level that could ultimately affect the protein function, and EBEs and SNPs present in the promoters that could alter the recognition by TAL effectors, and thus the manipulation of rice promoters by *X. oryzae* pathogens.

Besides their involvement in the CRL3 complex, BTB containing proteins are components of proteins involved in immunity, such as OsNPR1, a regulator of systemic acquired resistance (Rochon et al., 2006, Yuan et al., 2007), and AtPOB1 and AtPOB2, negative regulators of defense responses to fungal pathogens (Qu et al., 2010). Comparison of nucleotide and amino acid sequences of MATH-BTB between resistant and susceptible lines of MAGIC AILs and founders revealed structural variations and residue changes that could translate into different expression patterns of these genes. As MATH and BTB domains facilitate protein interactions, even single residue changes could affect their function or their ability to interact with their substrates. In fact, specific residues in the BTB domain are required for dimerization (Orosa et al., 2017, Melnik et al., 2000). In Arabidopsis, a highly conserved aspartic acid residue and a leucine are required for BTB dimerization (Weber et al., 2005). In this study, the MATH domain of OsMrBTB2 was disrupted and an extra residue in the BTB was detected in susceptible lines. Moreover, an

additional aspartic acid was found in the resistant lines. In *OsMBTB8*, a substitution from a leucine to a valine was found in the BTB domain in the susceptible line. Therefore, *OsMrBTB2* and *OsMBTB8* are promising candidates for future characterization. Additional experiments are required to reveal possible substrates of the MATH-BTB proteins in qXO-4-1 as well as to confirm if they are differentially transcribed upon *X. oryzae* infection in resistant and susceptible lines.

MATH-BTB promoters were pinpointed as possible targets of different *X. oryzae* TAL effectors. So far, evidence has supported that *Xoc* and *Xoo* TAL target different genes in rice (Cai et al., 2017, Verdier et al., 2012). Known targets of *Xoc* TAL are sulfur transporter genes (Cernadas et al., 2014), whereas several *Xoo* TAL effectors target host sucrose transporter genes (Chen et al., 2010). *OsMBTB8* promoter rises as an interesting candidate because it is putatively targeted by both *Xoc* and *Xoo* strains. Not only that, but it can also be a new example of an allele for the loss of susceptibility type of resistance (Hutin et al., 2015). Further analyses are needed to validate *OsMBTB8* promoter as a target of *X. oryzae* TAL effectors. To this end, sequencing of the promoter region among the eight MAGIC founders could also confirm the polymorphisms detected in the IR46 founder and *X. oryzae* inoculation with single TAL with subsequent gene expression analyses could reveal the association of this *MATH-BTB* genes with disease resistance.

4.4. MATERIALS AND METHODS

DNA, RNA extraction and cDNA syntesis

Genomic DNA (gDNA) from MAGIC AILs 163 and 194, MAGIC founders IR4630-22-2-5-1-3 (IR46) and Fedearroz 50 (Fed), and Nipponbare (Nipp) was extracted from 50 mg of ground plant tissue using the Invitrogen Easy-DNA™ Kit, protocol # 3 for plant leaves, following the

manufacturer's recommendations. Total RNA was extracted from 100 mg of ground plant tissue of MAGIC AIL 194 using the Sigma® Spectrum™ Plant Total RNA Kit, protocol B. A 50 µl aliquot of total RNA was treated with DNaseI using the Ambion® TURBO DNA-free™ Kit and reverse-transcribed with the qScript™ Flex cDNA Synthesis Kit (Quanta Biosciences™), using a mix of oligo dT and random primers.

PCR amplification, cloning and sequencing

Gene-specific primers were designed to amplify *MATH-BTB* genes present in qXO-4-1 (Table 4.2), using the MSU7 rice reference annotation (Kawahara et al., 2013). Each PCR reaction was prepared with a final volume of 50 µl, containing 100 ng of gDNA or cDNA (AIL 194), 0.2 mM dNTPs, 0.2 µM of each primer, 3% DMSO, 1X Phusion HF buffer and 1 unit of Phusion® High-Fidelity DNA Polymerase (New England BioLabs, Thermo Scientific®).

Touchdown PCR was used to amplify *OsMrBTB2* and *OsMBTB6*. Gene-specific conditions were: *OsMrBTB2* (LOC_Os04g53390), 30 sec at 98°C, 5 cycles of 10 sec at 98°C, 30 sec at 63°C, 45 sec at 72°C, 5 cycles of 10 sec at 98°C, 30 sec at 62°C, 45 sec at 72°C, 25 cycles of 10 sec at 98°C, 30 sec at 61°C, 45 sec at 72°C, and lastly, 5 min at 72°C; *OsMBTB6* (LOC_Os04g53400), 30 sec at 98°C, 5 cycles of 10 sec at 98°C, 30 sec at 67°C, 45 sec at 72°C, 5 cycles of 10 sec at 98°C, 30 sec at 66°C, 45 sec at 72°C, 25 cycles of 10 sec at 98°C, 30 sec at 65°C, 45 sec at 72°C, and lastly, 5 min at 72°C; *OsMBTB7* (LOC_Os04g53410), 30 sec at 98°C, 35 cycles of 10 sec at 98°C, 30 sec at 57°C, 45 sec at 72°C, and lastly, 5 min at 72°C; *OsMBTB8* (LOC_Os04g53430), 30 sec at 98°C, 35 cycles of 10 sec at 98°C, 30 sec at 59°C, 45 sec at 72°C, and lastly, 5 min at 72°C.

PCR products were separated by electrophoresis using a 1.2% agarose gel in buffer TAE 0.5X, stained with GelRed® (Biotium). The fragment size was confirmed using 1 Kb Ladder (Gold Biotechnology®). DNA products were purified from gel using QIAquick® Gel Extraction Kit (Qiagen). Purified products were cloned into pENTR™/D-TOPO® vector (Thermo Fisher Scientific), following the manufacturer's instructions. Each cloning product was transformed into One Shot™ TOP10 Chemically Competent *Escherichia coli* (Thermo Fisher Scientific), according to the manufacturer's protocol. Transformed *E. coli* cells were grown overnight in Luria–Bertani (LB) medium with kanamycin at 50 mg/ml at 37°C. Transformants were tested by colony PCR. Colony PCR was conducted using M13F and M13R primers, with a final volume of 25 µl, containing 0.2 mM dNTPs, 0.2 µM of each primer, 3% DMSO, and 1X GoTaq® Green Master Mix (Promega). The following conditions were used: 10 min at 95°C, 30 cycles of 30 sec at 95°C, 40 sec at 56°C, 2 min at 72°C, and lastly, 5 min at 72°C. PCR products were confirmed by electrophoresis as described above.

The plasmid DNA of a single positive transformant for each cloning reaction was purified using the GeneJET Plasmid Miniprep Kit (Thermo Scientific). Plasmids were extracted from *E. coli* that were grown overnight at 37°C in a liquid LB culture with kanamycin at 50mg/ml. Selected plasmids were sequenced at Integrated DNA Technologies (IDT) using M13F y M13R and internal primers (Table 4.2).

Sequence analysis

Raw sequences were analyzed using Geneious Pro 4.8.5 (Kearse et al., 2012), and a consensus sequence was confirmed for each gene. Consensus sequences for each variety were

translated to amino acid using the same software. Domain predictions were carried out using Prosite (de Castro et al., 2006).

TAL effector EBE prediction

Promoter sequences from the rice variety Nipponbare were extracted from the MSU7 rice reference annotation (Kawahara et al., 2013). Promoter regions were defined as the 1 Kb region upstream of the transcription start site. Promoter sequences from the eight indica MAGIC founders were extracted from the 3,000 genomes database (3K.R.G.P., 2014) by aligning Nipponbare gene sequences to the MAGIC founders. TALomes, i.e. repertoires of TAL effector genes, from 35 *X. oryzae* sequenced strains (14 *Xoc* and 21 *Xoo*) were used to extract the TAL sequences for each *X. oryzae* strain (Chapter 3, Table 3.4). EBE prediction in the rice variety Nipponbare (MSU7 reference annotation) was conducted using Talvez 3.2 (Perez-Quintero et al., 2013), defining qXO-4-1 QTL limits (30,862,506-32,134,600 Mb) as the target region. Predictions were conducted against both strands, with no position correction, using minimum score 8, keeping the top 500 targets per TAL, and using the RVD-DNA matrix published in Perez-Quintero et al. (2015).

4.5 FIGURES

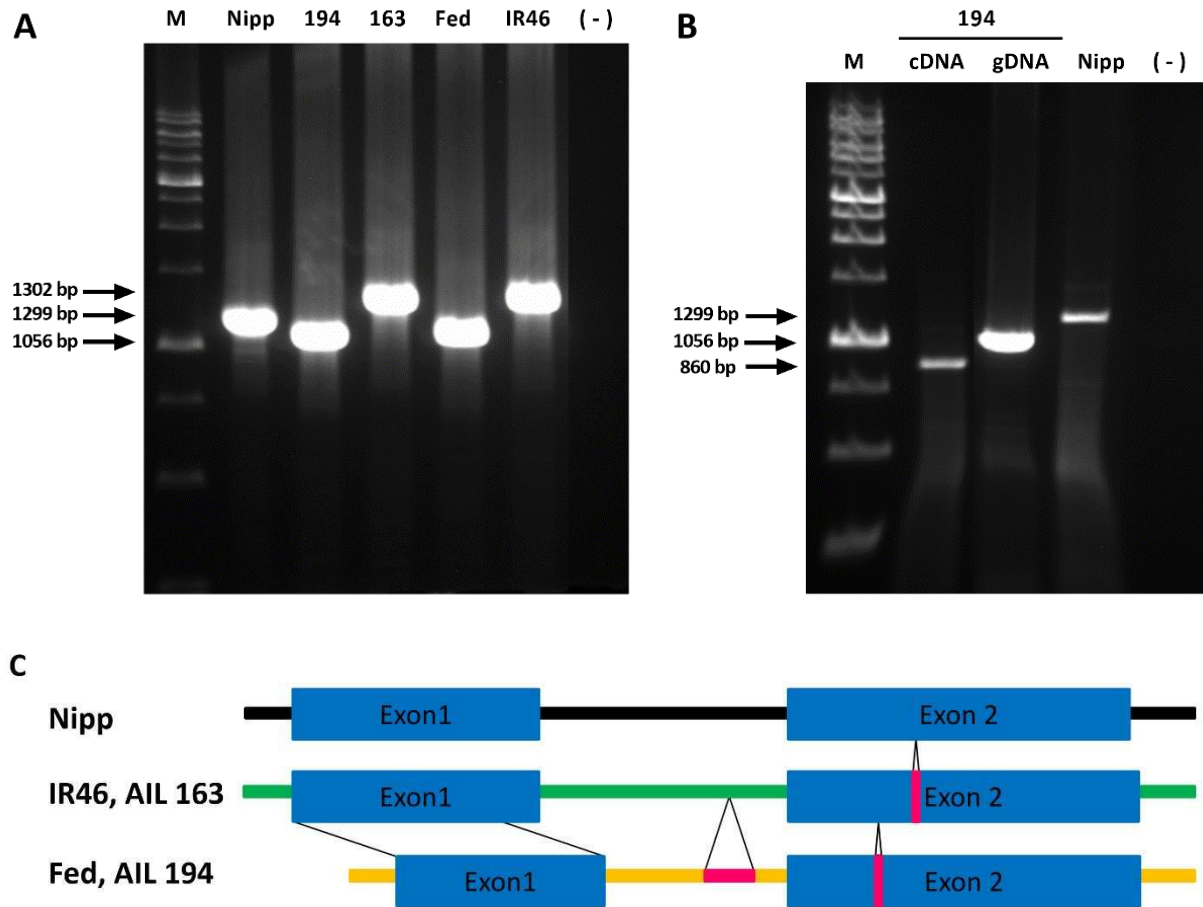


Figure 4.1. *OsMrBTB2* varies among MAGIC resistant and susceptible lines. **A.** PCR products of the complete coding sequence of *OsMrBTB2* from Nipponbare (Nipp), MAGIC AILs 194 and 163, and MAGIC founders Fedearroz 50 (Fed) and IR4630-22-2-5-1-3 (IR46). PCR product sizes were: 1,299 bp (Nipp), 1,302 bp (resistant lines 163 and IR46), and 1,056 bp (susceptible lines 194 and Fed). **B.** PCR products of the complete coding sequence of *OsMrBTB2* from cDNA and gDNA of MAGIC AIL 194, and gDNA of Nipp. PCR product sizes were: 1,299 bp (Nipp), 1,056 bp (gDNA of AIL 194), and 860 bp (cDNA of AIL 194). **C.** Gene model of *OsMrBTB2* in Nipp, resistant lines (IR46, AIL 163) and susceptible lines (Fed, AIL 194). Exons are indicated in blue are indicated, insertions are shown in pink.

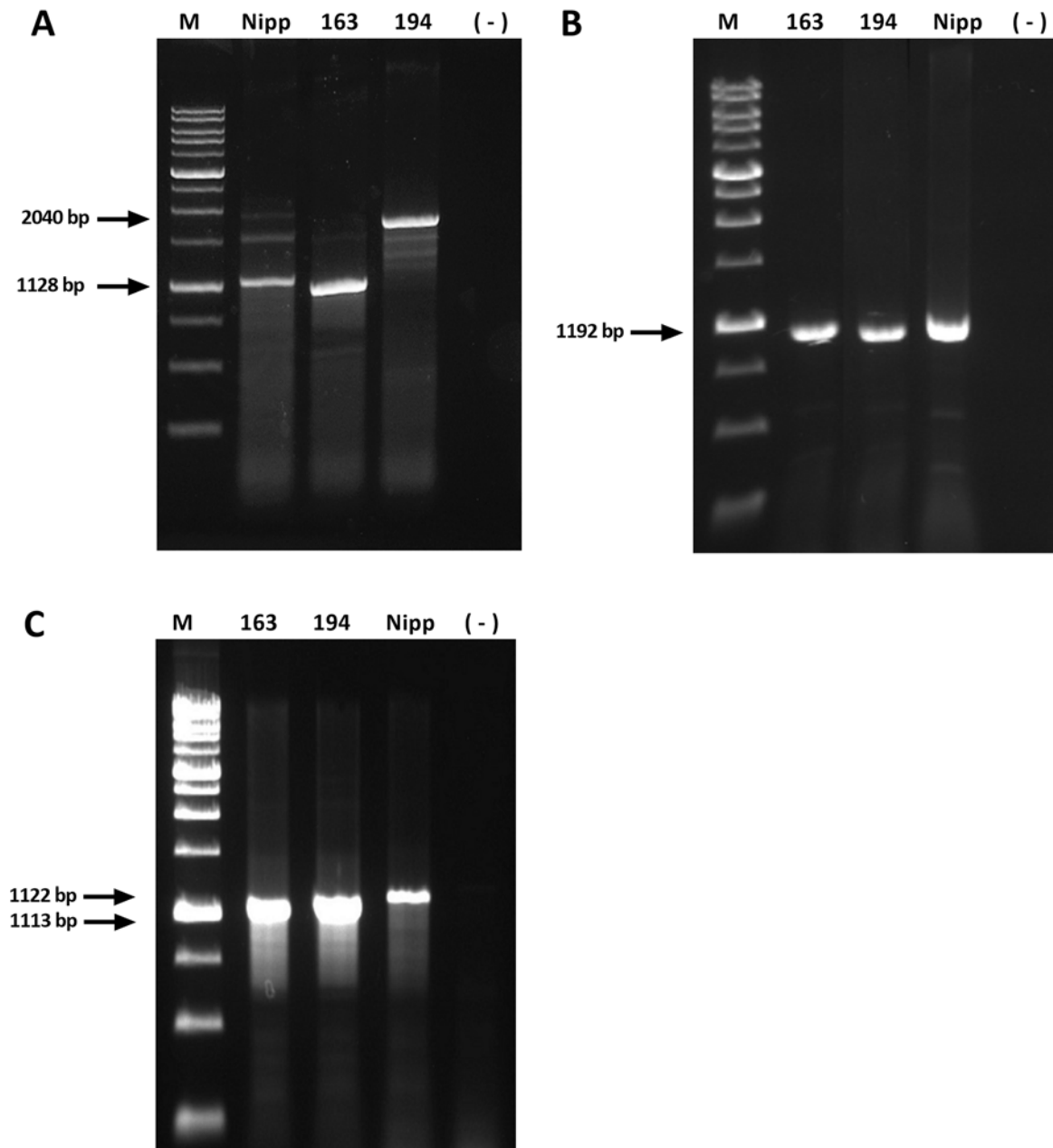


Figure 4.2. *MATH-BTB* genes vary in size among MAGIC resistant and susceptible AILs. **A.** PCR products of the complete coding sequence of *OsMBTB6* from Nipponbare (Nipp), MAGIC AILs 163 and 194. PCR product sizes were: 1,128 bp (Nipp and resistant AIL 163) and 2,040 bp (susceptible AIL 194). **B.** PCR products of the complete coding sequence and 100bp upstream of *OsMBTB7* from AILs 163 and 194, and Nipp. A product of 1,192 bp was obtained in all three varieties. **C.** PCR products of the complete coding sequence of *OsMBTB8* from AILs 163 and 194, and Nipp. PCR product sizes were: 1,122 bp (Nipp and susceptible AIL 194) and 1,113 bp (resistant AIL 163).

		MATH domain
OsMrBTB2_Nippon	1	MASSSTSSRCLTASVTGTHNLEVTSYSLLEGMGVGKFSSTTFSVAGYDWNLRFPDGIT
OsMrBTB2_IR46	1	MASSSTSSRCLTASVTGTHNLEVTSYSLLEGMGVGKFSSTTFSVAGYDWNLRFPDGIT
OsMrBTB2_163	1	MASSSTSSRCLTASVTGTHNLEVTSYSLLEGMGVGKFSSTTFSVAGYDWNLRFPDGIT
OsMrBTB2_Fed	1	MASSSTSSRCLTASVTGTHNLEVTSYSLLEGMGVGKFSSTTFSVAGYDWNLRFPDGIT
OsMrBTB2_194	1	MASSSTSSRCLTASVTGTHNLEVTSYSLLEGMGVGKFSSTTFSVAGYDWNLRFPDGIT
<hr/>		
OsMrBTB2_Nippon	61	DNDRKEGYGAIVMLASVYQISIAKEHAIRRI RFTGNDSFKIECSLTVISESRAEDVSTIP
OsMrBTB2_IR46	61	DNDRKEGYGAIVMLASVYQN SIAKEHAIRRI RFTGNDSFKIECSLTVISESRAEDVSTIP
OsMrBTB2_163	61	DNDRKEGYGAIVMLASVYQN SIAKEHAIRRI RFTGNDSFKIECSLTVISESRAEDVSTIP
OsMrBTB2_Fed	61	D-----EHAIGRI RFTGNDSFKIECSLTVISESRAEDVSTIP
OsMrBTB2_194	61	D-----EHAIGRI RFTGNDSFKIECSLTVISESRAEDVSTIP
		* * *
<hr/>		
		BTB domain
OsMrBTB2_Nippon	121	VPPSNLHQHLAGMLHGVEIADVEFSVG-GE PFRAHACVLAARSPVFRAELLGPAAARS IK
OsMrBTB2_IR46	121	VPPSNLHQHLAGMLHGVEIADVEFSVG-GE PFRAHACVLAARSPVFRAELLGPAAARS IK
OsMrBTB2_163	121	VPPSNLHQHLAGMLHGVEIADVEFSVG-GE PFRAHACVLAARSPVFRAELLGPAAARS IK
OsMrBTB2_Fed	98	VPPSNLHQHLAGMLHGGEIADVEFSVGG GE PFRAHACVLAARSPVFRAELLGPAAARS IK
OsMrBTB2_194	98	VPPSNLHQHLAGMLHGG E IADVEFSVGG GE PFRAHACVLAARSPVFRAELLGPAAARS IK
		* *
<hr/>		
OsMrBTB2_Nippon	180	IDD-DDDMEPATFKALLHFIIYTDHLPNDSGF GKDAAMQRRLLV AADRYGVDR LRAMCGVK
OsMrBTB2_IR46	180	IDDDDDMEPATFKALLHFIIYTDHLPNDSGF GKDAAMQRRLLV AADRYGVDR LRAMCGVK
OsMrBTB2_163	180	IDDDDDMEPATFKALLHFIIYTDHLPNDSGF GKDAAMQRRLLV AADRYGVDR LRAMCGVK
OsMrBTB2_Fed	158	IDD-DDDMEPATFKALLHFIIYTDHLPNDSGF GKDAAMQRRLLV AADRYGVDR LRAMCEAK
OsMrBTB2_194	158	IDD-DDDMEPATFKALLHFIIYTDHLPNDSGF GKDAAMQRRLLV AADRYGVDR LRAMCEAK
		* **
<hr/>		
OsMrBTB2_Nippon	239	LYKS SVSGTVVD SLFAEKHHCAQLKDACL GFMASPNVLGVVRKT DGF KRLVEGC PWVLK
OsMrBTB2_IR46	240	LYKS SVSGTVVD SLFAEKHHCAQLKDACL GFMASPNVLGVVRKT DGF KRLVEGC PWVLK
OsMrBTB2_163	240	LYKS SVSGTVVD SLFAEKHHCAQLKDACL GFMASPNVLGVVRKT DGF KRLVEGC PWVLK
OsMrBTB2_Fed	217	LYES VSGTVVD SLFAEKHHCAQLKDACL GFMASPNVL DVVRKT DGF MRLVEGC PWVLK
OsMrBTB2_194	217	LYES VSGTVVD SLFAEKHHCAQLKDACL GFMASPNVL DVVRKT DGF MRLVEGC PWVLK
		* * *
OsMrBTB2_Nippon	299	EILDKVPRF
OsMrBTB2_IR46	300	EILDKVPRF
OsMrBTB2_163	300	EILDKVPRF
OsMrBTB2_Fed	277	EILDKVPRF
OsMrBTB2_194	277	EILDKVPRF

		MATH domain	
OsMBTB6_Nipponb	1	MGNSLF	SMASSTASPSDGRSPRLPETLSRCVTASVAAAHNFEVTRYSLLAGVGAGEFVTS
OsMBTB6_163	1	MGNSLF	SMASSTASPSDGRSPRLPETLSRCVTASVAAAHNFEVTRYSLLAGVGAGEFVTS
OsMBTB6_194	1	MGNSLF	SMASSTASPSDGRSPRLPETLSRCVTASVAAAHNFEVTRYSLLAGVGAGEFVTS
OsMBTB6_Nipponb	61	GTFSID	DGHNWNIQVYPDRWKQEMNAGYVSVFLCLCGGATGVRKYTL
OsMBTB6_163	61	GTFSID	DGHNWNIQVYPDRWKQEMNAGYVSVFLCLCGGATGVRKYTL
OsMBTB6_194	61	GTFSVD	DGHNWNIQVYPDGWKQEMNAGYVSVFLCLCGGATGVRKYTL
		*	*
OsMBTB6_Nipponb	121	LTHRFD	TVGAFWGFPRFMERPRLRQWLLRRGPGGGDDCVTFRCSLTVIREPRTEGVAAVA
OsMBTB6_163	121	LTHRFD	TVGAFWGFPRFMERPRLRQWLLRRGPGGGDDCVTFRCSLTVIREPRTEGVAAVA
OsMBTB6_194	121	LTHRFD	TVGAFWGFPRFMERPRLRQWLLRRGPGGGDDCVTFRCSLTVIREPRTEGVAAVA
		BTB domain	
OsMBTB6_Nipponb	181	VPPSDM	RRRHMANMLRGGDGADVVLVRDQPFRAHRCVLAARSPVFRAELFGGGHMRERRT
OsMBTB6_163	181	VPPSDM	RRRHMANMLRGGDGADVVLVRDQPFRAHRCVLAARSPVFRAELFGGGHMRERRT
OsMBTB6_194	181	VPPSDM	RRRHMANMLRGGDGADVVLVRDQPFRAHRCVLAARSPVFRAELFGGGHMRERRT
OsMBTB6_Nipponb	241	SCVVVD	DMEPSIFSAFLHFIYTD
OsMBTB6_163	241	SCVVVD	DMEPSIFSAFLHFIYTD
OsMBTB6_194	241	SCVVVD	DMEPSIFSAFLHFIYTD
OsMBTB6_Nipponb	301	EEKLCR	GIDVQTVATTLLALAEQHQ
OsMBTB6_163	301	EEKLCR	GIDVQTVATTLLALAEQHQ
OsMBTB6_194	301	EEKLCR	GIDVQTVATTLLALAEQHQ
OsMBTB6_Nipponb	361	IMVDIL	DKVASVMSK
OsMBTB6_163	361	IMVDIL	DKVASVMSK
OsMBTB6_194	361	IMVDIL	DKVASVMSK

Figure 4.4. Deduced amino acid sequence of OsMBTB6 from MAGIC AILs compared to Nipponbare. Solid black line above peptide sequences indicate the MATH and BTB domains. Amino acid differences between the resistant (163) and the susceptible (194) AILs are shaded and represented by a (*).

			MATH domain
OsMBTB7_Nipponb	1	MGDHRDPAFPAAAGGCRLPKTSSVSVTESVTAVHDFKVTGYSLIEGLGIGRYVSSSTFTV	
OsMBTB7_163	1	MGDHRDPAFPAAAGGCRLPKTSSVSVTESVTAVHDFKVTGYSLIEGLGIGRYVSSSTFTV	
OsMBTB7_194	1	MGDHRDPAFPAAAGGCRLPKTSSVSVTESVTAVHDFKVTGYSLIEGLGIGRYVSSSTFTV	
OsMBTB7_Nipponb	61	GGVDWAVRFYPDGSTVTCLGNASAFLYYCGREKEVTRFTLNLLGKDGKLSQVTNSYMKH	
OsMBTB7_163	61	GGVDWAVRFYPDGSTVTCLGNASAFLYYCGREKEVTRFTLNLLGKDGKLSQVTNSYMKH	
OsMBTB7_194	61	GGVDWAVRFYPDGSTVTCLGNASAFLYYCGREKEVTRFTLNLLGKDGKLSQVTNSYMKH	
OsMBTB7_Nipponb	121	TFSPASDNWGFIFKFAEKSKLQSSPFLHNDCLTIRCLLTVVRESHTKDVEVNSVVVPPSNL	
OsMBTB7_163	121	TFSPASDNWGFIFKFAEKSKLQSSPFLHNDCLTIRCLLTVVRESHTKDVEVNSVVVPPSNL	
OsMBTB7_194	121	TFSPASDNWGFIFKFAEKSKLQSSPFLHNDCLTIRCLLTVVRESHTKDVEVNSVVVPPSNL	
			BTB domain
OsMBTB7_Nipponb	181	HTDFENMLQDGE GSDVTF TVGGQEFRAH K CVLAFRSPVFKAELFGPMKENG TQCIKIDDM	
OsMBTB7_163	181	HTDFENMLQDGE GSDVTF TVGGQEFRAH K CVLAFRSPVFKAELFGPMKENG TQCIKIDDM	
OsMBTB7_194	181	HTDFENMLQDGE GSDVTF TVGGQEFRAH R CVLAFRSPVFKAELFGPMKENG TQCIKIDDM	*
OsMBTB7_Nipponb	241	EPEVFEALLHFIYTDRLPDSCRDGKAAAMQHLLVAADRYGVDRLRLICERRLSETIDVET	
OsMBTB7_163	241	EPEVFEALLHFIYTDRLPDSCRDGKAAAMQHLLVAADRYGVDRLRLICERRLSETIDVET	
OsMBTB7_194	241	EPEVFEALLHFIYTDRLPDSCRDGKAAAMQHLLVAADRYGVDRLRLICERRLSETIDVET	
OsMBTB7_Nipponb	301	VATTLVLAEQHHC SQLRQACIGFVASPNMLGPVIESDGFKHLVESCPLIMKEILSKVSHI	
OsMBTB7_163	301	VATTLVLAEQHHC SQLRQACIGFVASPNMLGPVIESDGFKHLVESCPLIMKEILSKVSHI	
OsMBTB7_194	301	VATTLVLAEQHHC SQLRQACIGFVASPNMLGPVIESDGFKHLVESCPLIMKEILSKVSHI	
OsMBTB7_Nipponb	361	WIDKSC	
OsMBTB7_163	361	WIDKSC	
OsMBTB7_194	361	WIDKSC	

Figure 4.5. Deduced amino acid sequence of OsMBTB7 from MAGIC AILs compared to Nipponbare. Solid black line above peptide sequences indicate the MATH and BTB domains. Amino acid differences between the resistant (163) and the susceptible (194) AILs are shaded and represented by a (*).

			MATH domain
OsMBTB8_Nipponb	1	MLTSSAARTSSRSVWEGIT	GTGTHDFEVVGYSLMDGFGAGRHVCSGDFS
OsMBTB8_163	1	MLTSSAARTSSRSVWEGIT	WTGTHDFEVVGYSLMDGFGAGRHVCSGDFS
OsMBTB8_194	1	MLTSSAARTSSRSVWEGIT	GTGTHDFEVVGYSLMDGFGAGRHVCSGDFS
			*
OsMBTB8_Nipponb	61	GLDQDSAGYASACLAYRGKERLVRAKYSLSLVARDGRASPLAGD	TLRSHYFTPTSR
OsMBTB8_163	61	GLDQDSAGYASACLAYRGKERFVRAKYSLSLVARDGRASPLAGD	TLRSHYFTPTSR
OsMBTB8_194	61	GLDQDSAGYASACLAYRGKERFVRAKYSLSLVARDGRASPLAGD	TLRSHYFTPTSR
			.
OsMBTB8_Nipponb	121	LKFVEKSNLSSSPSSSSYSCLDDDTLTIRC	VTVVTGPRVSVAPAKERGPRVTVP
OsMBTB8_163	121	LKFVEKSKLSSSPSSSSYSCLDDDTLTIRC	VV---TGPRVESVAPAKERGPRVTVP
OsMBTB8_194	121	LKFVEKSKLSSSPSSSSYSCLDDDTLTIRC	VTVVTGPRVESVAPAKERGPRVTVP
			.
			BTB domain
OsMBTB8_Nipponb	181	HEHLARMLRDGRGSDVAFRVGGRVLAHRCVLAARSPVFDAELLGPM	METTAPCIEIHGV
OsMBTB8_163	178	HEHLARMLRDGRGSDLAFRVGGVLAHRCVLAARSPVFDAELLGPM	METTAPCIEIHGV
OsMBTB8_194	181	HEHLARMLRDGRGSDVAFRVGGRVLAHRCVLAARSPVFDAELLGPM	METTAPCIEIHGV
			*
OsMBTB8_Nipponb	241	EPAAFEALLRFVYTDWPLAGVDVAATVRLLSAADRYGLERLR	LMCEEKLEHGEDVDNAA
OsMBTB8_163	238	EPAAFEALLRFVYTDWPLAGVDVAATVRLLSAADRYGLERLR	LMCEEKLEHGEDVDNAA
OsMBTB8_194	241	EPAAFEALLRFVYTDWPLAGVDVAATVRLLSAADRYGLERLR	LMCEEKLEHGEDVDNAA
			.
OsMBTB8_Nipponb	301	DVLAMAEELHHCSQLRDACVAFIASPSTLGPVLASSGFEDL	IMATGASVTKEILHKVSESW
OsMBTB8_163	298	DVLAMAEELHHCSQLRDACVAFIASPSTLGPVLASSGFEDL	IMATGASVTKEILHKVSESW
OsMBTB8_194	301	DVLAMAEELHHCSQLRDACVAFIASPSTLGPVLASSGFEDL	IMATGASVTKEILHKVSESW
			.
OsMBTB8_Nipponb	361	SGPGNRNNSKRK	
OsMBTB8_163	358	SGPGNRNNSKRK	
OsMBTB8_194	361	SGPGNRNNSKRK	

Figure 4.6. Deduced amino acid sequence of OsMBTB8 from MAGIC AILs compared to Nipponbare. Solid black line above peptide sequences indicate the MATH and BTB domains. Amino acid differences between the resistant (163) and the susceptible (194) AILs are shaded and represented by a (*). Amino acid differences between both MAGIC AILs and Nipponbare are represented by a (·).

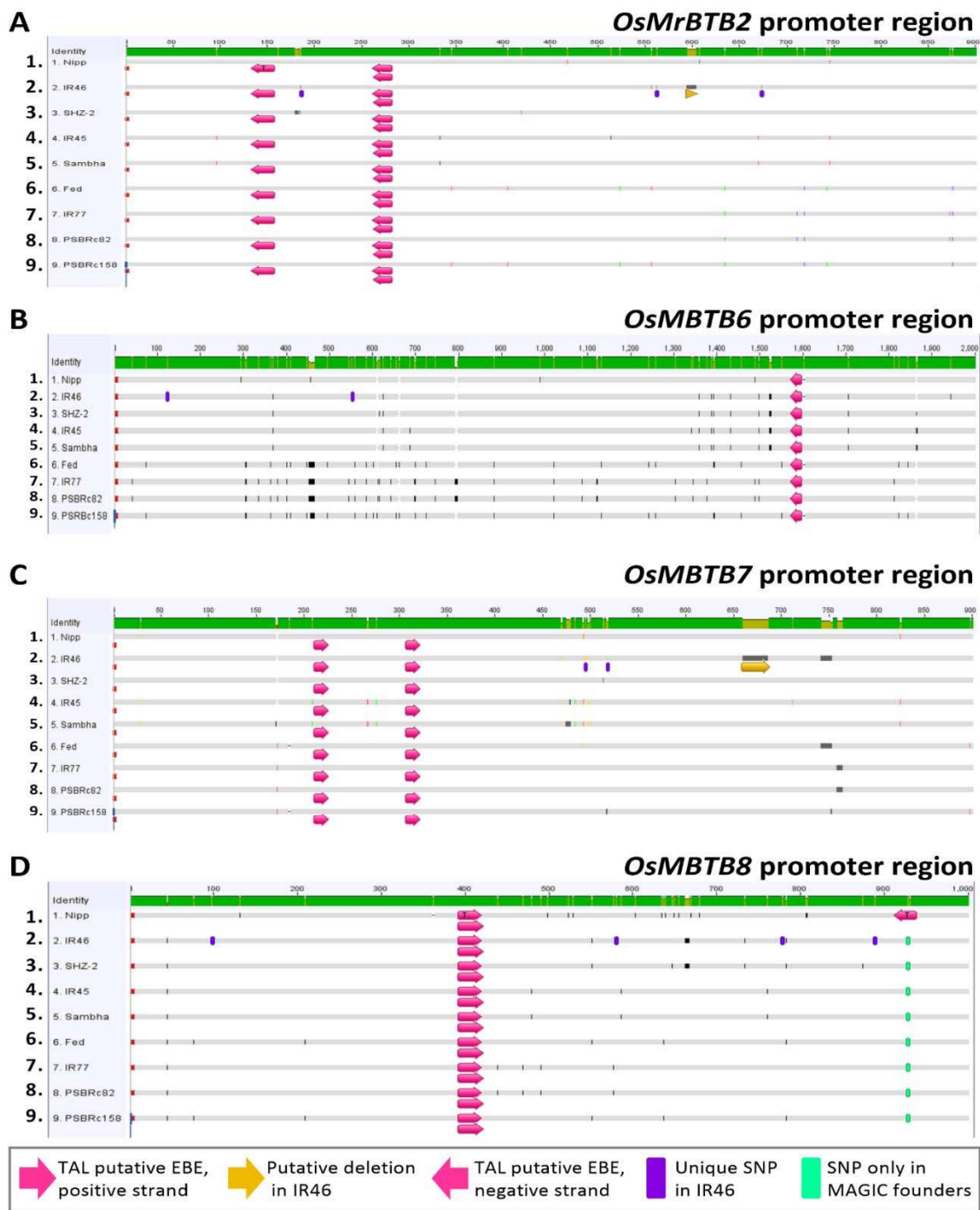


Figure 4.7. Predicted EBEs for *X. oryzae* TAL effectors in *MATH-BTB* promoter regions. **A.** 900 bp region upstream of transcription start site (TSS) of *OsMrBTB2*. **B.** 2 Kb region upstream of TSS of *OsMBTB6*. **C.** 900 bp region upstream of TSS of *OsMrBTB7*. **D.** 1 Kb region upstream of TSS of *OsMrBTB8*. Rice promoter sequences follow this order: 1. Nipponbare (Nipp); 2. IR4630-22-2-5-1-3 (IR46); 3. Shan-Huang Zhan-2 (SHZ-2); 4. IR45427-2B-2-2B-1-1 (IR45); 5. Sambha Mahsuri + Sub1 (Sambha); 6. Fedearroz 50 (Fed); 7. IR77298-14-1-2-10 (IR77); 8. PSBRc82 and 9. PSBRc 158.

4.6 TABLES

Table 4.1. Summary of criteria for selection of *MATH-BTB* genes.

Locus†	Gene	Position		SNPs			CMR		Predicted EBE targeted by <i>X. oryzae</i> TAL						
		Start	End	SNPs	Feature	Effect	CRM4	CRM5	<i>Xoc</i> Africa	<i>Xoc</i> Asia	<i>Xoo</i> Africa	<i>Xoo</i> Asia	Total EBE	Total strains	Total TAL
Os04g53390	<i>OsMrBTB2</i>	31,801,934	31,803,232	3	Exon	Non synonymous variant	Both	Both			1	3	3	4	5
Os04g53400	<i>OsMBTB6</i>	31,809,708	31,810,835									11	1	11	11
Os04g53410	<i>OsMBTB7</i>	31,812,018	31,813,118	1	Exon	Synonymous variant			2	2			2	4	8
Os04g53430	<i>OsMBTB8</i>	31,817,625	31,818,746				Both		2	1		7	3	10	10

† Prefix “LOC_” is omitted from the locus ID.

Table 4.2. Primers used for amplification and sequencing of *MATH-BTB* genes in qXO-4-1.

Primer name	Locus†	Gene	Sequence (5' - 3')	Sense	Tm (°C)	Purpose	Primer location	Expected product (bp)
53390b_Fwd	Os04g53390	<i>OsMrBTB2</i>	<u>CACCATGGCTAGCAGTTCGACATCGTCG</u>	Fwd	64.1	cloning	5' end	1,299
53390b_Rev			TCAGAACTAGGCACCTTGCTAAAATCTC	Rev	57.8	cloning	3'end	
P01	Os04g53390	<i>OsMrBTB2</i>	GAAGTCCACATCCGCGATCTC	Rev	57.7	sequencing		
53400b_Fwd	Os04g53400	<i>OsMBTB6</i>	<u>CACCATGGGCAACAGCTTGTTCTCCATG</u>	Fwd	63.5	cloning	5' end	1,128
53400b_Rev			TTACTTGCTCATGACGCTGGCAACCTTG	Rev	62.8	cloning	3'end	
P02	Os04g53400	<i>OsMBTB6</i>	GAGCTTGACGCATCGGTTTCGAC	Fwd	60.5	sequencing		
P08	Os04g53400	<i>OsMBTB6</i>	GTCGCCGCCCTCAGCATGTTC	Rev	65.2	sequencing		
53410_Fwd	Os04g53410	<i>OsMBTB7</i>	<u>CACCTTGATTGTGATGAAGTCATGGATATC</u>	Fwd	60.2	cloning	100bp upstream 5' end	1,192
53410_Rev			TCAGCAAGACTTGTCATCCAAATATGTG	Rev	57.5	cloning	3'end	
53430_Fwd	Os04g53430	<i>OsMBTB8</i>	<u>CACCATGTTGACTTCATCGGCTGC</u>	Fwd	60.6	cloning	5' end	1,122
53430_Rev			TCACCTTCTTTTGCTTGAATTATTCTGTTACCAGG	Rev	59.2	cloning	3'end	

† Prefix "LOC_" is omitted from the locus ID.

Table 4.3. Predicted EBEs in *MATH-BTB* promoter regions of qXO-4-1 for *X. oryzae* TAL effectors. MSU7 rice reference genome annotation was used for the predictions. Score was calculated using Talvez 3.2 (Perez-Quintero et al., 2013). Rank refers to the order of the scores. Shaded row indicate different EBEs for the same promoter.

Locus†	Gene	Pathovar	Strain	Origin	TAL	Score	Rank	EBE		
								Strand	Sequence	Distance to TSS
Os04g53390	<i>OsMrBTB2</i>	<i>Xoo</i>	PXO563	Asian	Tal5a	12.29	80	-	TGCTTTCCCCCCTCCCAT	-607
		<i>Xoo</i>	PXO71	Asian	Tal5a	12.29	80	-	TGCTTTCCCCCCTCCCAT	-621
		<i>Xoo</i>	PXO211	Asian	Tal5	12.38	104	-	TGCTTTCCCCCCTCCCAT	-621
		<i>Xoo</i>	MAI134	African	TalB	11.76	158	-	TCACCGGCCGTCCTCGCCTCCT	-621
		<i>Xoo</i>	PXO71	Asian	Tal5b	10.35	429	-	TGCTTTCCCCCCTCCCA	-745
Os04g53400	<i>OsMBTB6</i>	<i>Xoo</i>	KACC10331	Asian	YP_201652.1	10.24	370	-	TATATGTACAGAGGTATACAG	-607
		<i>Xoo</i>	MAFF311018	Asian	YP_451894.1	10.24	370	-	TATATGTACAGAGGTATACAG	-607
		<i>Xoo</i>	PXO145	Asian	Tal7a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO211	Asian	Tal2a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO236	Asian	Tal2a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO282	Asian	Tal7a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO524	Asian	Tal6a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO563	Asian	Tal6a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO602	Asian	Tal6a	10.24	370	-	TATATGTACAGAGGTATACAG	-65
		<i>Xoo</i>	PXO83	Asian	TalAG4	10.24	370	-	TATATGTACAGAGGTATACAG	-405
		<i>Xoo</i>	PXO86	Asian	Tal2a	10.24	370	-	TATATGTACAGAGGTATACAG	-405

Continuation Table 4.3.

Locus†	Gene	Pathovar	Strain	Origin	TAL	Score	Rank	EBE		
								Strand	Sequence	Distance to TSS
Os04g53410	<i>OsMBTB7</i>	<i>Xoc</i>	BLS303	Asian	Tal11e	9.70	384	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	BXORI	Asian	Tal11e	9.70	384	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	MAI10	African	Tal8d	9.70	384	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	BAI 5	African	Tal8d	9.70	384	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	BLS303	Asian	Tal11e	9.70	385	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	BXORI	Asian	Tal11e	9.70	385	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	MAI10	African	Tal8d	9.70	385	+	TCTCAGCCCTGAC	-405
		<i>Xoc</i>	BAI 5	African	Tal8d	9.70	385	+	TCTCAGCCCTGAC	-405
Os04g53430	<i>OsMBTB8</i>	<i>Xoc</i>	MAI10	African	Tal6b	12.30	47	+	TGCAGTCTATCGACGAGGCTCTCTCT	-405
		<i>Xoc</i>	BXORI	Asian	Tal9c	10.32	254	+	TGCAGTCTATCGACGAGGCTCTCT	-689
		<i>Xoc</i>	BAI 5	African	Tal6b	10.26	292	+	TGCAGTCTATCGACGAGGCTCTCT	-689
		<i>Xoo</i>	PXO236	Asian	Tal1	10.57	295	-	TCTAGCAACAAAGACACTTCTTT	-689
		<i>Xoo</i>	PXO524	Asian	Tal7	10.57	295	-	TCTAGCAACAAAGACACTTCTTT	-689
		<i>Xoo</i>	MAFF311018	Asian	YP_453043.1	10.51	304	-	TCTAGCAACAAAGACACTTCTTT	-593
		<i>Xoo</i>	PXO282	Asian	Tal8	10.51	304	-	TCTAGCAACAAAGACACTTCTTT	-593
		<i>Xoo</i>	PXO563	Asian	Tal7	10.51	304	-	TCTAGCAACAAAGACACTTCTTT	-593
		<i>Xoo</i>	PXO602	Asian	Tal7	10.51	304	-	TCTAGCAACAAAGACACTTCTTT	-593
		<i>Xoo</i>	PXO71	Asian	Tal7	10.51	304	-	TCTAGCAACAAAGACACTTCTTT	-621

† Prefix "LOC_" is omitted from the locus ID.

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CHAPTER 5

CONCLUSION

Durable and broad-spectrum resistance sources against BB and BLS of rice are critical to reduce losses and meet the production levels needed for feeding the growing global population. This dissertation exploits the increased diversity in a rice indica MAGIC population to identify novel, broad-spectrum and durable sources of resistance to BB and BLS.

In Chapter 2, multiple *Xoo* and *Xoc* strains were used to screen early and advanced generations of MAGIC AILs under greenhouse and field conditions. A particular focus was placed on strains of *Xoo* and *Xoc* strains from Sub-Saharan Africa, due to the lack of effective BB and BLS resistance in currently cultivated germplasm in this region. A total of 11 BSR, three pathovar-specific, and 37 strain-specific QTL were identified. Moreover, single alleles associated with resistance and susceptibility in three BSR QTL were detected. These findings will enable a better understanding of how the affected genes contribute to resistance or susceptibility. Unanswered questions remain, such as whether the same or different genes within each QTL are involved in the defense response to each of the *X. oryzae* pathovars, if there are QTL interactions that favor the defense response, and how these QTL are transcriptionally modulated. A valuable addition for the ultimate use of these resistance sources in breeding programs, would be the assessment of the effectiveness of these QTL to other rice pathogens, such as *Magnaporthe oryzae* and *Rhizoctonia solani*.

In Chapter 3, 14 disease resistance QTL were analyzed to identify promoters with multiple CRMs, promoters with putative targets for multiple *X. oryzae* strains, and SNP markers associated with resistance to *X. oryzae* strains. Only four loci met the three parameters, an AP2 domain containing protein (LOC_Os02g42585), a zinc finger C3HC4 type domain containing protein (LOC_Os02g42690), a putative kinase (LOC_Os11g44430), and a putative thaumatin (LOC_Os11g47944). In addition, 100 more candidate genes for which at least two of these criteria were met were selected. Among these, 77 loci had multiple EBE and multiple CRM in their promoters, suggesting potential convergence points of PTI and ETI. MAGIC founders were evaluated for CRM polymorphisms between resistant and susceptible donors, identifying eight candidate loci on BSR QTL qXO-2-1, qXO-4-1, qXO-5-1 and qXO-11-2. However, only two of these loci were putative targets of at least ten different *X. oryzae* strains. Essential for the validation of these results is the evaluation of CRM structure in the MAGIC AILs, as well as the confirmation of detected EBE as putative targets. Expression analyses of candidate genes is also necessary to confirm or rule out identified candidates.

In Chapter 4, a cluster of four *MATH-BTB* genes in qXO-4-1 was analyzed for polymorphisms between resistant and susceptible MAGIC lines. Structural variations and amino acid changes were identified in MATH and BTB domains of all genes among resistant and susceptible lines. Single residue changes can potentially affect these proteins' ability to dimerize or to interact with their substrates, thus altering the defense response. Additionally, all the promoters of the *MATH-BTB* genes are predicted targets of at least three different *X. oryzae* strains. *OsMrBTB2* and *OsMBTB8* were pinpointed as promising candidates for further validation. The *OsMBTB8* promoter is putatively targeted by both *Xoc* and *Xoo* strains, and it can also be a

new example of an allele for the loss of susceptibility type of resistance. Future experiments should consider evaluating differential expression of *MATH-BTB* genes upon *X. oryzae* infection, and knock-out of *MATH-BTB* genes to assess their role in disease resistance. Also, sequencing promoters of resistant and susceptible MAGIC AILs to confirm polymorphisms; and *X. oryzae* inoculation with single TAL with subsequent gene expression analyses to reveal the association of *MATH-BTB* genes with disease resistance. Finally, protein-protein interaction experiments would reveal required substrates of the MATH-BTB proteins in qXO-4-1.

In Appendix A, an advanced generation of MAGIC AILs was screened for resistance to Tal7b, a virulence enhancing factor present in Asian *Xoo* strains. Unique disease resistance QTL to Tal7b were identified on chromosomes 8 and 12, *qtal7b-8* and *qtal7b-12-2*, respectively. A Tal7b gene target converge on *qtal7b-8*, suggesting that this QTL houses a minor yet significant susceptibility locus. Further sequencing of the MAGIC AILs promoters and gene expression studies during *X. oryzae* with Tal7b infection are required to validate these results.

Overall, the increased genetic diversity and recombination in the indica MAGIC population, allowed enhanced resolution for QTL mapping. This, together with novel prediction algorithms for prediction of BSR and putative targets of *X. oryzae* TAL effectors allowed the identification of putative targets important for rice – *X. oryzae* resistant and susceptible interactions. The use of MAGIC populations for the study of disease resistance can also expedite the understanding of the resistance and susceptibility mechanisms.

APPENDIX A

RESISTANCE AND SUSCEPTIBILITY QTL TO *Xanthomonas oryzae* pv. *oryzae* VIRULENCE EFFECTOR Tal7b IDENTIFIED IN A RICE MAGIC POPULATION⁴

OVERVIEW

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is the single most destructive bacterial disease of rice. The optimal agronomic practice to manage the disease is deployment of resistant varieties. However, effective and durable disease resistance for BB is a continuous challenge due to the pathogen's evolution and adaptation on cultivated varieties. Key to *Xoo* pathogenicity and virulence are Transcription Activator-Like (TAL) effectors, which activate expression of host susceptibility genes. TAL effectors differentially contribute to a strain's virulence, and some are essential to pathogen fitness. We hypothesize that effective and durable disease resistance is attainable by understanding the targets of important virulence factors. To test this hypothesis, we screened the indica Multi-Parent Advanced Generation Inter-Cross (MAGIC) population for resistance against *Xoo* strains PXO99^A carrying the empty vector control (EV) and PXO99^A carrying the virulence factor Tal7b (pHMI::tal7b). Genome-wide association and interval mapping analysis revealed 18 disease resistance QTL, nine specific to

⁴ Collaborative effort with these authors: Alejandra I. Huerta, Emily E. Delorean, Ana M. Bossa-Castro, Chitra Raghavan, Rene Corral, Hei Leung, Valérie Verdier, and Jan E. Leach. Author contributions: E.E.D., A.M.B.-C., and J.E.L. designed research; A.I.H., E.E.D., A.M.B.-C., performed research; A.I.H., E.E.D., A.M.B.-C., and J.E.L. analyzed data. A.M.B.-C. mentored E.E.D. during her master project, participated in research design, performed IM analyses, and analyzed data.

PXO99^A pHMI::*tal7b* and nine to PXO99^A pHMI::EV. The top ranking predicted gene target for Tal7b correlated to a QTL on chromosome 8, *qta7b-8*. Together, our data suggest that this Tal7b target is a disease susceptibility gene that contributes to *Xoo* fitness in rice, and that the resistance locus identified on chromosome 8 falls under the loss of susceptibility TAL effector-associated resistance mechanism. The diversity of putative Tal7b rice gene targets that are associated with resistance or susceptibility provides an interesting perspective on effector-triggered susceptibility, that of one effector targeting multiple small effect susceptibility genes, or quantitative susceptibility.

A.1. INTRODUCTION

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is the most devastating bacterial disease of rice (*Oryza sativa* L.). In the field, BB severity depends on host genotype, pathogen pressure and environmental conditions. Typical yield reductions for BB range between 20-50% (Ou 1985), but under heavy disease pressure and lack of disease resistance in deployed varieties, yield losses may reach up to 70% (Reddy et al. 1979; Mew & Misra 1994). The optimal agronomic practice to manage BB is deployment of resistant varieties. Historically, available resistance to manage BB has relied on major resistance (*R*) genes. Unfortunately, the efficacy of *R* genes is frequently lost over time due to the pathogen's adaptation to a genotype and the evolution of new pathogenic races. For instance, the widespread release of rice varieties carrying the *R* gene *Xa4* in the Philippines in the early 1970's drove a pathogen population shift, where *Xoo* strains avirulent to *Xa4* were displaced by strains virulent to *Xa4* (Quibod et al. 2016; Mew et al. 1992). Identifying new sources of resistance that are

effective and durable for BB is a challenge that needs to be met considering the potential negative impacts of increased global agricultural trade, and erratic changing climate patterns.

Collectively, effectors dictate bacterial virulence and pathogenicity. One strain or pathogen population may carry multiple effectors with redundant function and some populations can house highly variable effector repertoires (Leach et al. 2001). Some effectors significantly contribute to bacterial virulence, in addition to providing a selective advantage to the pathogen in the absence of a corresponding host target, while others contribute less or nothing at all (Bai et al. 2000; Cunnac et al. 2011). Moreover, research suggests that one effector may target more than one host gene (Hogenhout et al. 2009; Cox et al. 2017). Knowing the contribution of each effector to pathogen virulence and their multiple minor effect susceptibility gene targets can guide breeding strategies towards more durable resistance (Leach et al. 2001).

Key to *Xoo* virulence are Transcription Activator-Like (TAL) effectors (Liu et al. 2014; Yang & White 2004; Sugio et al. 2007). Many TAL effectors are virulence factors, inducing expression of host susceptibility (*S*) genes that enhance microbial fitness via a highly conserved central repeat region (CRR). CRRs consist of a variable number of 33-34 amino acid repeats that differ from each other in amino acid composition at positions 12-13, called the Repeat Variable Diresidues (RVD) (Moscou & Bogdanove 2009; Boch et al. 2009). RVDs mediate TAL effector DNA binding specificity to sequences in the target host gene promoter, termed the effector binding element (EBE). Three different types of TAL effector-associated resistance mechanisms have been described in rice: 1) Dominant non-transcriptional, including NLR resistance proteins which fall under the typical ligand receptor mechanism (Triplett et al. 2016; Schornack et al. 2004); 2) Dominant TAL effector-dependent resistance, activated when TAL effectors such as AvrXa27,

AvrXa10 and AvrXa23 bind the EBE of major *R* genes triggering a hypersensitive response (HR) (Zhang, Yin, and White 2015); and 3) Recessive resistance, commonly referred to as loss of susceptibility, which result from polymorphisms in the EBE of host *S* genes that inhibit TAL effector binding, and disable activation of virulence-enhancing genes (Huang et al. 2016; Hutin et al. 2015).

Functional and bioinformatics approaches have deciphered the specificity in which different amino acid pairs (RVD) bind the host DNA. Knowing the TAL effector code has allowed scientists to predict TAL effector gene targets, and thus, identify putative TAL effector-induced susceptibility or resistance genes. A number of useful bioinformatic tools have been developed that allow prediction of TAL targets: Talvez (Perez-Quintero et al. 2013), Storyteller (Perez-Quintero et al. 2013), TALgetter (Grau et al. 2013) and Target Finder (Doyle et al. 2012). Each of these programs predict TAL effector targets by scoring RVD sequences against plant genomes using RVD-nucleotide association frequencies from known TAL effector-target pairs using different algorithms and strategies for target prediction.

In a recent comparative genomic study, a total of 181 TAL effectors were identified from ten Philippine *Xoo* isolates that represented different Philippine races. Based on RVD compositions, these effectors were categorized into 30 TAL effector families (TEF) (Quibod et al. 2016). TEF correlated to TAL effector clustering, suggesting that TAL effectors within a TEF have similar functions and thus similar gene targets. However, function has only been characterized for nine of the 30 TEF, based on one or two representative TAL effectors for each family. One TAL family containing nine effectors that remains to be characterized in detail is TEF7 (Quibod et al. 2016). Within this family, one member, Tal7b, has been identified to play an incremental, but

significant role in bacterial virulence (Bai et al. 2000). Considering each *Xoo* strain may have anywhere between nine to 20 TAL effectors, their diversity and especially their conservation among strains raises the question '*why are TAL effectors conserved and what are their host targets?*'

Assuming *R* gene durability is linked to the relative importance of effectors to pathogen virulence, one potential strategy to select for long-lasting resistance in the field is to screen for sources of resistance that target important and highly conserved virulence effectors such as Tal7b (Vera Cruz et al. 2000; Leach et al. 2001). To this end, we took a two-pronged approach aimed at identifying new sources of resistance targeting this specific TAL effector. We used a Multi-parent Advance Generation Inter-Cross (MAGIC) population generated from eight elite parents from the indica subgroup of rice. The indica MAGIC is a powerful resource because it captures the genetic diversity of multiple parents, which have been recombined over several generations to create a population with large phenotypic diversity ideal for high-resolution trait mapping (Bandillo et al. 2013; Raghavan et al. 2017). We also exploited the deciphered TAL effector code to predict Tal7b susceptibility and resistance gene targets (Boch et al. 2009; Doyle et al. 2012; Perez-Quintero et al. 2013).

In this study, we report the identification of 18 disease resistance QTL for BB, six of which are unique to the strain harboring virulence effector Tal7b. Additionally, we identify Tal7b predicted gene targets near or within these loci. Our results suggest that Tal7b contributes to *Xoo* virulence by targeting multiple *S* genes in rice. At least one of the resistance loci identified in this study is predicted to harbor polymorphisms in or near the Tal7b gene target, and thus, disables activation of one of the multiple predicted *S* gene targets. Altogether, our data provides

an interesting and unexplored perspective on pathogen triggered susceptibility, that of small effect effector-induced susceptibility, or quantitative susceptibility.

A.2. RESULTS

Tal7b is a conserved TAL effector in Asian *Xoo* isolates

Previous work showed that Tal7b plays a minor, yet important, role to pathogen fitness and aggressiveness (Bai et al. 2000), and thus, it was selected as the ideal virulence factor to screen for resistance. The effector was cloned from *Xoo* strain PXO86 and sequenced. Our sequence analysis revealed that the CRR is composed of 18 modules, each with 34 amino acid repeats. The CRR was flanked by the characteristic TAL effector Type III Secretion System (TTSS) signal sequences and at the C-terminus by the nuclear localization sequences (NLS) and activation domain (AD) (Figure A.1a) (Boch et al., 2009, Moscou & Bogdanove, 2009). Our *tal7b* sequence matched the recently reported *tal7b* gene sequence of *Xoo* strain PXO86 (Booher et al. 2015).

Next, we used the Tal7b sequence (GenBank accession AJQ83546.1) as a query in a BLAST search for Tal7b homologues in all 135 sequenced strains of *Xoo* and *X. oryzae* pv. *oryzicola* (*Xoc*). The results of this search revealed that Tal7b was not present in any of the 110 publically available *X. oryzae* draft genomes or in any of the complete genomes of *Xoc*. Homologues of Tal7b were found in all complete genomes of Asian *Xoo* isolates but not in any of African origin. At least one copy of the effector was found in representatives of the ten different races present in the Philippine Archipelago (Quibod et al. 2016). Two copies of the gene were found in PXO99^A, the strain we used to screen the indica MAGIC population, , named *tal8a* and *tal7a*, as a consequence of a near perfect tandem duplication (Booher et al. 2015). A Tal7b variant with two additional

repeats in the CRR was also found in Japanese, Korean, and Philippine race 8 isolates, MAF3111018, KACC20331 and PXO211, respectively (Figure A.1b). Although they varied at the DNA level, sequence alignment of all Tal7b homologues indicate 100% similarity in RVD composition (Figure A.1b). These results indicate that Tal7b is a conserved TAL effector in Asian *Xoo* strains and suggest evolutionary selection for the function of this effector in bacterial fitness.

Indica MAGIC population segregates for resistance to *Xoo* PXO99^A pHMI::EV and PXO99^A pHMI::tal7b

At the eight selfed generation, a subset of 330 advanced intercross lines (AILs) and founders of the indica MAGIC population were screened for resistance to PXO99^A carrying the empty vector (EV) and PXO99^A pHMI::tal7b (Figure A.2, Appendix B.2, Table S.A.1.). The responses to both strains were measured as lesion length (LL). Longer lesion lengths were observed on AILs challenged with PXO99^A pHMI::tal7b compared to those inoculated with PXO99^A pHMI::EV (Figure A.2; Appendix B.2, Table S.A.2). Variance of lesion lengths caused by PXO99^A pHMI::EV and PXO99^A pHMI::tal7b were significantly different (Tukey adjusted *P*-value < 0.001), indicating potential *S* and *R* gene targets responsive to Tal7b in the indica MAGIC population (Figure A.2; Appendix B.2, Table S.A.3). Although the variance of interaction of AILs by strain was not significant (*P*-value = 0.88), the t-test comparing strain LS-Means on individual AILs showed 63 lines with significantly different responses to both strains, nine with Tukey adjusted *P*-value < 0.001, and 54 with *P*-values of < 0.05 (Figure A.2b). The overall average lesion length calculated for PXO99^A pHMI::EV was 13.7 cm, compared to 17.1 cm for PXO99^A pHMI::tal7b (Appendix B.2, Table S.A.2). Longer lesion lengths were observed on 96 AILs compared to the founders. These data confirm that Tal7b is indeed a virulence factor that

contributes to *Xoo* virulence and further suggest that its contribution is incremental yet significant.

Of the eight founders used to generate the MAGIC population, none displayed a strong resistance phenotype (LL < 5 cm) to either strain (Figures A.2c, A.2d; Appendix B.2, Table S.A.4). However, 24 and 32 of the AILs screened were more resistant to PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*, than the most resistant parent for each treatment, Samba Mahsuri-*sub1* (LL = 9.8 cm) and PSBRc158 (LL = 11.5 cm), respectively. At the opposite extreme, one and 96 AILs were found to be more susceptible, than the most susceptible parent IR4527-2B-2-2B-1-1, to PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*, respectively (Figures A.2c, A.2d). The normal distribution and continuous variation observed in the phenotypic response of AIL screened to PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*, in conjunction with the transgressive segregation observed for both strains, indicate that this MAGIC population segregates for resistance and susceptibility (Figure A.2). Moreover, the lack of strong resistance suggests that these traits are controlled by multiple small effect resistance and susceptibility loci.

Marker assisted analyses identify loci associated with resistance to *Xoo* PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*

Genome-wide association studies (GWAS) and interval mapping (IM) analyses were used to map resistance and susceptibility loci targeting one important virulence factor, *Tal7b*, in the indica MAGIC population. GWAS revealed significantly associated SNP (P -value ≤ 0.001) on chromosomes 5 and 11 for PXO99^A pHMI::EV and on chromosomes 5, 8, 11 and 12 for PXO99^A pHMI::*tal7b* (Figure A.3; Appendix B.2, Tables S.A.5, and S.A.6). For PXO99^A pHMI::EV, 43

significantly associated SNP markers were detected by GWAS, with the major cluster (33 SNP) located on chromosome 5 (Appendix B.2, Table S.A.5). For PXO99^A pHMI::*tal7b*, 29 significantly associated SNP markers were identified, also with a major cluster on chromosome 5 (Appendix B.2, Table S.A.6).

IM analyses identified a total of 18 QTL implicated in disease resistance to both strains. Nine QTL, named qPXO99^A, were detected in response to PXO99^A pHMI::EV on chromosomes 1, 5, 7, 8, 10, 11 and 12 (Appendix B.2, Figure S.A.1; Table S.A.7). Similarly, nine QTL were also identified for PXO99^A pHMI::*tal7b*, and named *qta7b* on chromosomes 1, 3, 5, 8, 10, 11, and 12 (Appendix B.2, Figure S.A.1; Table S.A.8). For PXO99^A pHMI::EV, only the QTL on chromosome 5 was supported by GWAS and IM, instead, for PXO99^A pHMI::*tal7b* QTL on chromosomes 5, 8 and 12 were supported by both methodologies.

MAGIC population reveals unique resistance QTL to PXO99^A pHMI::*tal7b*

The IM-identified QTL on chromosomes 5, 10, and 11 were consistent to both strains, whereas QTL on chromosomes 1, 7, 8 and 12 were unique to PXO99^A pHMI::EV, and those on chromosomes 1, 3, 8, 11 and 12 were unique to PXO99^A pHMI::*tal7b* (Appendix B.2, Figure S.A.1; Tables S.A.7, and S.A.8). Twenty of the 29 significant SNP markers to PXO99^A pHMI::*tal7b* clustered on chromosome 5. The other nine SNP markers were distributed into smaller clusters and were unique to PXO99^A pHMI::*tal7b* (Table A.1). Four SNP markers converged on *qta7b-8*, the PXO99^A pHMI::*tal7b* specific QTL on chromosome 8, and four converged on *qta7b-12-2*, the QTL on chromosome 12. Overall, six unique QTL associated with resistance to PXO99^A pHMI::*tal7b* were identified in the indica MAGIC population. Two of these QTL, *qta7b-8* and

qtal7b-12-2, were confirmed by both GWAS and IM analyses (Figures A.3 and A.4; Appendix B.2, Figure S.A.1; Tables S.A.6 and S.A.8).

qtal7b*-8 harbors a susceptibility allele to PXO99^A pHMI::*tal7b

The QTL that was mapped to chromosome 8 and was unique to PXO99^A pHMI::*tal7b*, *qtal7b*-8, was selected to further characterize the resistance mechanism governing this locus. Fourteen MAGIC AILs with the resistant and susceptible marker alleles on chromosome 8 were selected from the 330 AILs originally screened. These lines were reevaluated for their responses to PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b* (AILs: 13, 24, 156, 163, 197, 210, 219, 222, 225, 229, 234, 237, 250, and 267) and Nipponbare which served as a positive control. A subset of these lines (13, 219, 229) and Nipponbare showed significantly longer lesions in response to PXO99^A pHMI::*tal7b* than to PXO99^A pHMI::EV (*P*-value <0.05) (Figure A.5., Appendix B.2, Table S.A.9). Among these four lines the average lesion length to PXO99^A pHMI::*tal7b* was 16.9 cm and 12.2 cm the for empty vector control, a significant lesion length difference of approximately 4.68 cm (*P*-value <0.001). The remaining 11 AILs that were re-screened, including lines 24, 163, 197, and 210 (Figure A.5., Appendix B.2, Table S.A.9) did not differ in the observed lesion lengths to either bacterial strain, regardless of the presence or absence of *tal7b*. Among these 11 lines, the average lesion length for PXO99^A pHMI::*tal7b* was 13.07 cm and 12.45 cm for PXO99^A pHMI::EV, a difference of 0.62 cm. In contrast to major *R* genes, the absence of this significant difference in the majority of lines with variant alleles in *qtal7*-8 suggests that this QTL houses a minor yet significant susceptibility allele.

Tal7b gene targets converge on QTL identified for PXO99^A pHMI::*tal7b*

A total of 97,219 putative gene targets of Tal7b were predicted using Talvez (Perez-Quintero et al. 2013). These targets and their positions were aligned with the physical position of the significantly associated SNP markers and QTL identified on chromosomes 5, 8, 11 and 12. This analysis resulted in a total of eight target candidates for Tal7b (Figure A.4, Table A.2). Among the most highly ranked, four homologues of the *SWEET* sucrose transporter genes that serve as major susceptibility genes in rice, cassava and cotton were detected (Cox et al. 2017). The remaining four targets included a putative brassinosteroid insensitive 1 associated receptor kinase 1 precursor (LOC_Os08g07760), a putative dehydrin (LOC_Os11g26790), a calmodulin binding protein (LOC_Os12g36920) and spotted leaf 11 (LOC_Os12g38210).

A.3. DISCUSSION

Towards identifying novel resistance loci specific to Tal7b, we conducted a virulence screen on the indica MAGIC population (Bandillo et al. 2013). In this study, we confirm our hypothesis that Tal7b is a virulence enhancing factor and report six rice QTL unique to PXO99^A pHMI::*tal7b*. Our results suggest that the mechanism of resistance for one of them, *qtal7b-8*, is loss of susceptibility (Figure A.4). The correlation between Tal7b putative gene targets and multiple QTL unique to PXO99^A pHMI::*tal7b* suggest that Tal7b may target multiple genes in the rice genome. Together our data are consistent with the hypothesis that one TAL effector may target multiple minor effect susceptibility genes leading to quantitative susceptibility, and thus each TAL target contributes incrementally to pathogen fitness and disease.

TAL effector virulence is family-member specific and not purely additive (Bai et al. 2000). Decades of functional characterization of TAL effectors have revealed that some effectors like AvrXa7, PthXo1 and PthXo3 of *Xoo*, Tal1c of *Xoc* and the recently characterized Avrb6 of *X. citri* subsp. *malvacearum* target the *OsSweet* family of sucrose transporter genes (Verdier et al. 2012; Cox et al. 2017; Yang, Sugio, & White 2006; Antony et al. 2010). Others, such as PthXo6, PthXo7, AvrBs3, PthA, PthB and PthC target transcription factors (Sugio et al. 2007). All of these TAL effectors target major susceptibility genes and have taken center stage because of their all or nothing phenotype, and thus, have overshadowed what we are referring to as TAL targeted minor effect susceptibility genes. Our current data suggests that one TAL effector may target multiple minor effect susceptibility genes, i.e. quantitative susceptibility, and that each target contributes incrementally to pathogen fitness and virulence.

For many years, the complexity associated with sequencing repetitive genomic regions, a characteristic of TAL effectors, restricted the accurate sequencing of TAL containing *Xanthomonas* genomes (Booher et al. 2015). That is, until the advent of single molecule real-time sequencing (PacBio), which has allowed for the complete sequencing of 20 *X. oryzae* isolates. Prior to this, TAL effectors were sequenced via cloning of individual genes, as was done for this study. As a result of the robust long-read sequencing provided by PacBio, a near perfect tandem duplication was found in the re-sequencing of PXO99^A (Booher et al. 2015). The 212 Kb duplication harbored two identical copies of *Tal7b*, named *Tal8a* and *Tal7a* (Booher et al. 2015; Quibod et al. 2016). We performed our experiments prior to the re-sequencing of PXO99^A therefore both PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b* used in this study carried *tal7a* and

tal8a. Whether these effectors are expressed in PXO99^A remains to be shown. However, we still observed a clear difference in virulence between both strains.

The conservation of Tal7b among *Xoo* Philippine races as well as isolates from other Asian countries indicate a strong selective pressure to retain the effector even in the presence of other major TAL effectors such as AvrXa7 and PthXo1, and confirms a role in pathogen fitness. Despite our ability to predict multiple TAL effector gene targets in a genome, little is known about the function of most of the predicted targets outside of the *SWEET* genes and the transcription factors. TAL effector research has focused on one TAL effector one gene target, except for whole genome transcriptional studies, and even these have alluded to the possibility of more than one target per TAL effector.

Multiple host targets have been described for non-TAL effectors such as AvrRpt2 and AvrPto from *Pseudomonas syringae*, Avr2 from *Fusarium oxysporum* and EPIC2B from *Phytophthora infestans*, all of which contribute to suppression of basal plant defenses. In a recent study, an integrated approach was used to identify the cotton genes targeted by the *X. citri* subsp. *malvacearum* TAL effector Avrbs6 (Cox et al. 2017). The top ten Avrbs6 gene targets include a *SWEET* gene, unknown proteins, a transcriptional factor and Cytochrome P450. A sulfate transporter gene was identified as the susceptibility gene target of Tal2g from *Xoc* (Cernadas et al. 2014). These discoveries suggest that TAL effectors target other genes with functions previously not identified and support our hypothesis that one TAL effector targets may target multiple susceptibility alleles, as we found for Tal7b.

MAGIC populations are powerful genetic resources that capture the genetic diversity of multiple parents, recombined over several generations, to ultimately generate a population with large phenotypic diversity (Bandillo et al. 2013). Because the parents of the indica MAGIC population we used are elite varieties, the resistance loci characterized here can then be readily introgressed into elite rice varieties in collaboration with rice breeders. While this study focuses on resistance to a bacterial disease of rice, the strategy for finding durable resistance based on knowledge of effector targeted susceptibility and the application of novel genetic resources is broadly applicable to other crops and diseases.

A.4. MATERIALS AND METHODS

Bacterial strains, plant material and growth conditions

The bacterial strains and plasmids used in this study are listed in Appendix B.2, Table S.A.1, along with relevant characteristics. *Xoo* strains were cultured on Peptone Sucrose Agar (PSA) (Karganilla, et al. 1973) at 28°C and *Escherichia coli* strains were cultured on Luria-Bertani (LB) medium (Miller 1992) at 37°C. When necessary, antibiotics were added to the medium at the following concentrations: 50 µg/L streptomycin, 50 µg/L spectinomycin.

Rice varieties used in this study include 330 AILs from the indica MAGIC population previously described (Bandillo et al. 2013; Raghavan et al. 2017) at the eighth generation of selfing (S8), as well as the eight founding parents: Fedearroz 50, IR45427-2B-2-2b-1-1, IR4630-22-2-5-1-3, IR77298-14-1-2-10, PSBRc82, Samba Mashuri + Sub1, Sanhuangzhan-2, and PSBRc158. Nipponbare and WAB-56-125 served as susceptible and resistant controls, respectively. Plants were grown and cared for as described (Bossa-Castro et al. 2018). Rice lines

were grown in triplicate using an incomplete random block (IRB) design. Each experiment was replicated three times.

Plasmid constructs

The *tal7b* gene, previously named *ab4.5* (Bai et al. 2000), was subcloned from a cosmid clone pXO6-33 derived from *Xoo* strain PXO86 (Hopkins et al. 1992) to generate pBS4.5b. The CRR of *tal7b* (*tal7b*) was then cloned as a *SphI* fragment into the single *SphI* site of the entry vector pCS466 to generate pCS466::*tal7b*. pCS466 is a derivative of the Gateway entry vector pCR8-GW (Invitrogen) that contains a truncated form of the *Xoc* BLS256 *Tal1c* gene, from which the *SphI* fragment that comprises the repeat region has been removed (Verdier et al. 2012). Using Gateway LR Clonase (Invitrogen), the *tal7b* CRR flanked by the *Tal1c* N- and C- termini was transferred to the broad host-range destination vector pKEB31 (Cermak et al. 2011) Addgene plasmid 31224, (www.addgene.org) to create pKEB31::*tal7b* for constitutive expression in *Xanthomonas*. Finally, *tal7b* was cloned into the low-copy cosmid vector pHM1 (Hopkins et al. 1992) by digesting pKEB31::*tal7b* with *HindIII* HF to extract the *tal7b* CRR flanked by the *tal1c* domains (Verdier et al. 2012). The resulting plasmid, pHM1::*tal7b* was transformed into *Xoo* PXO99^A by electroporation (Choi & Leach 1994). Transformants were selected on nutrient agar containing appropriate antibiotics. Colony PCR was performed with primers F4: CGCAATGCACTGACGGGTGC and R2458: CATGCAAAGACGCCTGATCCGG to confirm the presence of *Tal7b*. The PCR program included an initial denaturation step at 96°C for 4 min, followed by 25 repeats of a 15 sec 96°C denaturation, a 30 sec 58°C annealing, and a 45 sec 70°C elongation, with a final 70°C elongation step for 4 min. Finally, integrity of *Tal7b* was confirmed by Sanger sequencing.

Bacterial inoculations and phenotyping

Six-weeks post sowing, the two youngest, completely expanded leaves of each rice plant were leaf clip inoculated as described (Kauffman et al. 1973). Briefly, all strains were incubated for 24h on PSA medium amended with streptomycin and spectinomycin at 28°C. Inoculum was then prepared by suspending bacteria in sterile water to an optical density at 600 nm (OD₆₀₀) of 0.2, 10⁸ CFU/ml. Lesion lengths were measured in centimeters at 14 days post inoculation (dpi).

Genotyping

The 330 MAGIC AILs and the eight founder parents used in this study were genotyped using a 96-plex ApeKI genotyping by sequencing (GBS) protocol, as described (Bandillo et al. 2013; Elshire et al. 2011). Raw reads, publically available at <http://snpseek.irri.org/download.zul>, were trimmed and aligned to the Nipponbare reference genome MSU7 (Kawahara et al. 2013). SNP calling was conducted prior to filtering as described in Raghavan et al. (2017). The remaining SNP markers, where then filtered so that all AILs had at least 70% of sites. This generated the final SNP data set of 14,561 markers was used for both GWAS and IM.

Data analysis

Lesion lengths (LL), measured in centimeters (cm), were analyzed using SAS® software version 9.4 (SAS Institute Inc., 2013). Each of the two inoculated leaves per plant were treated as technical replicates and used to calculate simple means for each biological replicate. All biological replicate values were then averaged using the least square means (LS-Means) function in PROC MIXED. Bacterial strain, line, and bacterial strain by line interaction were treated as fixed effects. Block and replicates were treated as random effects. *P*-values were calculated using Tukey's

method for multiple comparisons. AILs with missing phenotypic data were removed from all analyses.

Genome-wide association studies

GWAS was performed using 14,561 SNP markers, as described in Bossa-Castro et al. (2018). Briefly, a kinship matrix was generated for the MAGIC population, excluding parents, to account for population structure using TASSEL version 5.0.2 (Bradbury et al. 2007). Statistics and allele effects were generated in TASSEL using the mixed linear model (MLM). Q-values, which assess the false discovery rate from GWAS, were calculated with q-value package (Storey and Tibshirani, 2003) in R. The linear model settings were set to default, where compression level was calculated using the optimum level and the variance component estimated using the P3D method. Results, are presented in Manhattan plots generated using the qqman R package (Turner 2014).

Interval Mapping

Interval mapping was carried out using the *mpIM* function from R package mpMap, a platform designed for QTL mapping of multi-parent populations, as described (Huang & George 2011). A linkage map was generated with the SNP data of each AIL and founder, as well as line pedigree. Interval mapping assumed true marker positions, no covariates and a step size of 1 cM. QTL position, founder effect estimate, and allele effect were determined as described (Raghavan et al. 2017).

Confirmation of resistance phenotype on chromosome 8

MAGIC AILs with variant allele in *qta17b-8* (13, 24, 156, 163, 197, 210, 219, 222, 225, 229, 234, 237, 250, 267) were used to confirm resistance phenotype identified on chromosome 8. Nipponbare was used as a control. Six plants per AIL served as biological replicates and two leaves per plant served as technical replicates for each bacterial treatment. The two bacterial treatments were PXO99^A pHMI::EV or PXO99^A pHMI::*tal7b*. At 14 dpi, lesion lengths were measured as described above for all leaves and data was analyzed using one-way ANOVA. Statistical analyses were carried out using JMP Pro 13 (SAS Institute Inc., Cary, NC).

Physical map of QTL identified in this study, predicted Tal7b gene targets and known resistance *R* gene/QTL.

All reported BB resistance genes and QTL compiled in Dejedatin et al., 2016 were used to generate a physical map of the QTL identified in this study with respect to and all known BB resistance loci. The maps were generated with *tidyverse*, a collection of R packages that include ggplot2. Each chromosome was derived with the physical location of the SNP markers generated in this study. A total of 706, 1178, 988, and 1527 SNPs were used to make chromosome 5, 8, 11 and 12, respectively.

Tal7b predicted targets

Tal7b gene targets were predicted using Talvez (Perez-Quintero et al. 2013).

A.5. FIGURES

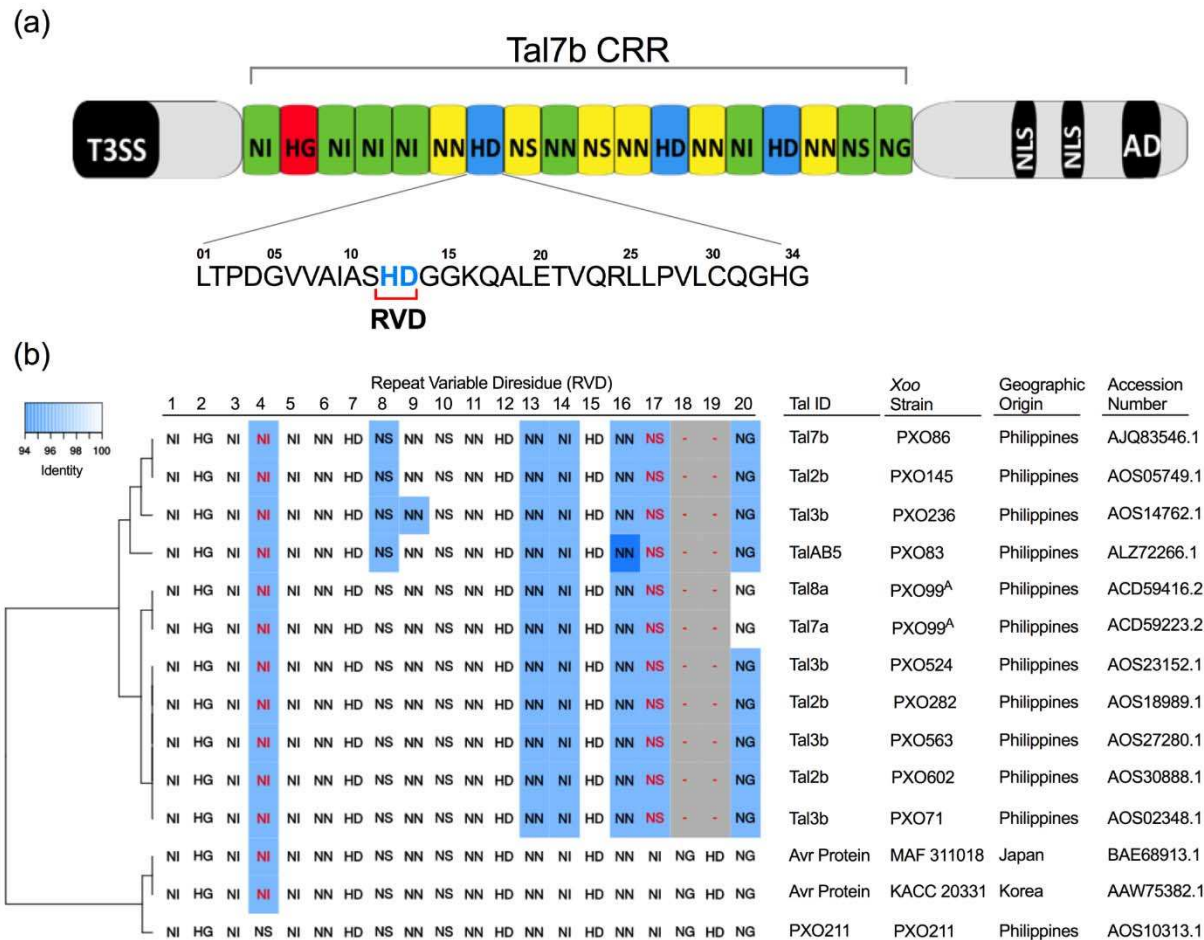


Figure A.1. A schematic representation of Tal7b. (a) The central repeat region (CRR) of Tal7b contains 18 modules of 34 amino acid repeats (represented in different colors) that differ from each other in amino acid composition at positions 12 and 13, called the repeat variable diresidues (RVD); RVDs are shown in bold inside colored repeat modules and represent the RVD sequence for Tal7b. The CRR is flanked by an N-terminus harboring a Type III Secretion Signal (TTSS), a C-terminus with nuclear localization signals (NLS), and an activation domain (AD). (b) Tal7b is present in multiple Asian strains of *Xoo* and all have identical RVD sequences. Amino acids that differ in RVD composition among Tal7b homologues are represented in red letters. Missing repeats and RVDs are represented as dashed red lines inside gray boxes. Blue shading overlaid on top of RVD sequences represent sequence mismatch in DNA alignment among Tal7b homologues. White shading represents 100% amino acid match.

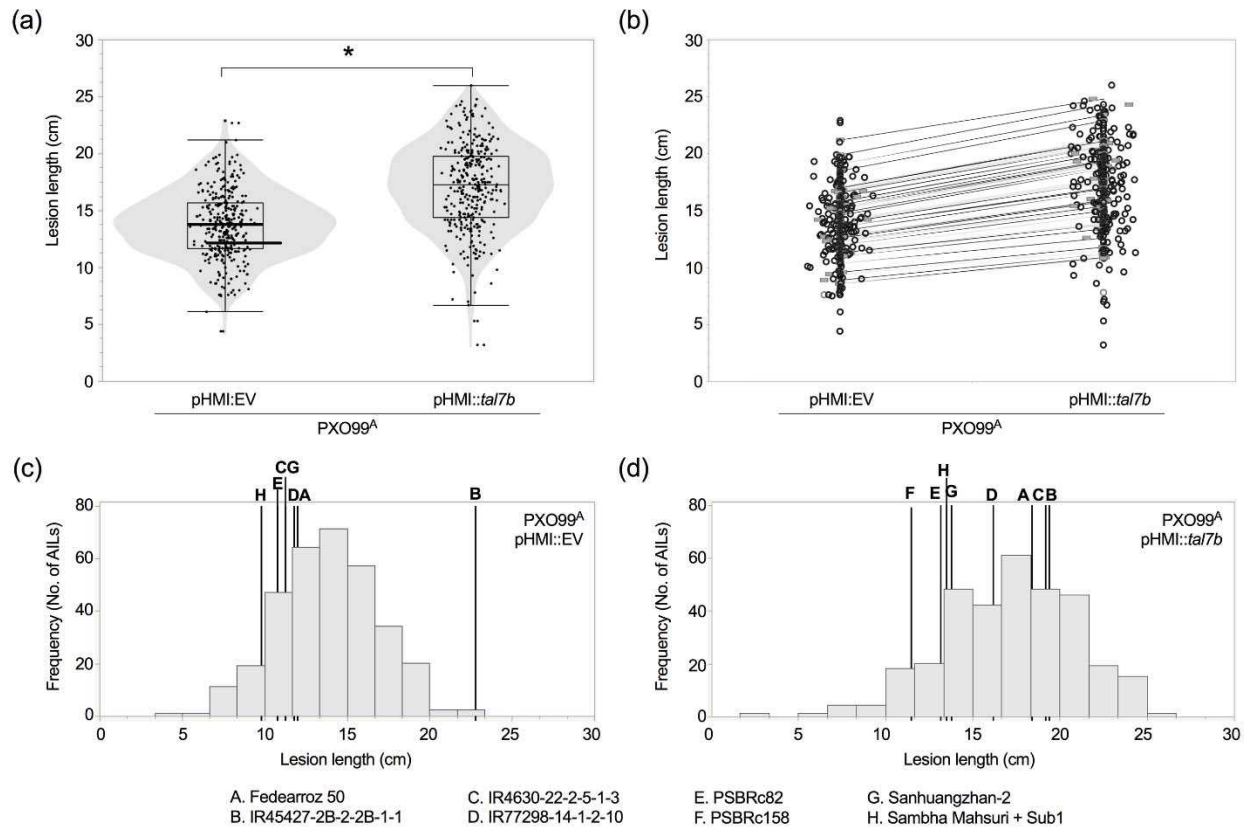


Figure A.2. *Tal7b* increases virulence of *Xoo* strain PXO99^A to MAGIC AILs. (a) Phenotypic distribution of the response of MAGIC AILs to *Xoo* strain PXO99^A with or without the plasmid borne copy of additional virulence factor, *Tal7b*. Violin plots represent the distribution of the Least Square Means (LS-Means) of bacterial blight disease lesion lengths (cm) on 330 MAGIC AILs and eight founding parents challenged with PXO99^A pHLMI empty vector (pHLMI::EV) or pHLMI carrying *Tal7b* (pHLMI::*tal7b*). Box-and-whisker plots imbedded in violin plots represent 50% of the values around the median (bold) and the asterisk (*) represents Tukey adjusted P -value < 0.001 . (b) Each symbol on the scattered plot represents the LS-Mean lesion length (cm) recorded for each of the 330 AIL screened. The black lines connecting each value highlights the 63 AIL with significantly longer lesion lengths in response to PXO99^A pHLMI::*tal7b* (left) compared to PXO99^A pHLMI::EV (right) (Tukey adjusted P -value < 0.05). Histograms representing the LS-Mean response, measured as lesion lengths (cm), of each of the MAGIC AILs after inoculation with: (c) PXO99^A pHLMI::EV and (d) PXO99^A pHLMI::*tal7b*. Histograms are overlaid on LS-Mean lesion lengths measured for the eight founding parents of the indica MAGIC AILs: (A) Fedearroz 50, (B) IR45427-2B-2-2B-1-1, (C) IR4630-22-2-5-1-3, (D) IR77298-14-1-2-10, (E) PSBRc82, (F) Samba Mashuri + Sub1, (G) Sanhuangzhan-2, and (H) PSBRc158.

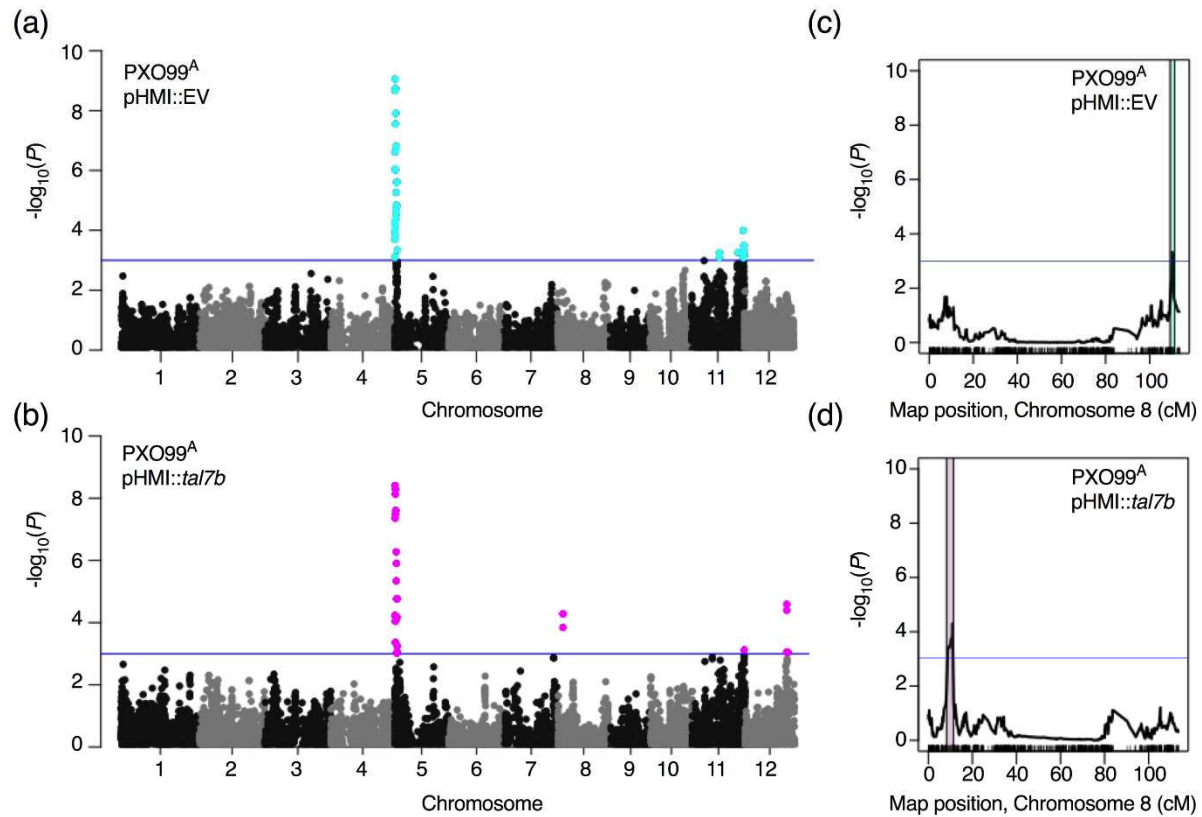


Figure A.3. QTL detection for *Xoo* PXO99^A with and without *tal7b*, highlighting unique QTL to *Tal7b*. (a, b). Manhattan plots show the negative logarithm of the *P*-values for the mixed linear model, by chromosome, using 14,561 SNPs. Solid blue line indicates genome-wide significance threshold of $P \leq 0.001$. (a) Screening of MAGIC AILs with *Xoo* PXO99^A pHMI::EV. Significantly associated SNPs identified on chromosomes 5 and 11, are shown in cyan and are listed in Appendix B.2, Table S.A.5. (b) Screening of MAGIC AILs with *Xoo* PXO99^A pHMI::*tal7b*. Significantly associated SNPs identified on chromosomes 5, 8, 11 and 12, are shown in magenta and are listed in Appendix B.2, Table S.A.6 (c, d) Simple interval mapping on chromosome 8 with significant QTL ($P \leq 0.001$). Highlighted regions indicate 1-LOD support intervals. (c) PXO99^A pHMI::EV shows a small QTL peak on chromosome 8, which is distinct from the peak identified for (d) PXO99^A pHMI::*tal7b*, supporting GWAS identification of unique QTL associated to virulence factor *tal7b*.

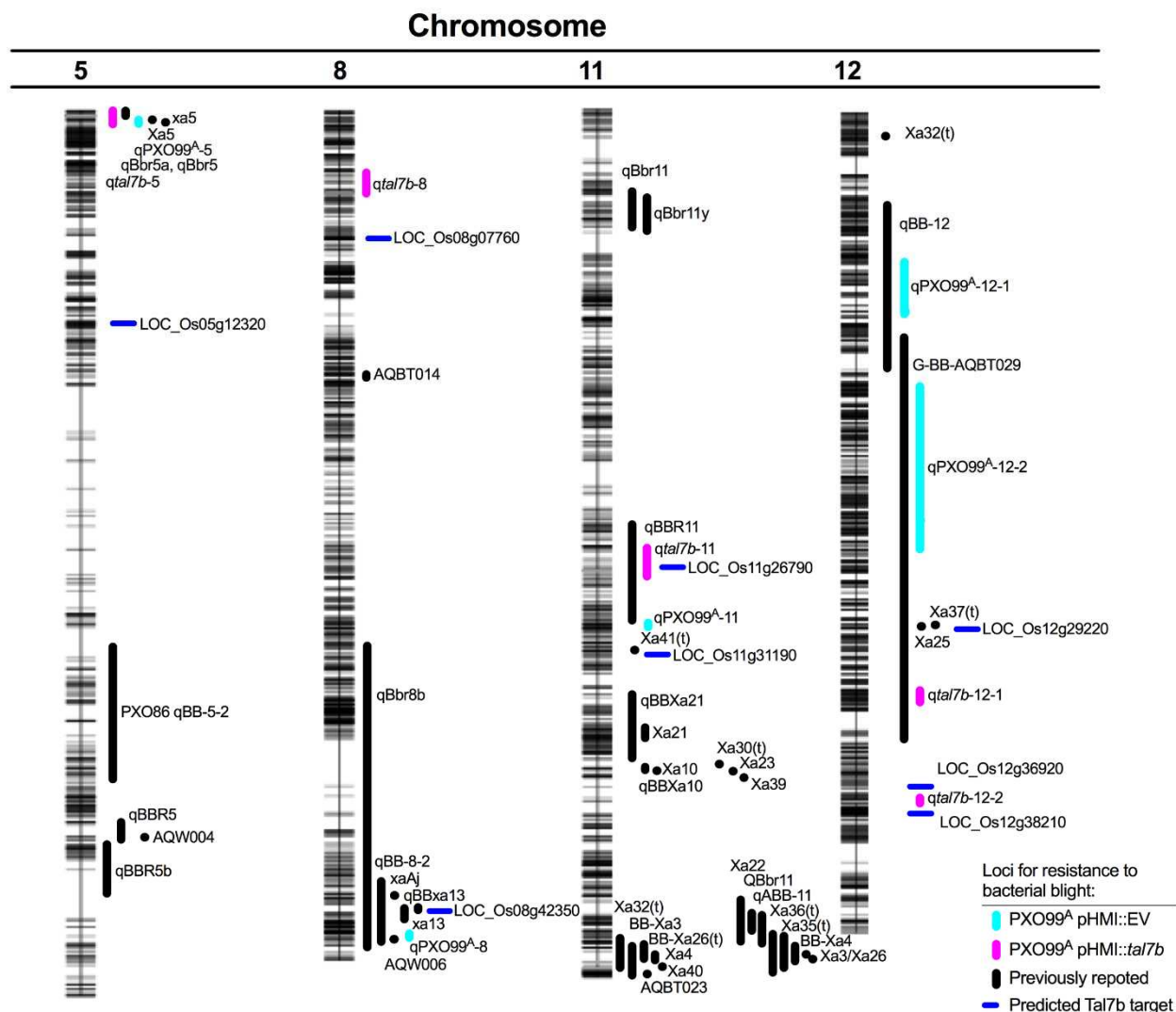


Figure A.4. Integrated physical map of rice chromosomes 5, 8, 11 and 12. Map shows the physical positions of QTL identified in this study, predicted Tal7b targets, and previously described loci for BB resistance. Cyan vertical lines indicate QTL identified in this study for PXO99^A pHMI::EV; magenta vertical lines represent QTL identified in this study for PXO99^A pHMI::*tal7b*, named qPXO99^A and *qta17b*, respectively. Blue horizontal lines show putative Tal7b targets; and black lines/dots indicate previously reported *R*, *S* genes and QTL.

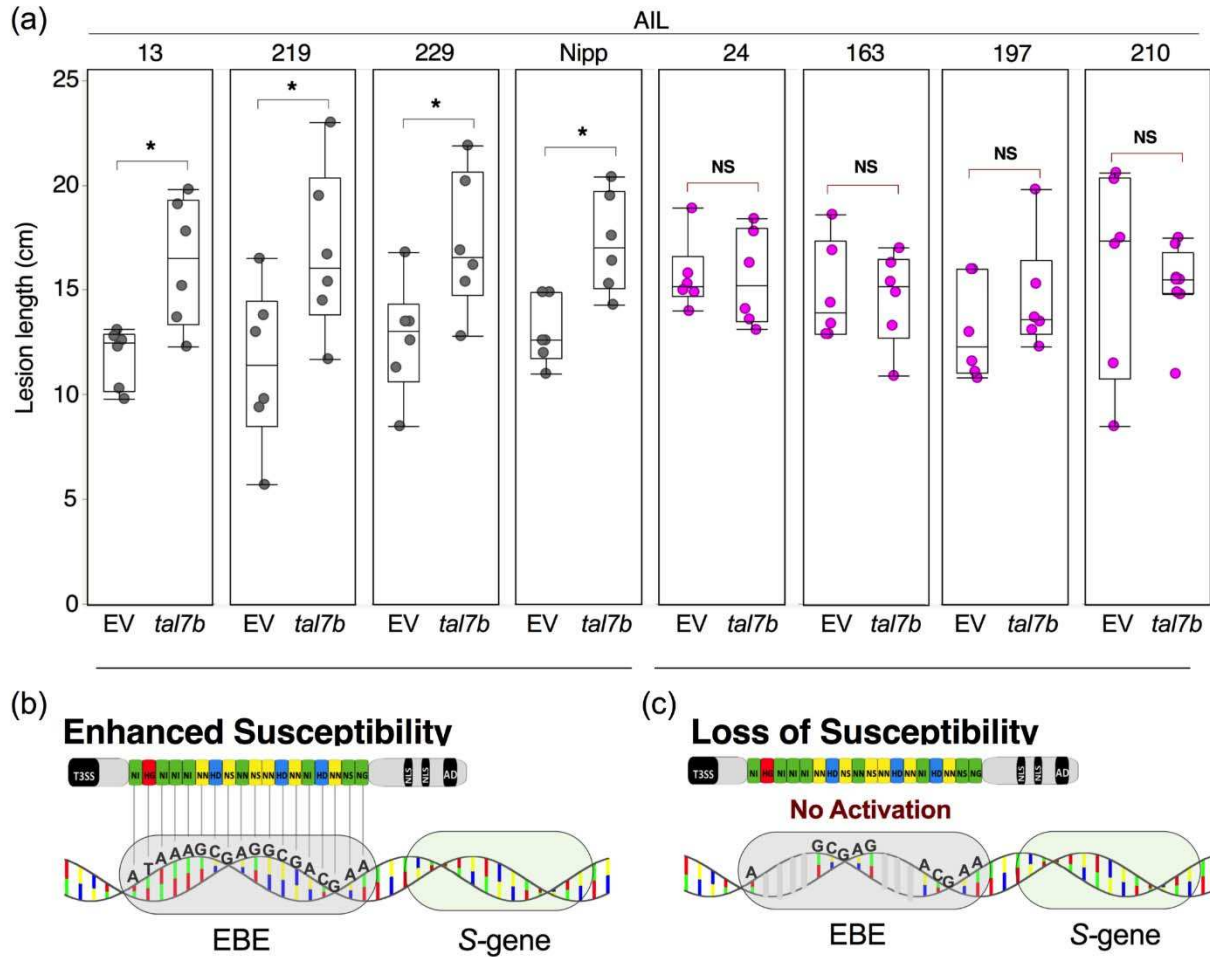


Figure A.5. Phenotypic response of selected MAGIC AILs with significant SNPs in *qta7b-8* and proposed model governing the resistance mechanism. (a) Lesion lengths (cm) in response to inoculation with PXO99^A pHMI::EV (EV) or PXO99^A pHM1::*tal7b* (*tal7b*). The AILs and control Nipponbare (Nipp) are listed above each pair-wise comparison box. Asterisks indicate significant differences in AIL response (lesion length) to EV vs. *tal7b*, as determined by one-way ANOVA (P -value ≤ 0.05). NS represents no significant differences between treatments. Eight of the 15 total AIL tested are shown, data for all 15 lines are shown in Appendix B.2, Table S.A.9. (b) Model proposing Tal7b target as a disease susceptibility gene contributing to pathogen fitness in rice. The virulence effector Tal7b binds its cognate effector binding element (EBE) in the promoter region of the target *S* gene leading to enhanced susceptibility [e.g., AILs 13, 219, 229 and Nipponbare (Nipp) shown in (a)]. (c) Model proposing how resistance loci identified in this study [AILs 24, 163, 197, and 210, shown in (a)] harbor polymorphisms in the Tal7b target EBE, disabling activation of *S* gene, leading to a loss of susceptibility type of resistance.

A.6. TABLES

Table A.1. Unique significantly associated SNPs and their effects on lesion length in response to PXO99^A pHMI::tal7b.

Marker ^a	P-value ^b	q-value ^c	Effect Estimate ^d	Allele ^e	Allele Ratio ^f
S8_2778495	5.22 x 10 ⁻⁵	4.46 x 10 ⁻²	-3.77	C/T	16/288
S8_2778496	5.22 x 10 ⁻⁵	4.46 x 10 ⁻²	3.77	C/T	288/16
S8_2778497	5.22 x 10 ⁻⁵	4.46 x 10 ⁻²	-3.77	G/T	16/288
S8_2774179	1.44 x 10 ⁻⁴	9.53 x 10 ⁻²	-3.54	A/G	16/290
S11_28697250	7.58 x 10 ⁻⁴	4.41 x 10 ⁻¹	2.54	C/G	36/268
S12_23092043	4.04 x 10 ⁻⁵	4.21 x 10 ⁻²	-2.27	C/T	196/93
S12_23120151	2.57 x 10 ⁻⁵	2.88 x 10 ⁻²	2.39	A/G	91/197

^a Physical coordinate of marker, number following S designates chromosome, number following underscore designates the physical location on the chromosome in bp.

^b Threshold for significance $P\text{-value} \leq 0.001$

^c Measure of significance in terms of the false discovery rate.

^d Effect estimate compares phenotypes, average lesion lengths (cm), with contrasting SNP allele. Negative effects correspond to a decrease in lesion length and a positive effect corresponds to an increase in lesion length.

^e Allele represents the SNP allele associated with the measured effect estimate in the numerator (Effect allele) whereas the Null allele is in the denominator.

^f Allele ratio represents the ratio of AILs with the Effect/Null allele as defined in Allele column.

Table A.2. Putative gene targets for Tal7b as predicted by Talvez.

Locus ID	Talvez score ^a	Annotation	Gene
LOC_Os05g12320	21.8	Nodulin MtN3 family protein	<i>OsSWEET</i>
LOC_Os08g42350	18.9	Nodulin MtN3 family protein	<i>OsSWEET</i>
LOC_Os08g07760	22.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	<i>OsSERK1/OsBAK1</i>
LOC_Os11g26790	21.1	Putative dehydrin	DHN
LOC_Os11g31190	21.2	Nodulin MtN3 family protein	<i>OsSWEET</i>
LOC_Os12g29220	15.6	Nodulin MtN3 family protein	<i>OsSWEET</i>
LOC_Os12g36920	16.9	Calmodulin binding protein	CaM-binding protein
LOC_Os12g38210	20.7	Spotted leaf 11	<i>SPL11</i>

^a Score was calculated using Talvez 3.2, as described by Perez-Quintero et al., 2013.

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APPENDIX B

Supplementary material

B.1. CHAPTER 2 SUPPLEMENTARY MATERIAL

Supplementary Figures

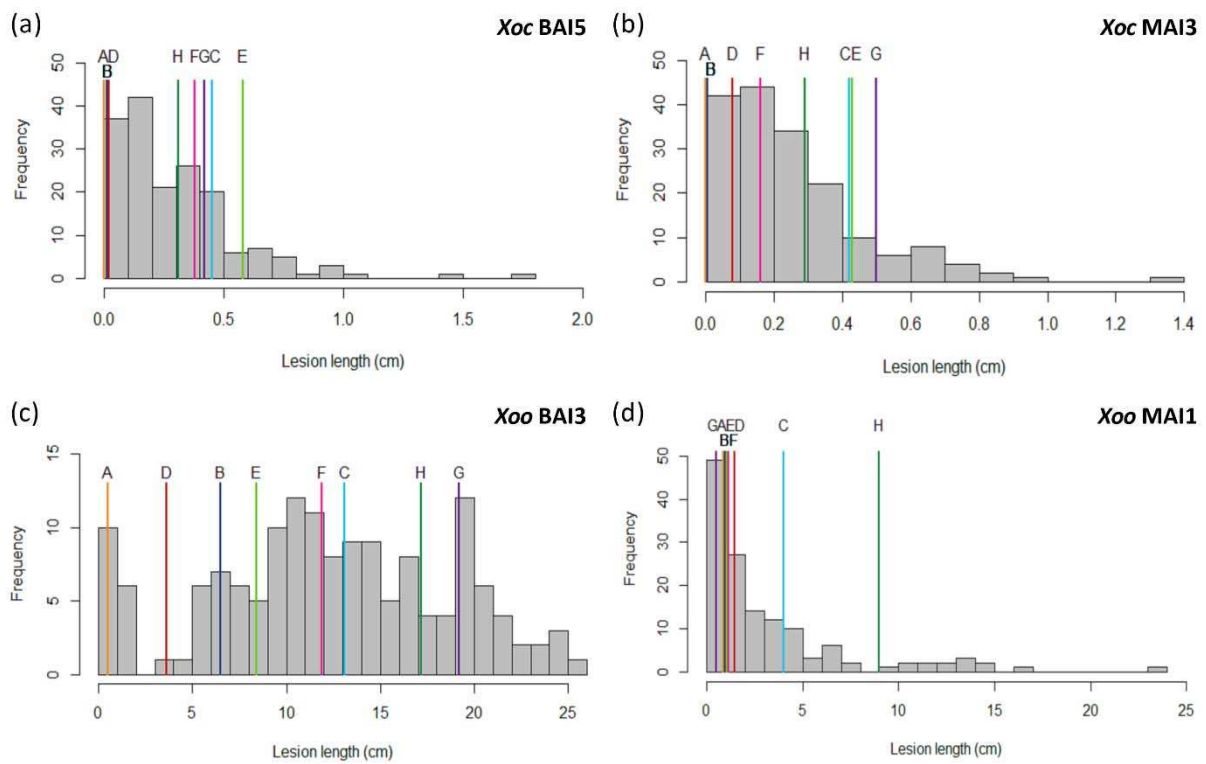


Figure S2.1. Distribution of lesion length (cm) of indica MAGIC founders and S4 subset. (a) Screening of 171 AILs in growth chamber with *Xoc* BAI5. (b) Screening of 174 AILs in growth chamber with *Xoc* MAI3. (c) Screening of 152 AILs in the greenhouse with *Xoo* BAI3. (d) Screening of 137 AILs in the greenhouse with *Xoo* MAI1. Histograms represent mean values of MAGIC lines. Mean lesion lengths of founders are indicated with vertical lines (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1).

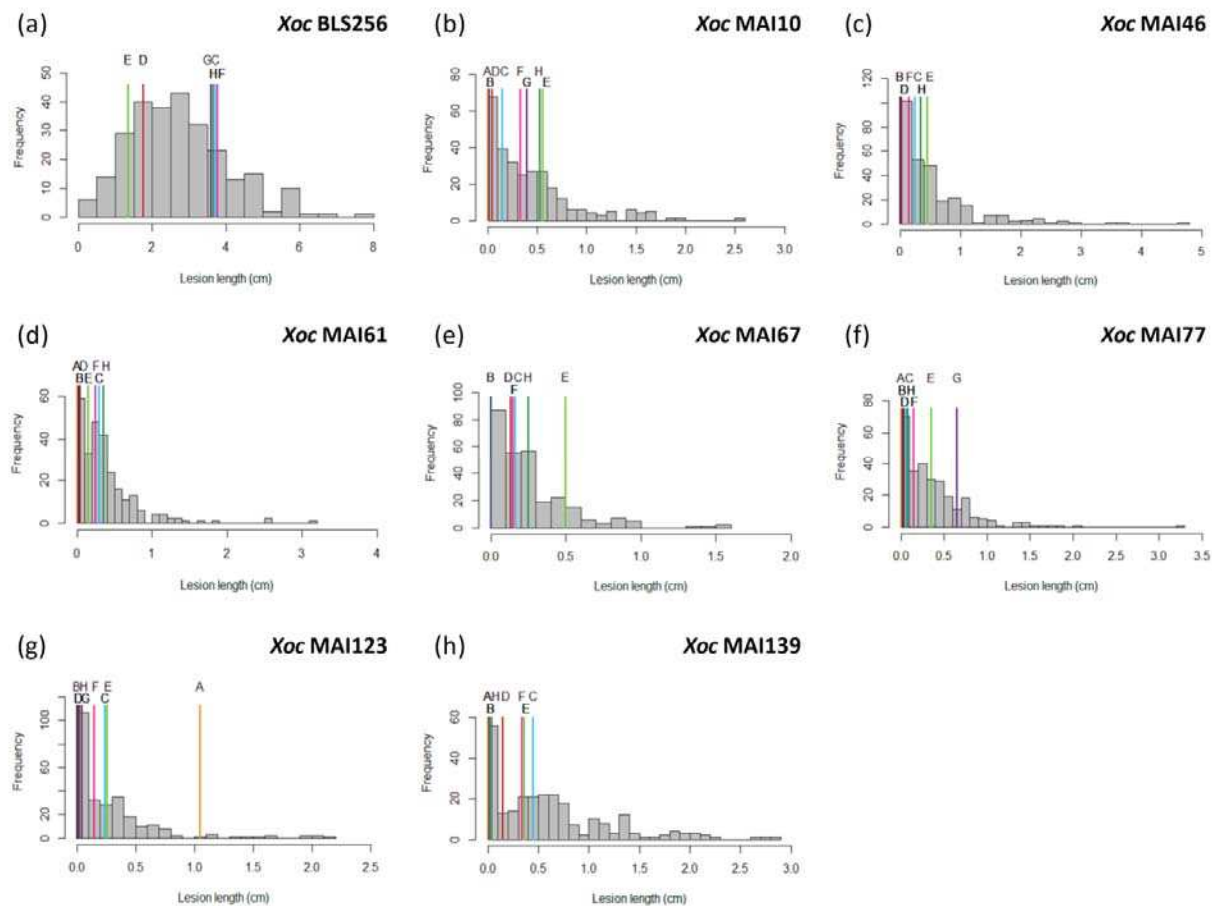


Figure S2.2. Distribution of lesion length (cm) of indica MAGIC founders and S8 subset screened with multiple *Xoc* strains. (a) Screening of 268 AILs with *Xoc* BLS256. (b) Screening of 290 AILs with *Xoc* MAI10. (c) Screening of 288 AILs with *Xoc* MAI46. (d) Screening of 270 AILs with *Xoc* MAI61. (e) Screening of 281 AILs with *Xoc* MAI67. (f) Screening of 280 AILs with *Xoc* MAI77. (g) Screening of 265 AILs with *Xoc* MAI123. (h) Screening of 252 AILs with *Xoc* MAI139. *Xoc* BLS256 was screened in the greenhouse, the rest of strains screened in the field. Histograms represent mean values of MAGIC lines. Mean lesion lengths of founders are indicated with vertical lines (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1). For strains BLS256, MAI46, MAI61, MAI67 and MAI139 some phenotypic values of founders are missing due to lack of germination.

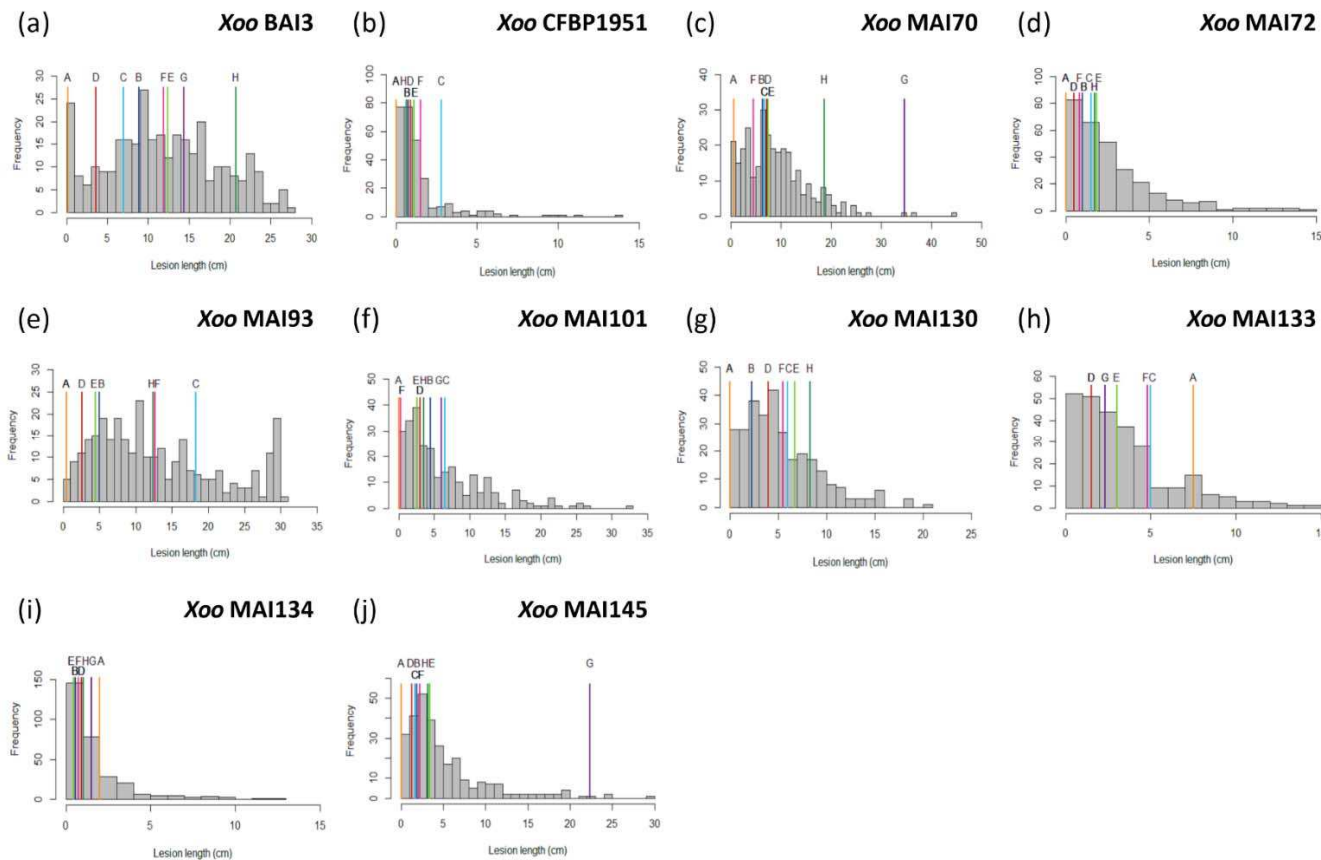


Figure S2.3. Distribution of lesion length (cm) of indica MAGIC founders and S8 subset screened with multiple *Xoo* strains. (a) Screening of 325 AILs with *Xoo* BAI3. (b) Screening of 281 AILs with *Xoo* CFBP1951. (c) Screening of 309 AILs with *Xoo* MAI70. (d) Screening of 296 AILs with *Xoo* MAI72. (e) Screening of 295 AILs with *Xoo* MAI93. (f) Screening of 270 AILs with *Xoo* MAI101. (g) Screening of 296 AILs with *Xoo* MAI130. (h) Screening of 276 AILs with *Xoo* MAI133. (i) Screening of 295 AILs with *Xoo* MAI134. (j) Screening of 286 AILs with *Xoo* MAI145. *Xoo* BAI3 was screened in the greenhouse, the rest of strains screened in the field. Histograms represent mean values of MAGIC lines. Mean lesion lengths of founders are indicated with vertical lines (A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1). For strains CFBP1951, MAI72, MAI93, MAI130, MAI133 and MAI134 some phenotypic values of founders are missing due to lack of germination.

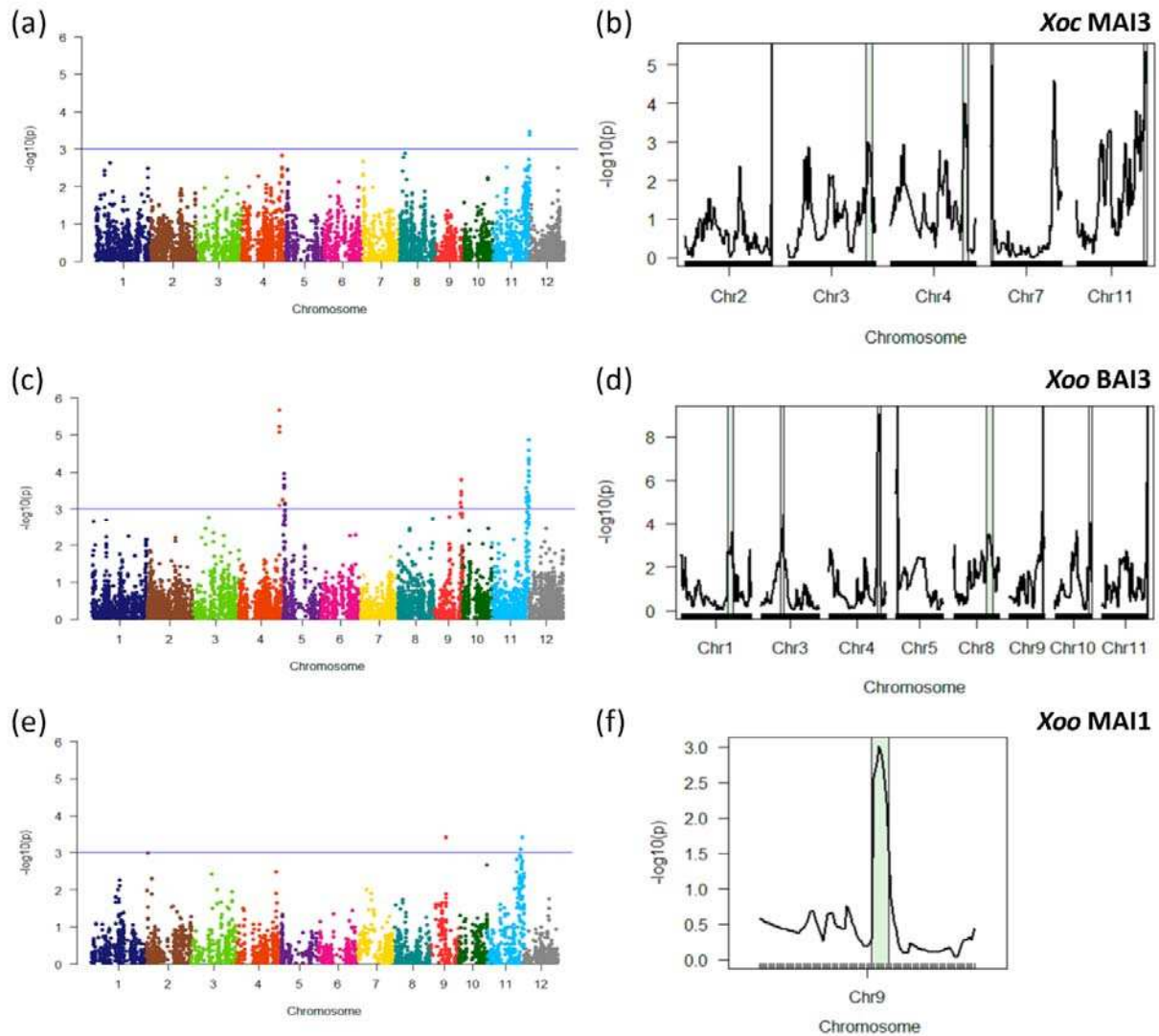


Figure S2.4. QTL detection for resistance to *Xoc* MAI3 and *Xoo* BAI3 and MAI1 in indica MAGIC S4 subset. (a, b) *Xoc* MAI3 (Markers=6,894). (c, d) *Xoo* BAI3 (Markers =7,390). (e, f) *Xoo* MAI1 (Markers =3,669). (a, c, e) Manhattan plots show the negative logarithm of the P -values for the mixed linear model, by chromosome. Solid blue line indicates significance threshold (P -value < 0.001). (b, d, f) Simple interval mapping showing chromosomes with significant QTL (P -value < 0.001). Green regions indicate 1-LOD support intervals.

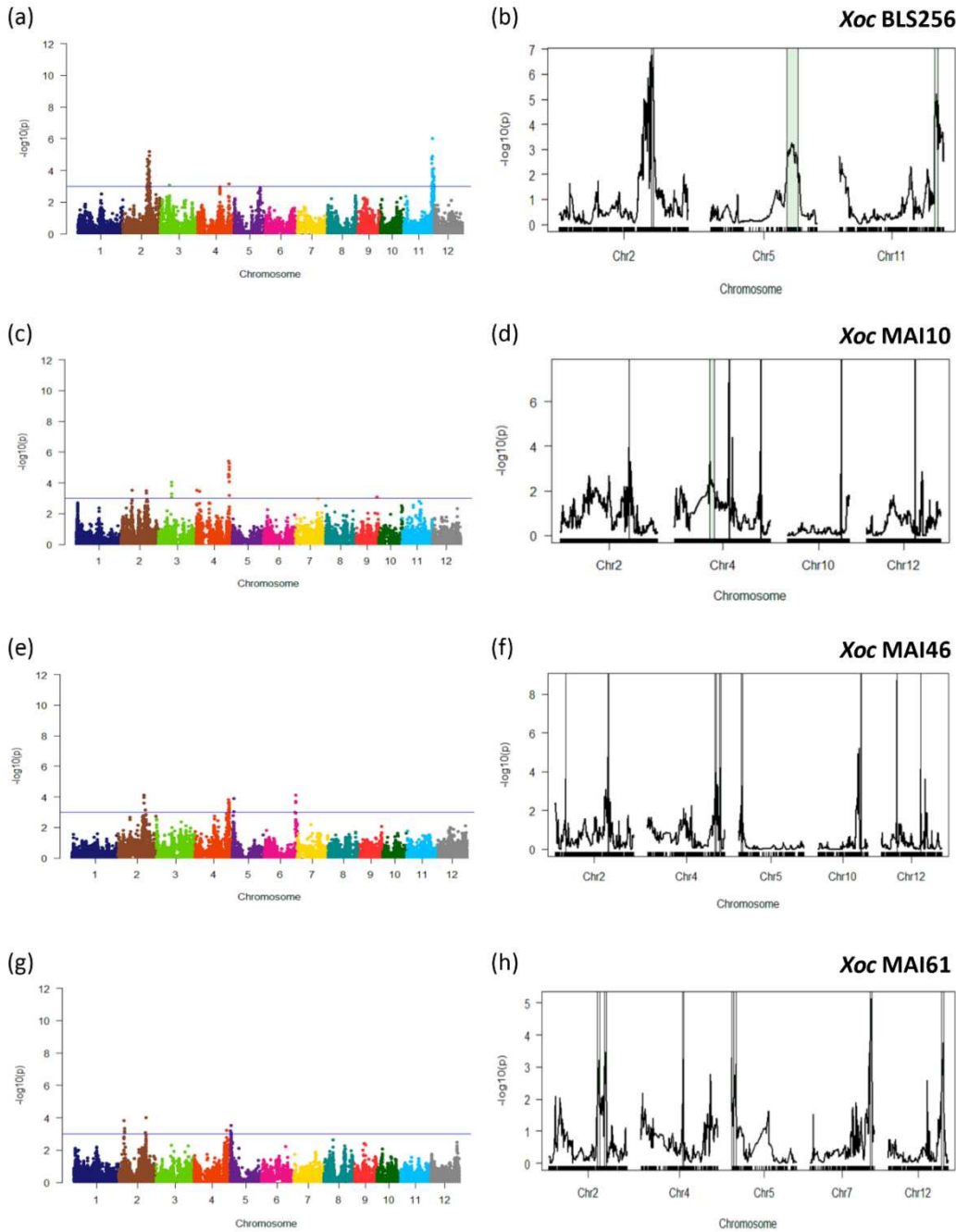
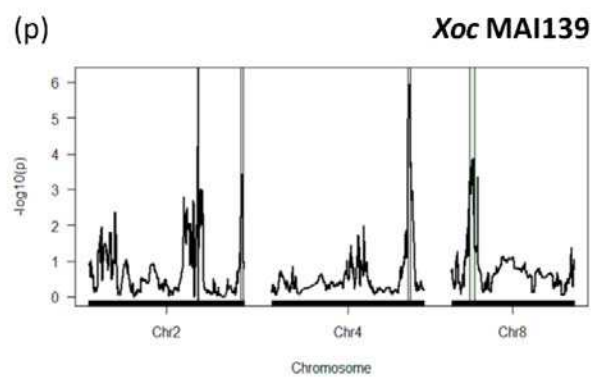
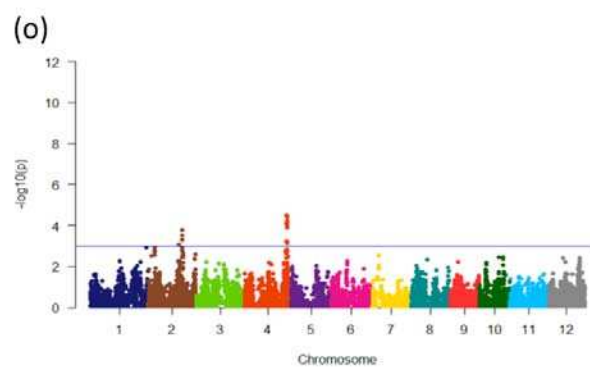
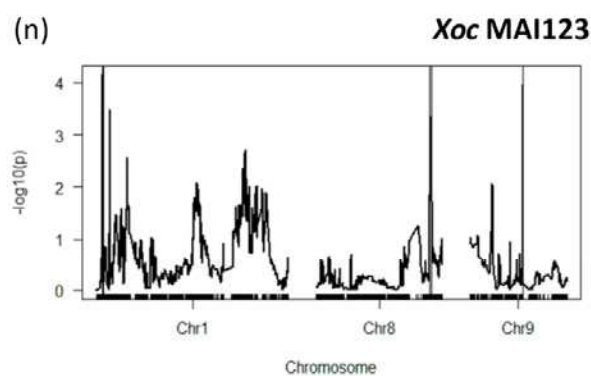
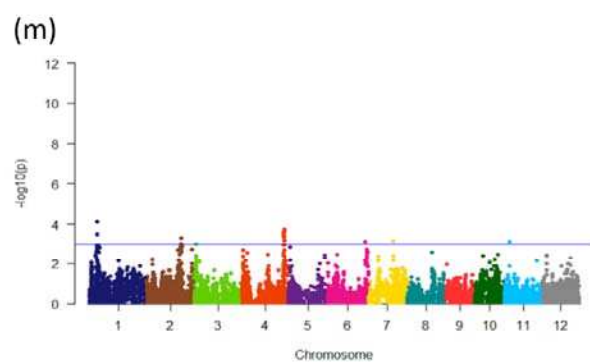
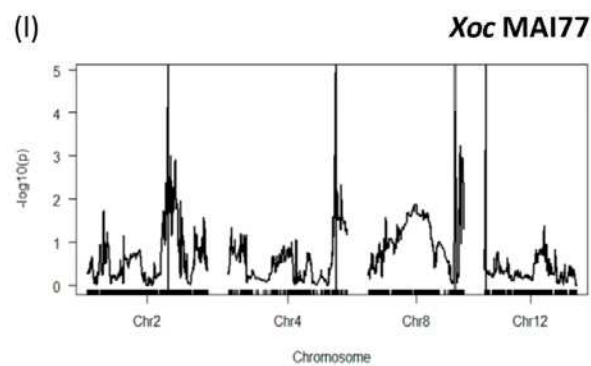
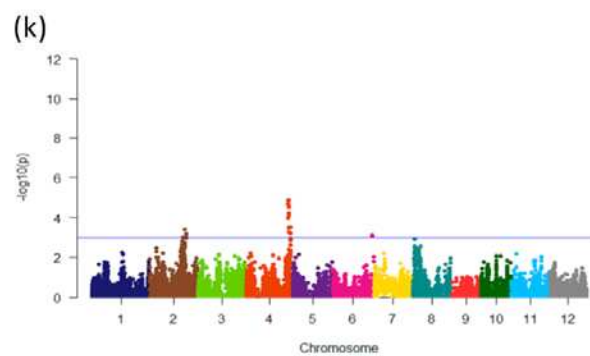
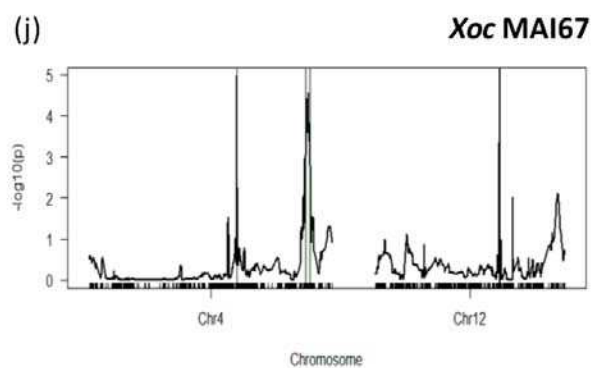
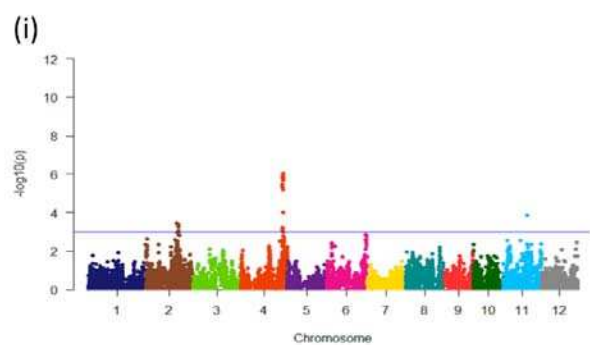


Figure S2.5. QTL detection for resistance to *Xoc* strains in indica MAGIC S8 subset. (a, b) *Xoc* BLS256; (c, d) *Xoc* MAI10; (e, f) *Xoc* MAI46; (g, h) *Xoc* MAI61; (i, j) *Xoc* MAI67; (k, l) *Xoc* MAI77; (m, n) *Xoc* MAI123; (o, p) *Xoc* MAI139. SNP markers used for all strains =14,475. (a, c, e, g, i, k, m, o). Manhattan plots show the negative logarithm of the *P*-values for the mixed linear model, by chromosome. Solid blue line indicates significance threshold (*P*-value < 0.001). (b, d, f, h, j, l, n, p) Simple interval mapping showing chromosomes with significant QTL (*P*-value < 0.001). Green regions indicate 1-LOD support intervals.



Continuation Figure S2.5.

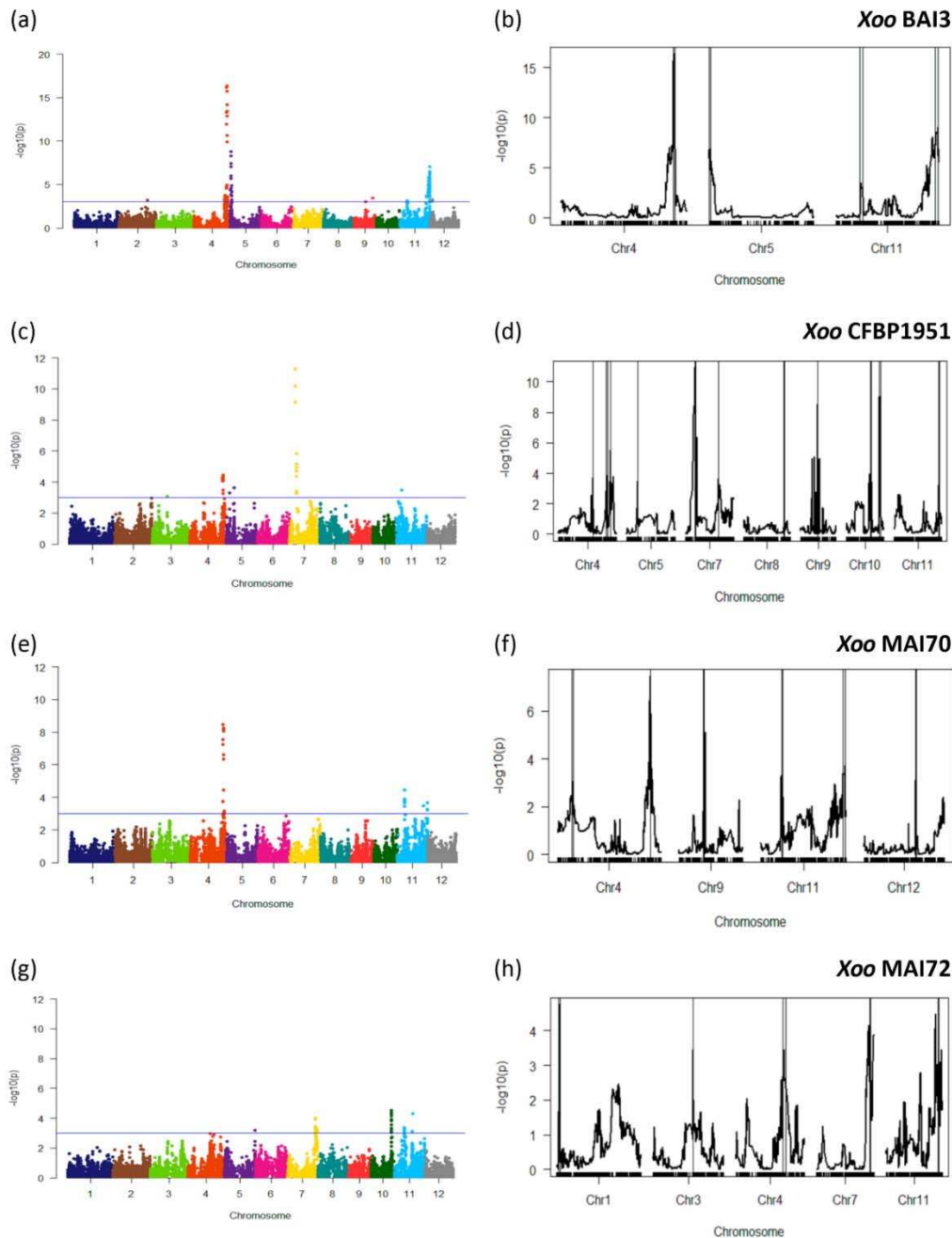
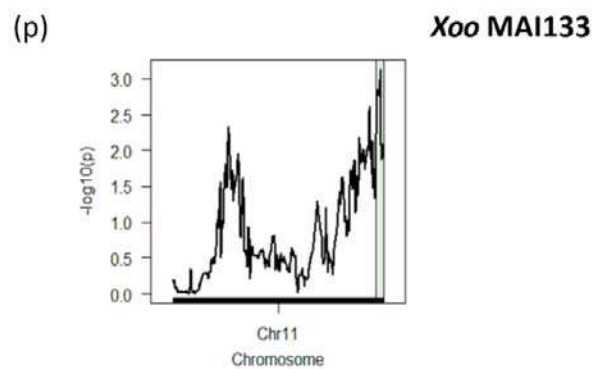
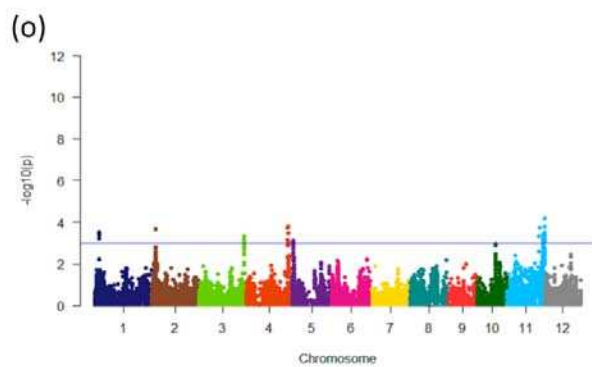
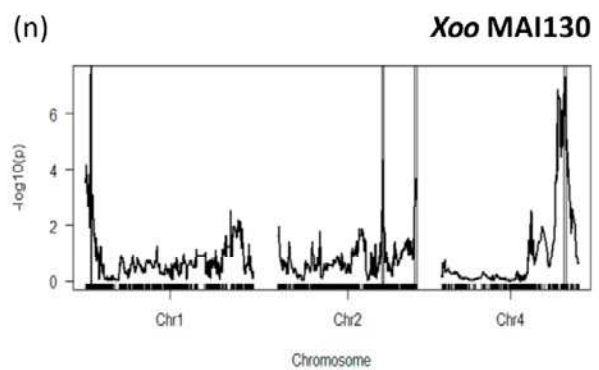
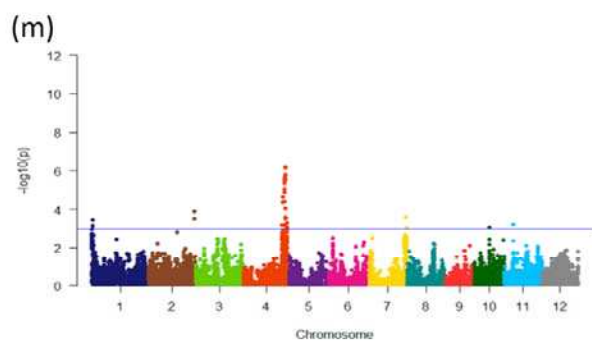
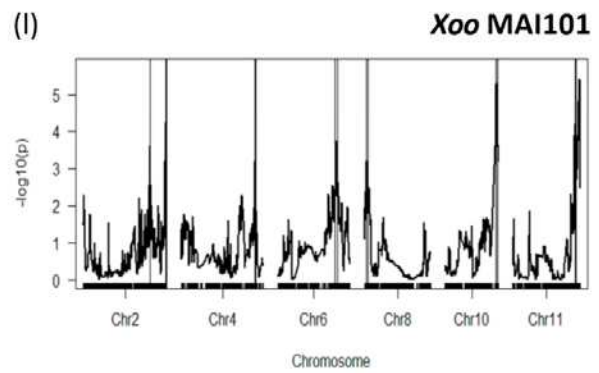
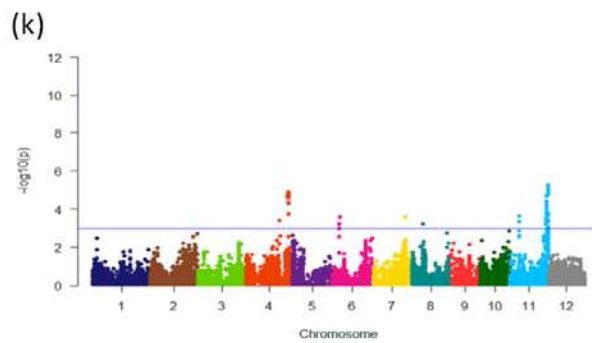
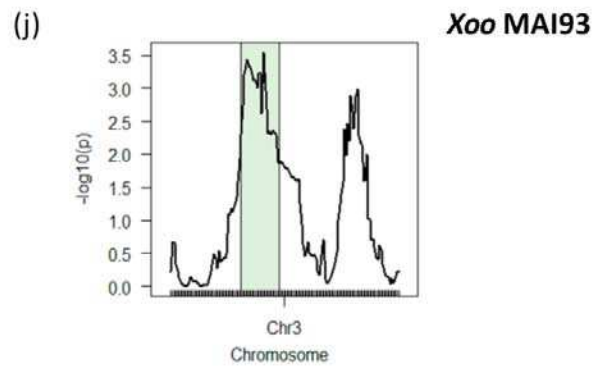
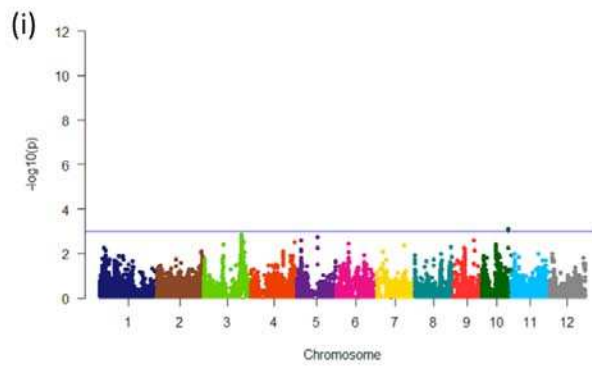
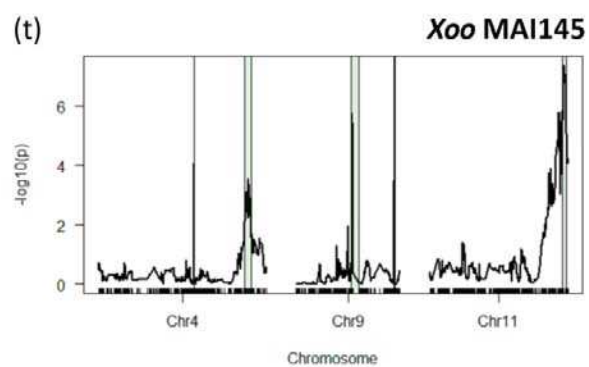
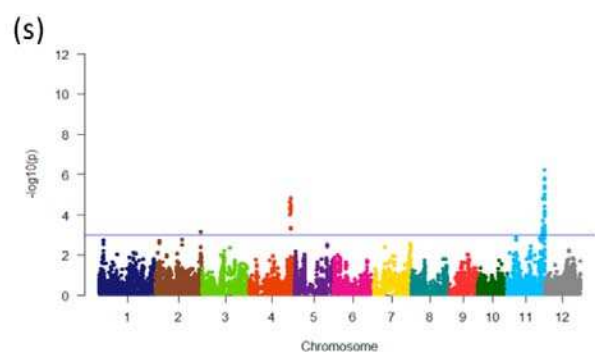
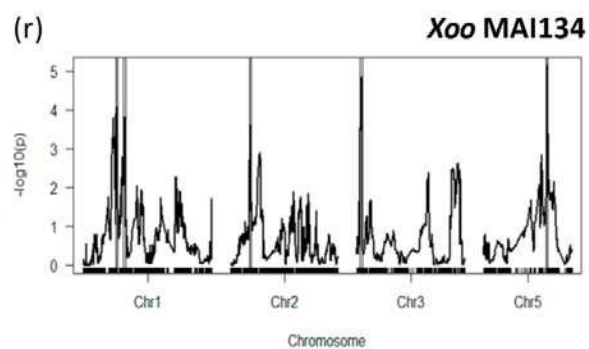
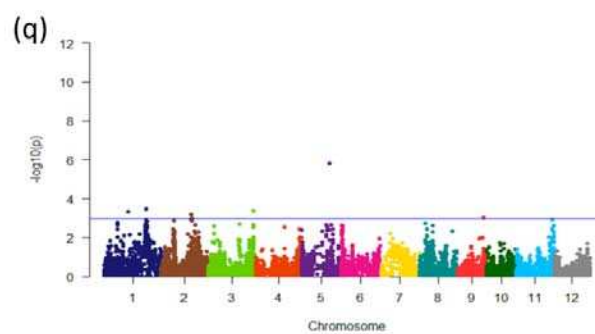


Figure S2.6. QTL detection for resistance to *Xoo* strains in indica MAGIC S8 subset. (a, b) *Xoo* BAI3; (c, d) *Xoo* CFBP1951; (e, f) *Xoo* MAI70, Note: first QTL on Chr 4 discarded (P -value > 0.001); (g, h) *Xoo* MAI72; (i, j) *Xoo* MAI93; (k, l) *Xoo* MAI101; (m, n) *Xoo* MAI130; (o, p) *Xoo* MAI133; (q, r) *Xoo* MAI134; (s, t) *Xoo* MAI145, Note: first QTL on Chr 9 discarded (P -value > 0.001). SNP markers used for all strains = 14,475. (a, c, e, g, i, k, m, o, q, s). Manhattan plots show the negative logarithm of the P -values for the mixed linear model, by chromosome. Solid blue line indicates significance threshold (P -value < 0.001). (b, d, f, h, j, l, n, p, r, t) Simple interval mapping showing chromosomes with significant QTL (P -value < 0.001). Green regions indicate 1-LOD support intervals.



Continuation Figure S2.6.



Continuation Figure S2.6.

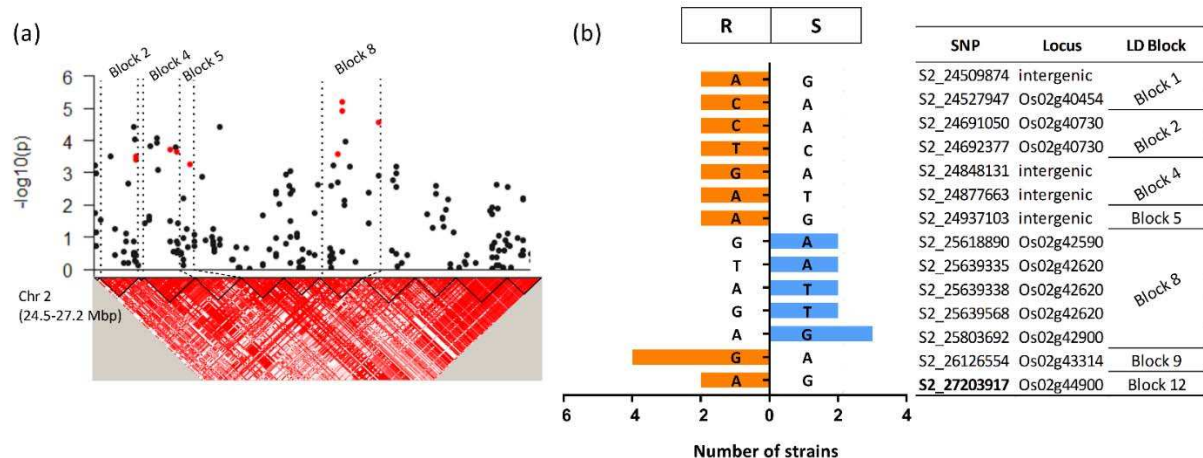


Figure S2.7. Complete haplotype block analyses and SNP effects in a hotspot region for *X. oryzae* resistance on chromosome 2. (a) Local Manhattan plot of *Xoc* BLS256 (top) and linkage disequilibrium (LD) with haplotype block analysis (bottom) of 24.5 – 27.2 Mbp region on chromosome 2. Red filled circles indicate SNPs that are significant to multiple for *X. oryzae* strains. LD heatmap shows the standard Haploview color scheme to display LD with bright red for strong LD ($LOD = 2$, $D' = 1$), pink ($LOD = 2$, $D' < 1$), and blue ($LOD < 2$, $D' = 1$) for intermediate LD, and white for no LD ($LOD < 2$, $D' < 1$). (b) Summary of SNP effects to *X. oryzae* strains on chromosome 2. Size of the bars denote the number of strains for which a SNP was significant (P -value < 0.001), color and direction of the bars indicate the sign of the estimated effect, either negative (left, orange) or positive (right, blue). A negative effect is associated with a more resistant phenotype (R), and a positive effect with a more susceptible phenotype (S). For each SNP the correspondent allele for the estimated effect is shown. SNP in bold denote the SNP was significant in both pathovars (*Xoc* and *Xoo*), otherwise the SNP was significant only for *Xoc* strains. The locus ID for each SNP (prefix “LOC_” is omitted), was predicted from the MSU7 rice reference annotation.

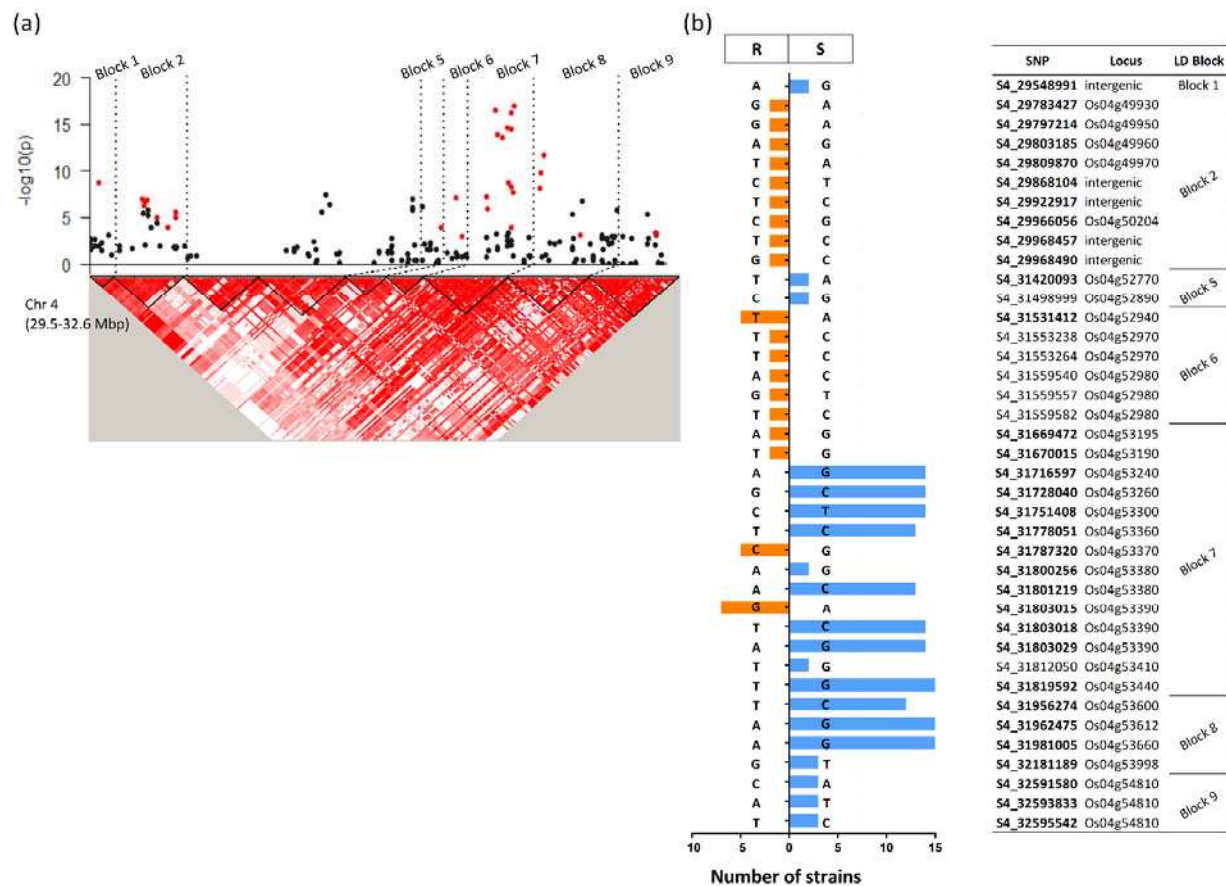


Figure S2.8. Complete haplotype block analyses and SNP effects in a hotspot region for *X. oryzae* resistance on chromosome 4. (a) Local Manhattan plot of *Xoc* BAI5 (top) and linkage disequilibrium (LD) with haplotype block analysis (bottom) of 29.5 – 32.6 Mbp region on chromosome 4. Red filled circles indicate SNPs that are significant to multiple *X. oryzae* strains. LD heatmap shows the standard Haploview color scheme to display LD with bright red for strong LD ($LOD = 2$ $D' = 1$), pink ($LOD = 2$ $D' < 1$), and blue ($LOD < 2$ $D' = 1$) for intermediate LD, and white for no LD ($LOD < 2$, $D' < 1$). (b) Summary of SNP effects to *X. oryzae* strains on chromosome 4. Size of the bars denote the number of strains for which a SNP was significant (P -value < 0.001), color and direction of the bars indicate the sign of the estimated effect, either negative (left, orange) or positive (right, blue). A negative effect is associated with a more resistant phenotype (R), and a positive effect with a more susceptible phenotype (S). For each SNP the correspondent allele for the estimated effect is shown. SNPs in bold denote the SNP was significant in both pathovars (*Xoc* and *Xoo*), otherwise the SNP was significant only for *Xoc* strains. The locus ID for each SNP (prefix "LOC_" is omitted), was predicted from the MSU7 rice reference annotation.

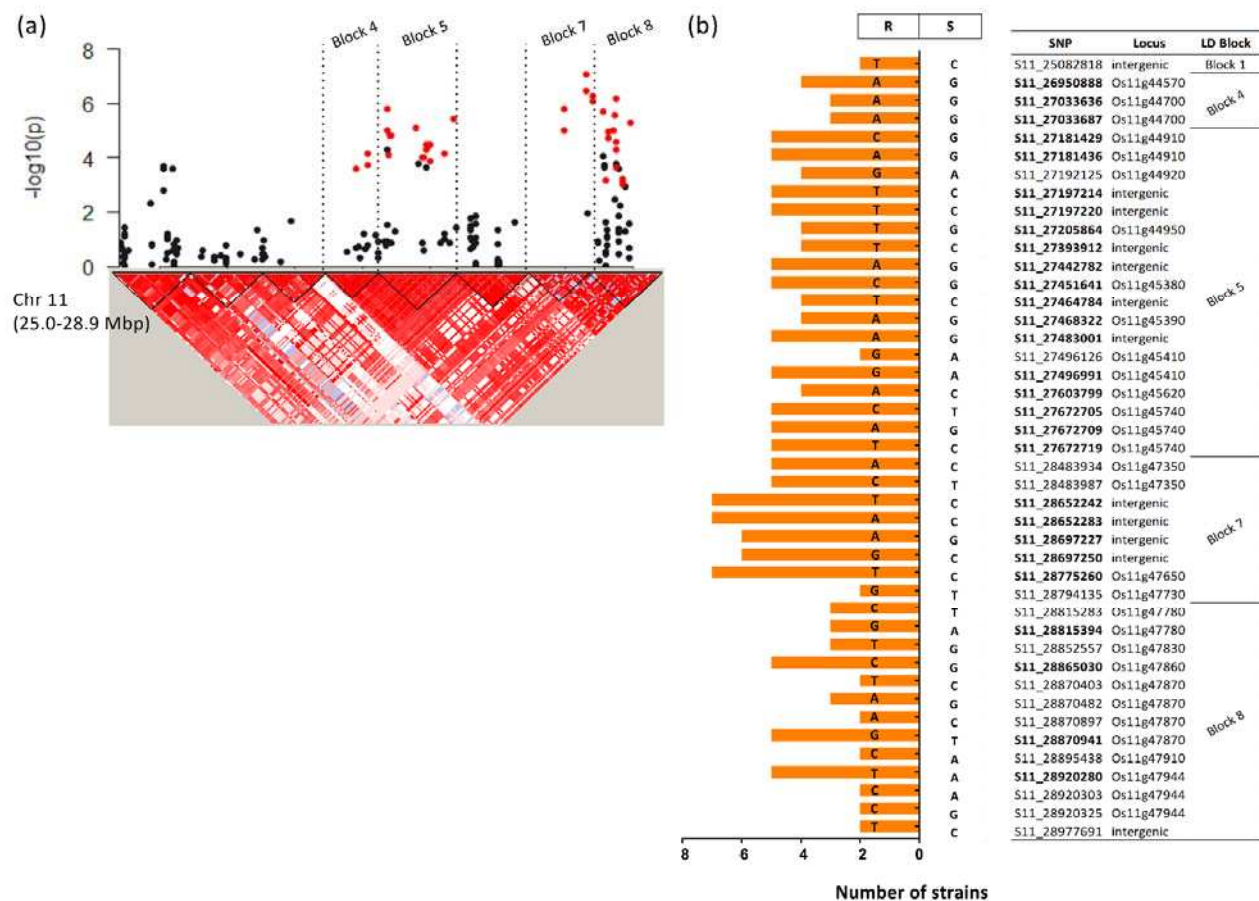


Figure S2.9. Complete haplotype block analyses and SNP effects in a hotspot region for *X. oryzae* resistance on chromosome 11. (a) Local Manhattan plot of *Xoo* BAI3 (top) and linkage disequilibrium (LD) with haplotype block analysis (bottom) of 25.8 – 28.9 Mbp region on chromosome 11. Red filled circles indicate SNPs that are significant to multiple for *X. oryzae* strains. LD heatmap shows the standard Haploview color scheme to display LD with bright red for strong LD ($LOD = 2$, $D' = 1$), pink ($LOD = 2$, $D' < 1$), and blue ($LOD < 2$, $D' = 1$) for intermediate LD, and white for no LD ($LOD < 2$, $D' < 1$). (b) Summary of SNP effects to *X. oryzae* strains on chromosome 11. Size of the bars denote the number of strains for which a SNP was significant (P -value < 0.001), color and direction of the bars indicate the sign of the estimated effect, either negative (left, orange) or positive (right, blue). A negative effect is associated with a more resistant phenotype (R), and a positive effect with a more susceptible phenotype (S). For each SNP the correspondent allele for the estimated effect is shown. SNPs in bold denote the SNP was significant in both pathovars (*Xoc* and *Xoo*), otherwise the SNP was significant only for *Xoo* strains. The locus ID for each SNP (prefix "LOC_" is omitted), was predicted from the MSU7 rice reference annotation.

Supplementary Tables

Table S2.1. Agronomic traits of MAGIC indica founders (modified from (Bandillo et al., 2013)).

Designation	Germoplasm/Variety	Origin	IRIS ID	GID [†]	Known <i>R</i> genes	Agronomic relevance
A	IR4630-22-2-5-1-3	IRRI	IRIS 313-15898	56023	<i>Xa4</i>	Salt tolerance
B	Fedearroz 50	Colombia	IRIS 313-15896	1846419	<i>Xa4</i>	Delayed senescence, quality traits, disease tolerance, breeding progenitor
C	IR77298-14-1-2-10	IRRI	IRIS 313-15901	2154106	<i>Xa4</i>	Drought tolerance, tungro resistance, IR64
D	Shan-Huang Zhan-2 (SHZ-2)	China	IRIS 313-15897	402862	<i>Xa4</i>	Blast resistance, high yielding, breeding
E	PSBRc82 (IRRI123 or IR64633-87-2-2-3-3)	IRRI	CX358	94801	<i>Xa4</i> , <i>xa5</i>	High yielding, most popular variety of Philippines
F	Sambha Mahsuri + Sub1 (IR 07F287)	IRRI	IRIS 313-15900	2254836		Mega variety, good grain quality, submergence tolerance
G	PSBRc 158 (IRRI146 or IR77186-122-2-2-3)	IRRI	IRIS 313-15902	1111266	<i>Xa4</i>	High yielding in new plant type II (NPT) background
H	IR45427-2B-2-2B-1-1	IRRI	IRIS 313-15899	1935108	<i>Xa4</i>	Iron toxicity tolerance

[†]GID, germplasm identification.

Table S2.2. *Xanthomonas oryzae* strains used for inoculations.

Pathovar	Strain	Origin	Region - Site	Race	XopAJ (avrXo1)	Screening	Screening site	Reference
<i>Xoc</i>	BAI5	Burkina Faso	Hauts Bassins - Vallée du Kou		-	S4, S8	Growth chamber, greenhouse	(Wonni et al., 2014)
<i>Xoc</i>	BLS256	Philippines	Los Baños		+	S8	Greenhouse	(Bogdanove et al., 2011‡)
<i>Xoc</i>	MAI3	Mali	O. Niger - Niono		+	S4	Growth chamber	(Gonzalez et al., 2007)
<i>Xoc</i>	MAI10	Mali	O. Niger - Niono		-	S8	Field	(Gonzalez et al., 2007)
<i>Xoc</i>	MAI46	Mali	Koulikoro - Baguineda		+	S8	Field	(Wonni et al., 2014)
<i>Xoc</i>	MAI61	Mali	O.Niger - Madina		+	S8	Field	unpublished
<i>Xoc</i>	MAI67	Mali	O. Niger - Niono		+	S8	Field	unpublished
<i>Xoc</i>	MAI77	Mali	Sikasso - Sélingué		+	S8	Field	unpublished
<i>Xoc</i>	MAI123	Mali	O.Niger - Bewani		+	S8	Field	unpublished
<i>Xoc</i>	MAI139	Mali	O.Niger Kogoni		+	S8	Field	unpublished
<i>Xoo</i>	BAI3	Burkina Faso	East center - Bagre	A1		S4, S8	Greenhouse	(Gonzalez et al., 2007)
<i>Xoo</i>	CFBP1951	Mali	Kayes	A3		S8	Field	unpublished
<i>Xoo</i>	MAI1	Mali	O. Niger - Niono	A3		S4	Greenhouse	(Gonzalez et al., 2007)
<i>Xoo</i>	MAI70	Mali	O. Niger - Niono	A6		S8	Field	unpublished
<i>Xoo</i>	MAI72	Mali	O. Niger - Niono	A5		S8	Field	unpublished
<i>Xoo</i>	MAI93	Mali	O. Niger - Niono	A7		S8	Field	unpublished
<i>Xoo</i>	MAI101	Mali	O. Niger - Niono	A4		S8	Field	unpublished
<i>Xoo</i>	MAI130	Mali	O. Niger - Bewani 2	A9		S8	Field	unpublished
<i>Xoo</i>	MAI133	Mali	O. Niger - Bewani 10	A9		S8	Field	unpublished
<i>Xoo</i>	MAI134	Mali	O. Niger - Kala 3	A3		S8	Field	unpublished
<i>Xoo</i>	MAI136	Mali	O. Niger - Kala 9	A8		S8	Field	unpublished
<i>Xoo</i>	MAI145	Mali	O. Niger - Kouroumari	A6		S8	Field	unpublished

‡ Bogdanove, A.J., Koebnik, R., Lu, H., Furutani, A., Angiuoli, S.V. *et al.* (2011) Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas* spp. *J Bacteriol* **193**, 5450-5464.

Table S2.3. SNP markers and MAGIC AILs used for GWAS and IM analyses in S4 and S8 subsets.

MAGIC subset	Pathovar	Strain	N° AILs screened	Initial SNP dataset	Final dataset used
S4	<i>Xoc</i>	BAI5	171	634,103	7,258
	<i>Xoc</i>	MAI3	174		6,894
	<i>Xoo</i>	BAI3	152		7,390
	<i>Xoo</i>	MAI1	137		3,669
S8	<i>Xoc</i>	BAI5	323	396,361	14,475
	<i>Xoc</i>	BLS256	268		
	<i>Xoc</i>	MAI10	290		
	<i>Xoc</i>	MAI46	288		
	<i>Xoc</i>	MAI61	270		
	<i>Xoc</i>	MAI67	281		
	<i>Xoc</i>	MAI77	280		
	<i>Xoc</i>	MAI123	265		
	<i>Xoc</i>	MAI139	252		
	<i>Xoo</i>	BAI3	325		
	<i>Xoo</i>	CFBP1951	281		
	<i>Xoo</i>	MAI70	309		
	<i>Xoo</i>	MAI72	296		
	<i>Xoo</i>	MAI93	295		
	<i>Xoo</i>	MAI101	270		
	<i>Xoo</i>	MAI130	296		
	<i>Xoo</i>	MAI133	276		
	<i>Xoo</i>	MAI134	295		
	<i>Xoo</i>	MAI136	276		
	<i>Xoo</i>	MAI145	286		

Table S2.4. Significant SNPs in indica MAGIC S4 subset associated with disease resistance to African *Xoc* and *Xoo*, using MLM (P -value < 0.001). Effect estimate corresponds to the phenotypic estimated deviation from the mean of the effect allele at each SNP (a negative effect indicates shorter lesion lengths than the mean and a positive effects indicates the opposite). Effect estimate is calculated in millimeters (mm) for *Xoc* strains and centimeters (cm) for *Xoo* strains. Stars (*) in significance correspondence panel indicate level of significance for GWAS (P -value < 0.001 and q -value > 0.05).

Pathovar	Strain	Marker (Chr_Pos)	P -value	q -value	R^2	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance
<i>Xoc</i>	BAI5	S4_31266738	8.4E-04	6.9E-02	6.9	2.7	A/G	153/13	*
<i>Xoo</i>	BAI3	S4_31716597	8.6E-06	1.5E-01	15.5	9.5	G/A	131/8	*
<i>Xoo</i>	BAI3	S4_31751408	6.1E-06	1.6E-01	16.3	10.0	T/C	132/8	*
<i>Xoo</i>	BAI3	S4_31779189	8.1E-04	8.6E-02	8.6	5.2	C/T	122/15	*
<i>Xoo</i>	BAI3	S4_31803018	2.2E-06	1.8E-01	18.0	10.6	C/T	128/8	*
<i>Xoo</i>	BAI3	S4_34659203	5.6E-04	9.0E-02	9.0	7.4	G/T	139/8	*
<i>Xoo</i>	BAI3	S5_227187	2.3E-04	1.1E-01	10.9	7.3	C/A	118/12	*
<i>Xoo</i>	BAI3	S5_285834	2.3E-04	1.1E-01	10.7	7.3	G/A	129/12	*
<i>Xoo</i>	BAI3	S5_353165	1.1E-04	1.1E-01	11.4	6.8	C/T	126/15	*
<i>Xoo</i>	BAI3	S5_440644	1.5E-04	1.0E-01	10.4	6.7	G/A	127/15	*
<i>Xoo</i>	BAI3	S5_759048	2.7E-04	1.0E-01	10.2	-5.3	C/T	26/108	*
<i>Xoo</i>	BAI3	S5_849560	7.0E-04	9.7E-02	9.7	6.2	C/T	105/17	*
<i>Xoo</i>	BAI3	S5_1200961	7.5E-04	8.4E-02	8.4	5.7	G/A	123/20	*
<i>Xoc</i>	BAI5	S5_1829611	1.2E-04	1.0E-01	10.2	-2.1	C/A	111/33	*
<i>Xoc</i>	BAI5	S5_1833139	2.4E-04	8.7E-02	8.7	-1.9	T/A	119/35	*
<i>Xoc</i>	BAI5	S8_5250168	4.1E-04	8.0E-02	8.0	-3.2	C/T	152/9	*
<i>Xoc</i>	BAI5	S8_5469156	6.4E-04	7.5E-02	7.5	-2.0	C/T	118/34	*
<i>Xoo</i>	MAI1	S9_12266970	3.9E-04	1.1E-01	10.9	-6.2	G/C	121/7	*
<i>Xoo</i>	BAI3	S9_21002076	6.6E-04	9.7E-02	9.7	4.2	G/A	57/68	*
<i>Xoo</i>	BAI3	S9_21176469	8.8E-04	8.8E-02	8.8	-7.6	G/T	123/9	*
<i>Xoo</i>	BAI3	S9_21243301	4.2E-04	1.1E-01	11.0	5.7	T/C	26/96	*
<i>Xoo</i>	BAI3	S9_21291790	3.4E-04	1.2E-01	12.0	5.4	T/C	26/102	*
<i>Xoo</i>	BAI3	S9_21291867	1.6E-04	1.2E-01	12.4	5.9	A/C	27/104	*

Continuation Table S2.4.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance
Xoo	MAI1	S11_26195519	8.1E-04	1.0E-01	10.0	-4.3	C/A	114/12	*
Xoo	BAI3	S11_27412501	4.8E-04	9.0E-02	9.0	6.1	C/G	16/120	*
Xoo	BAI3	S11_27412530	6.4E-04	8.7E-02	8.7	6.0	C/T	16/119	*
Xoo	BAI3	S11_27437727	2.7E-04	1.0E-01	10.5	6.0	G/A	19/113	*
Xoo	MAI1	S11_27451641	3.8E-04	1.2E-01	11.9	-4.0	C/G	103/17	*
Xoo	BAI3	S11_27677943	3.4E-04	1.0E-01	10.2	-7.7	A/G	124/11	*
Xoo	BAI3	S11_27677963	3.4E-04	1.0E-01	10.2	-7.7	T/C	124/11	*
Xoo	BAI3	S11_28652283	8.1E-04	8.9E-02	8.9	-5.1	A/C	112/25	*
Xoo	BAI3	S11_28697227	1.8E-04	1.1E-01	11.5	5.5	G/A	27/104	*
Xoo	BAI3	S11_28733787	4.4E-04	9.4E-02	9.4	-7.1	C/A	130/13	*
Xoo	BAI3	S11_28760878	1.8E-04	1.3E-01	13.5	-6.0	C/T	96/25	*
Xoo	BAI3	S11_28793592	2.5E-05	1.5E-01	15.1	-9.3	C/T	110/11	*
Xoo	BAI3	S11_28807359	5.1E-04	8.8E-02	8.8	-7.2	G/A	137/12	*
Xoo	BAI3	S11_28809570	1.4E-05	1.6E-01	15.8	-8.7	C/G	124/13	*
Xoo	BAI3	S11_28809652	4.9E-05	1.2E-01	11.9	-7.8	C/G	133/14	*
Xoo	BAI3	S11_28809654	4.8E-05	1.2E-01	11.9	-7.9	A/G	132/14	*
Xoo	BAI3	S11_28865030	9.2E-05	1.2E-01	11.8	-5.9	C/G	112/27	*
Xoo	BAI3	S11_28870403	1.2E-04	1.2E-01	12.0	-5.7	T/C	105/26	*
Xoo	BAI3	S11_28870482	4.4E-05	1.5E-01	14.7	-6.4	A/G	99/24	*
Xoo	BAI3	S11_28870897	6.0E-04	9.1E-02	9.1	-5.2	A/C	108/24	*
Xoo	BAI3	S11_28870941	6.0E-05	1.3E-01	13.2	-6.2	G/T	107/25	*
Xoc	MAI3	S11_28871165	4.3E-04	8.5E-02	8.5	-2.6	G/C	147/13	*
Xoo	BAI3	S11_28871228	9.1E-04	9.4E-02	9.4	5.0	C/G	25/99	*
Xoo	BAI3	S11_28896330	1.8E-04	1.0E-01	10.5	-8.0	A/G	137/11	*
Xoo	BAI3	S11_28896471	1.3E-04	1.2E-01	12.4	-7.4	G/A	110/14	*
Xoo	BAI3	S11_28920280	5.3E-04	1.0E-01	10.3	5.6	A/T	23/104	*
Xoc	MAI3	S11_28920303	3.3E-04	9.1E-02	9.1	-2.5	C/A	140/14	*

Table S2.5. Significant SNPs in indica MAGIC S8 subset associated with disease resistance to African and Asian *Xoc* and *Xoo*, using MLM (P -value < 0.001). Effect estimate corresponds to the phenotypic estimated deviation from the mean of the effect allele at each SNP (a negative effect indicates shorter lesion lengths than the mean and a positive effects indicates the opposite). Effect estimate is calculated in millimeters (mm) for *Xoc* strains and centimeters (cm) for *Xoo* strains. Stars in significance correspondence panel indicate level of significance of GWAS markers as follows: (*) P -value < 0.001 and q-value > 0.05; (**) P -value < 0.001 and q-value < 0.05; (***) P -value < 0.0001 and q-value < 0.05. Bold: significant SNP detected by more than one *X. oryzae* strain. The locus ID for each SNP was predicted from the MSU7 rice reference annotation. Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes.

Pathovar	Strain	Marker (Chr_Pos)	P -value	q-value	R^2	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI130	S1_485081	3.5E-04	2.2E-01	4.9	3.0	C/G	28/231	*	LOC_Os01g01890	expressed protein
<i>Xoo</i>	MAI130	S1_498819	7.3E-04	3.5E-01	4.2	2.8	T/C	29/248	*	LOC_Os01g01920	HD domain containing protein 2, putative, expressed
<i>Xoo</i>	MAI133	S1_2867144	5.9E-04	3.4E-01	5.0	-1.7	C/A	198/46	*	LOC_Os01g06000	PPR repeat containing protein, expressed
<i>Xoo</i>	MAI133	S1_2885468	4.1E-04	3.4E-01	5.4	-1.7	A/G	199/50	*	LOC_Os01g06030	expressed protein
<i>Xoo</i>	MAI133	S1_2885521	3.0E-04	3.4E-01	5.7	-1.8	T/C	198/45	*	LOC_Os01g06030	expressed protein
<i>Xoo</i>	MAI133	S1_2899652	4.4E-04	3.4E-01	5.4	-1.7	G/A	198/47	*	LOC_Os01g06070	expressed protein
<i>Xoc</i>	MAI123	S1_5574004	3.2E-04	5.2E-01	5.2	-2.6	A/G	199/36	*		intergenic
<i>Xoc</i>	MAI123	S1_5593624	7.4E-05	5.2E-01	7.1	-2.9	A/T	182/36	*	LOC_Os01g10530	expressed protein
<i>Xoo</i>	MAI134	S1_18200721	4.5E-04	9.1E-01	5.5	-1.8	C/G	236/16	*		intergenic
<i>Xoo</i>	MAI134	S1_32124854	3.2E-04	9.1E-01	5.2	-1.2	T/C	234/40	*	LOC_Os01g55770	expressed protein
<i>Xoo</i>	MAI133	S2_2838357	2.1E-04	3.4E-01	5.8	1.4	T/G	131/112	*	LOC_Os02g05770	expressed protein
<i>Xoc</i>	MAI61	S2_5164029	1.5E-04	9.1E-01	5.9	-2.2	C/T	141/84	*		intergenic
<i>Xoc</i>	MAI61	S2_5254453	8.3E-04	9.1E-01	4.6	-1.9	G/A	166/82	*	LOC_Os02g10090	expressed protein
<i>Xoc</i>	MAI61	S2_5259884	4.6E-04	9.1E-01	5.1	-2.0	G/T	158/82	*	LOC_Os02g10100	leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed
<i>Xoc</i>	MAI61	S2_5281537	7.3E-04	9.1E-01	4.6	-2.0	C/T	160/77	*	LOC_Os02g10120	lipoxygenase, putative, expressed
<i>Xoc</i>	MAI10	S2_10360915	2.9E-04	3.0E-01	5.0	-2.4	A/G	139/119	*	LOC_Os02g17880	glycosyl hydrolases family 16, putative, expressed
<i>Xoo</i>	MAI134	S2_23098915	6.8E-04	9.1E-01	4.7	-1.6	A/C	252/19	*	LOC_Os02g38180	expressed protein
<i>Xoc</i>	MAI139	S2_23223948	8.5E-04	6.8E-01	5.7	-4.2	G/A	183/32	*		intergenic
<i>Xoo</i>	MAI134	S2_23384851	9.9E-04	9.1E-01	4.3	-1.5	A/G	268/21	*	LOC_Os02g38690	protein phosphatase 2C containing protein, expressed
<i>Xoc</i>	BLS256	S2_23384882	3.7E-04	1.1E-01	5.5	-11.7	T/G	212/24	*	LOC_Os02g38690	protein phosphatase 2C containing protein, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI67	S2_23467758	3.7E-04	3.7E-01	4.9	-1.7	T/G	201/51	*	LOC_Os02g38820	expressed protein
<i>Xoc</i>	BLS256	S2_23593375	7.7E-04	1.7E-01	4.4	-11.0	C/T	232/24	*	intergenic	
<i>Xoc</i>	BLS256	S2_23684061	7.5E-04	1.7E-01	4.5	-11.0	C/T	232/24	*	LOC_Os02g39210	expressed protein
<i>Xoc</i>	BLS256	S2_23819009	1.9E-05	3.6E-02	7.3	-10.7	A/T	204/45	***	LOC_Os02g39470	cyclin, N-terminal domain containing protein, expressed
<i>Xoc</i>	BLS256	S2_23826988	1.6E-04	8.6E-02	6.3	-8.0	C/A	150/79	*	LOC_Os02g39480	protein phosphatase 2C, putative, expressed
<i>Xoc</i>	BLS256	S2_23827020	9.0E-04	1.8E-01	5.1	-7.1	A/G	154/75	*	LOC_Os02g39480	protein phosphatase 2C, putative, expressed
<i>Xoc</i>	BLS256	S2_23874924	5.6E-05	5.7E-02	6.5	-11.7	A/G	218/31	*	LOC_Os02g39550	calcium-binding mitochondrial protein anon-60Da, putative, expressed
<i>Xoc</i>	BLS256	S2_24006214	3.0E-05	4.2E-02	7.9	-12.1	C/T	188/33	***	LOC_Os02g39750	inorganic phosphate transporter, putative, expressed
<i>Xoc</i>	BLS256	S2_24108025	7.6E-04	1.7E-01	4.7	-7.3	A/C	166/71	*	intergenic	
<i>Xoc</i>	BLS256	S2_24122049	9.6E-04	1.9E-01	4.7	-6.7	T/G	141/92	*	intergenic	
<i>Xoc</i>	BLS256	S2_24135986	1.8E-04	8.6E-02	5.6	-12.5	C/T	227/24	*	LOC_Os02g39910	B4-BTB1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with B4 subfamily conserved sequence, expressed
<i>Xoc</i>	BLS256	S2_24234623	7.0E-04	1.7E-01	4.5	-10.9	A/G	229/26	*	intergenic	
<i>Xoc</i>	BLS256	S2_24273471	3.6E-04	1.1E-01	5.1	-11.5	A/G	224/25	*	LOC_Os02g40090	transporter-related, putative, expressed
<i>Xoc</i>	MAI46	S2_24278919	2.6E-04	2.9E-01	5.2	-5.9	G/C	255/21	*	LOC_Os02g40100	plant protein of unknown function DUF869 domain containing protein, expressed
<i>Xoc</i>	BLS256	S2_24405470	7.3E-04	1.7E-01	4.7	-10.3	G/A	223/28	*	LOC_Os02g40320	PINHEAD, putative, expressed
<i>Xoc</i>	BLS256	S2_24479319	3.3E-04	1.1E-01	5.1	-11.4	C/G	226/26	*	intergenic	
<i>Xoc</i>	BLS256	S2_24480075	4.0E-04	1.2E-01	4.9	-11.6	T/C	229/25	*	intergenic	
<i>Xoc</i>	BLS256	S2_24504679	6.1E-04	1.6E-01	4.7	-8.3	A/G	196/51	*	intergenic	
<i>Xoc</i>	MAI10	S2_24509874	4.6E-04	3.9E-01	4.5	-3.9	A/G	260/19	*	intergenic	
<i>Xoc</i>	MAI46	S2_24509874	7.9E-05	2.9E-01	6.5	-6.7	A/G	258/19	*	intergenic	
<i>Xoc</i>	MAI10	S2_24527947	3.2E-04	3.1E-01	4.9	-4.0	G/A	257/19	*	LOC_Os02g40454	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI46	S2_24527947	1.1E-04	2.9E-01	5.8	-6.5	G/A	256/19	*	LOC_Os02g40454	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B, putative, expressed
<i>Xoc</i>	BLS256	S2_24575274	3.1E-04	1.0E-01	5.1	-5.8	A/G	239/20	*	LOC_Os02g40514	h/ACA ribonucleoprotein complex subunit 3, putative, expressed
<i>Xoc</i>	BLS256	S2_24679759	3.7E-05	4.2E-02	6.8	-11.3	C/T	215/36	***	intergenic	
<i>Xoc</i>	BLS256	S2_24688545	9.4E-05	6.8E-02	7.0	-10.5	C/G	190/38	*	LOC_Os02g40720	expressed protein
<i>Xoc</i>	BLS256	S2_24691050	3.0E-04	1.0E-01	5.7	-8.0	A/G	165/61	*	LOC_Os02g40730	ammonium transporter protein, putative, expressed
<i>Xoc</i>	MAI77	S2_24691050	1.0E-03	6.4E-01	4.6	-2.0	A/G	166/69	*	LOC_Os02g40730	ammonium transporter protein, putative, expressed
<i>Xoc</i>	BLS256	S2_24692377	3.9E-04	1.2E-01	5.1	-9.4	G/T	210/37	*	LOC_Os02g40730	ammonium transporter protein, putative, expressed
<i>Xoc</i>	MAI67	S2_24692377	4.4E-04	4.1E-01	4.9	-1.8	G/T	216/41	*	LOC_Os02g40730	ammonium transporter protein, putative, expressed
<i>Xoc</i>	BLS256	S2_24754613	1.5E-04	8.6E-02	5.7	-10.1	G/A	215/38	*	LOC_Os02g40840	alcohol oxidase, putative, expressed
<i>Xoc</i>	BLS256	S2_24786166	1.1E-04	7.6E-02	5.8	-10.4	C/T	218/37	*	LOC_Os02g40900	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	BLS256	S2_24786718	8.3E-05	6.7E-02	6.1	-10.8	A/C	216/36	*	LOC_Os02g40900	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	BLS256	S2_24791557	8.3E-04	1.7E-01	4.6	-8.9	C/G	208/38	*	intergenic	
<i>Xoc</i>	BLS256	S2_24848131	1.8E-04	8.6E-02	5.5	-9.2	A/T	203/49	*	intergenic	
<i>Xoc</i>	MAI67	S2_24848131	9.9E-04	5.7E-01	4.7	-1.5	A/T	211/50	*	intergenic	
<i>Xoc</i>	BLS256	S2_24874086	1.6E-04	8.6E-02	5.6	-9.5	G/A	202/47	*	LOC_Os02g41500	OsWAK13 - OsWAK receptor-like protein kinase, expressed
<i>Xoc</i>	BLS256	S2_24877663	2.2E-04	8.8E-02	5.4	-9.1	T/A	203/49	*	intergenic	
<i>Xoc</i>	MAI67	S2_24877663	9.5E-04	5.7E-01	4.7	-1.5	T/A	211/50	*	intergenic	
<i>Xoc</i>	BLS256	S2_24937103	5.3E-04	1.4E-01	5.2	-8.4	G/A	193/51	*	intergenic	
<i>Xoc</i>	MAI67	S2_24937103	5.5E-04	4.8E-01	4.7	-1.6	G/A	199/56	*	intergenic	
<i>Xoc</i>	BLS256	S2_25075755	3.7E-05	4.2E-02	7.0	-11.4	G/A	200/37	***	LOC_Os02g41720	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	BLS256	S2_25400243	8.7E-04	1.7E-01	4.4	-10.8	C/T	230/23	*	LOC_Os02g42220	transposon protein, putative, unclassified, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BLS256	S2_25596670	5.7E-04	1.5E-01	4.7	8.0	T/C	53/199	*	LOC_Os02g42585	AP2 domain containing protein, expressed
<i>Xoc</i>	BLS256	S2_25618890	2.6E-04	9.2E-02	5.8	6.7	G/A	107/137	*	LOC_Os02g42590	WD-40 repeat family protein, putative, expressed
<i>Xoc</i>	MAI139	S2_25618890	5.2E-04	5.3E-01	5.3	2.9	G/A	104/123	*	LOC_Os02g42590	WD-40 repeat family protein, putative, expressed
<i>Xoc</i>	BLS256	S2_25639335	6.3E-06	3.0E-02	8.5	8.6	T/A	139/108	***	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	MAI139	S2_25639335	3.0E-04	3.3E-01	5.9	3.1	T/A	134/97	*	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	BLS256	S2_25639338	6.3E-06	3.0E-02	8.5	8.6	A/G	139/108	***	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	MAI139	S2_25639338	3.0E-04	3.3E-01	5.9	3.1	A/G	134/97	*	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	BLS256	S2_25639568	1.2E-05	3.6E-02	7.9	8.4	C/T	140/107	***	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	MAI139	S2_25639568	1.7E-04	2.2E-01	6.5	3.2	C/T	135/96	*	LOC_Os02g42620	protein kinase, putative, expressed
<i>Xoc</i>	BLS256	S2_25654974	1.1E-04	7.3E-02	6.1	7.2	C/A	115/132	*	LOC_Os02g42650	expansin precursor, putative, expressed
<i>Xoc</i>	BLS256	S2_25672672	6.6E-04	1.6E-01	5.0	7.0	T/C	82/143	*	LOC_Os02g42690	zinc finger, C3HC4 type domain containing protein, expressed
<i>Xoc</i>	BLS256	S2_25803692	2.8E-05	4.2E-02	7.2	7.8	A/C	102/140	***	LOC_Os02g42900	expressed protein
<i>Xoc</i>	MAI46	S2_25803692	7.1E-04	5.4E-01	4.5	3.0	A/C	114/145	*	LOC_Os02g42900	expressed protein
<i>Xoc</i>	MAI61	S2_25803692	8.6E-04	9.1E-01	4.5	1.8	A/C	107/137	*	LOC_Os02g42900	expressed protein
<i>Xoc</i>	BLS256	S2_25885474	6.5E-04	1.6E-01	4.7	6.3	C/G	119/124	*	LOC_Os02g43000	cysteine-rich repeat secretory protein 15 precursor, putative, expressed
<i>Xoc</i>	BAI5	S2_26070743	2.8E-04	7.5E-02	4.6	-6.1	A/T	216/79	*	intergenic	
<i>Xoc</i>	BAI5	S2_26126554	4.8E-04	1.2E-01	4.7	-6.1	C/A	201/68	*	LOC_Os02g43314	expressed protein
<i>Xoc</i>	MAI61	S2_26126554	9.5E-05	9.1E-01	6.3	-2.6	C/A	167/60	*	LOC_Os02g43314	expressed protein
<i>Xoc</i>	MAI77	S2_26126554	3.8E-04	3.9E-01	5.2	-2.2	C/A	169/62	*	LOC_Os02g43314	expressed protein
<i>Xoc</i>	MAI123	S2_26126554	5.2E-04	5.8E-01	5.1	-2.1	C/A	163/58	*	LOC_Os02g43314	expressed protein
<i>Xoc</i>	BAI5	S2_26329353	7.3E-04	1.7E-01	3.9	5.2	G/T	117/174	*	LOC_Os02g43630	hypothetical protein
<i>Xoc</i>	BAI5	S2_26349262	8.7E-04	1.9E-01	3.8	-5.6	G/A	220/76	*	LOC_Os02g43670	transferase family protein, putative, expressed
<i>Xoc</i>	MAI77	S2_27203917	6.3E-04	5.2E-01	4.8	-2.6	A/G	204/35	*	LOC_Os02g44900	expressed protein
<i>Xoo</i>	BAI3	S2_27203917	5.9E-04	8.8E-02	4.2	-4.2	A/G	237/40	*	LOC_Os02g44900	expressed protein
<i>Xoc</i>	MAI77	S2_27204005	9.8E-04	6.4E-01	4.1	-2.6	G/A	236/32	*	LOC_Os02g44900	expressed protein
<i>Xoo</i>	MAI136	S2_29845695	8.6E-04	3.2E-01	5.2	-3.3	C/G	184/37	*	intergenic	
<i>Xoo</i>	MAI145	S2_34796411	7.3E-04	2.5E-01	4.4	-2.2	G/T	160/101	*	LOC_Os02g56750	OsFBX65 - F-box domain containing protein, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI130	S2_35216593	1.2E-04	1.1E-01	5.6	-2.3	G/C	225/53	*	LOC_Os02g57460	RING-H2 finger protein ATL5G, putative, expressed
<i>Xoo</i>	MAI130	S2_35217191	2.9E-04	2.0E-01	4.9	-2.2	T/C	224/55	*	LOC_Os02g57460	RING-H2 finger protein ATL5G, putative, expressed
<i>Xoc</i>	BLS256	S3_9153681	8.5E-04	1.7E-01	4.6	9.1	A/G	214/29	*	intergenic	
<i>Xoc</i>	MAI10	S3_12629690	8.4E-04	5.8E-01	5.4	2.2	C/T	74/157	*	LOC_Os03g22040	expressed protein
<i>Xoc</i>	MAI10	S3_12647861	8.8E-05	1.2E-01	5.8	2.4	T/G	82/189	*	LOC_Os03g22070	expressed protein
<i>Xoc</i>	MAI10	S3_12647903	4.9E-04	3.9E-01	4.6	2.2	C/G	78/177	*	LOC_Os03g22070	expressed protein
<i>Xoc</i>	MAI10	S3_12647983	1.5E-04	1.8E-01	5.3	2.3	T/C	85/187	*	LOC_Os03g22070	expressed protein
<i>Xoo</i>	CFBP1951	S3_14528215	8.7E-04	4.4E-01	4.7	-1.4	T/G	214/20	*	LOC_Os03g25400	kinase, putative, expressed
<i>Xoo</i>	MAI133	S3_34779286	8.1E-04	3.4E-01	4.6	-2.1	A/G	216/26	*	LOC_Os03g61240	expressed protein
<i>Xoo</i>	MAI133	S3_34793557	6.7E-04	3.4E-01	5.8	-2.1	A/G	206/27	*	LOC_Os03g61270	OsMan04 - Endo-Beta-Mannanase, expressed
<i>Xoo</i>	MAI133	S3_34793568	6.7E-04	3.4E-01	5.8	-2.1	T/C	206/27	*	LOC_Os03g61270	OsMan04 - Endo-Beta-Mannanase, expressed
<i>Xoo</i>	MAI133	S3_34826622	4.5E-04	3.4E-01	5.3	-2.1	T/G	204/29	*	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed
<i>Xoo</i>	MAI133	S3_34826623	4.5E-04	3.4E-01	5.3	-2.1	A/C	204/29	*	LOC_Os03g61360	hydrolase, alpha/beta fold family domain containing protein, expressed
<i>Xoo</i>	MAI134	S3_34870865	4.4E-04	9.1E-01	5.4	-1.6	G/A	255/21	*	LOC_Os03g61470	uncharacterized Cys-rich domain containing protein, putative, expressed
<i>Xoc</i>	MAI10	S4_1000522	2.9E-04	3.0E-01	5.2	-2.3	C/T	98/157	*	LOC_Os04g02650	expressed protein
<i>Xoc</i>	MAI10	S4_3531897	3.6E-04	3.3E-01	5.6	-2.3	G/C	182/79	*	LOC_Os04g06700	expressed protein
<i>Xoo</i>	MAI101	S4_24924317	3.9E-04	1.4E-01	6.1	-5.1	A/G	198/22	*	LOC_Os04g42100	retrotransposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI101	S4_24924363	3.9E-04	1.4E-01	6.1	-5.1	G/A	198/22	*	LOC_Os04g42100	retrotransposon protein, putative, unclassified, expressed
<i>Xoc</i>	BAI5	S4_29482889	3.9E-05	1.2E-02	5.8	6.1	G/C	208/86	***	intergenic	
<i>Xoc</i>	BAI5	S4_29548991	1.7E-09	2.1E-06	12.4	13.1	G/A	273/35	***	intergenic	
<i>Xoo</i>	BAI3	S4_29548991	5.8E-04	8.8E-02	4.0	4.6	G/A	273/37	*	intergenic	
<i>Xoc</i>	BAI5	S4_29602194	8.0E-04	1.8E-01	3.7	9.6	G/A	289/20	*	intergenic	

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_29783427	1.1E-07	7.4E-05	9.8	-9.2	G/A	69/232	***	LOC_Os04g49930	sensitivity to red light reduced protein 1, putative, expressed
<i>Xoo</i>	BAI3	S4_29783427	5.9E-04	8.8E-02	3.9	-3.8	G/A	72/232	*	LOC_Os04g49930	sensitivity to red light reduced protein 1, putative, expressed
<i>Xoc</i>	BAI5	S4_29788028	3.7E-06	1.4E-03	8.1	-8.1	T/C	63/206	***	LOC_Os04g49940	expressed protein
<i>Xoc</i>	BAI5	S4_29797214	5.7E-07	3.0E-04	8.8	-8.7	G/A	69/230	***	LOC_Os04g49950	OsFBX150 - F-box domain containing protein, expressed
<i>Xoo</i>	BAI3	S4_29797214	6.5E-04	9.2E-02	4.0	-3.8	G/A	72/230	*	LOC_Os04g49950	OsFBX150 - F-box domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_29803185	1.6E-07	9.4E-05	9.6	-9.2	A/G	69/232	***	LOC_Os04g49960	glycosyl transferase, group 1 domain containing protein, expressed
<i>Xoo</i>	BAI3	S4_29803185	6.3E-04	9.0E-02	3.9	-3.8	A/G	72/232	*	LOC_Os04g49960	glycosyl transferase, group 1 domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_29809870	1.4E-07	8.7E-05	9.9	-9.1	T/A	70/231	***	LOC_Os04g49970	U-box, putative, expressed
<i>Xoo</i>	BAI3	S4_29809870	4.7E-04	7.6E-02	4.1	-3.8	T/A	73/231	*	LOC_Os04g49970	U-box, putative, expressed
<i>Xoc</i>	BAI5	S4_29817523	1.5E-06	6.7E-04	9.1	-8.5	T/G	61/210	***	LOC_Os04g49990	AT hook motif domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_29817535	5.8E-06	2.0E-03	7.9	-7.9	C/T	63/210	***	LOC_Os04g49990	AT hook motif domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_29817550	5.8E-06	2.0E-03	7.9	-7.9	G/A	63/210	***	LOC_Os04g49990	AT hook motif domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_29832522	1.0E-04	3.0E-02	5.5	-6.6	A/G	76/200	**	LOC_Os04g50030	DNA binding protein, putative, expressed
<i>Xoc</i>	BAI5	S4_29866691	3.6E-05	1.1E-02	6.0	-6.8	T/A	81/219	***	LOC_Os04g50080	expressed protein
<i>Xoc</i>	BAI5	S4_29868104	1.1E-05	3.6E-03	6.8	-7.4	C/T	78/219	***	intergenic	
<i>Xoo</i>	MAI130	S4_29868104	6.3E-04	3.3E-01	4.5	-2.1	C/T	73/198	*	intergenic	
<i>Xoc</i>	BAI5	S4_29922917	1.1E-04	3.2E-02	5.6	-6.5	T/C	73/196	**	intergenic	
<i>Xoo</i>	BAI3	S4_29922917	2.3E-04	4.3E-02	4.9	-3.9	T/C	76/196	**	intergenic	
<i>Xoc</i>	BLS256	S4_29965442	7.2E-04	1.7E-01	4.7	6.6	C/T	95/147	*	LOC_Os04g50204	protein transport protein-related, putative, expressed
<i>Xoc</i>	BAI5	S4_29966056	2.5E-06	1.0E-03	7.6	-8.1	C/G	67/234	***	LOC_Os04g50204	protein transport protein-related, putative, expressed
<i>Xoo</i>	BAI3	S4_29966056	1.8E-04	3.7E-02	4.7	-4.1	C/G	70/233	**	LOC_Os04g50204	protein transport protein-related, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_29968457	1.0E-05	3.4E-03	7.0	-7.5	T/C	68/227	***	intergenic	
<i>Xoo</i>	BAI3	S4_29968457	9.1E-04	1.2E-01	3.7	-3.6	T/C	71/227	*	intergenic	
<i>Xoc</i>	BAI5	S4_29968490	1.1E-05	3.6E-03	6.9	-7.5	G/C	67/231	***	intergenic	
<i>Xoo</i>	BAI3	S4_29968490	1.7E-04	3.5E-02	4.9	-4.1	G/C	70/231	**	intergenic	
<i>Xoo</i>	MAI130	S4_30019173	6.6E-04	3.3E-01	4.7	-1.9	G/A	101/170	*	LOC_Os04g50740	ara54-like RING finger protein, putative, expressed
<i>Xoo</i>	MAI130	S4_30047908	2.3E-05	2.6E-02	7.1	-2.4	T/A	84/185	***	LOC_Os04g50790	RNA recognition motif, putative, expressed
<i>Xoo</i>	MAI130	S4_30080184	4.2E-05	4.1E-02	6.5	-2.3	G/A	82/178	***	LOC_Os04g50860	expressed protein
<i>Xoc</i>	BAI5	S4_30764890	2.6E-06	1.0E-03	8.7	-7.7	A/G	77/194	***	LOC_Os04g51880	GHMP kinases ATP-binding protein, putative, expressed
<i>Xoc</i>	BAI5	S4_30790417	3.7E-08	3.4E-05	10.8	-8.9	G/T	79/213	***	intergenic	
<i>Xoc</i>	BAI5	S4_30808530	4.1E-07	2.3E-04	9.2	-8.6	A/G	75/219	***	LOC_Os04g51920	protein disulfide isomerase, putative, expressed
<i>Xoc</i>	BAI5	S4_31263800	1.0E-07	6.9E-05	9.5	15.7	C/T	295/16	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31263806	1.0E-07	6.9E-05	9.5	15.7	T/C	295/16	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31263820	1.0E-07	6.9E-05	9.5	15.7	C/T	295/16	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31263829	9.4E-07	4.6E-04	8.3	13.9	C/T	278/17	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31264880	1.7E-06	7.1E-04	8.1	13.9	A/G	278/17	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31264887	1.7E-06	7.1E-04	8.1	13.9	T/C	278/17	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31264905	8.1E-07	4.0E-04	8.1	14.4	G/A	294/17	***	LOC_Os04g52590	protein kinase domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_31316473	6.6E-07	3.4E-04	9.6	14.0	C/T	261/18	***	LOC_Os04g52630	leucine-rich repeat-containing protein kinase family protein, putative, expressed
<i>Xoc</i>	BAI5	S4_31420093	1.1E-04	3.2E-02	5.0	9.7	A/T	286/21	**	LOC_Os04g52770	helix-loop-helix DNA-binding domain containing protein, expressed
<i>Xoo</i>	BAI3	S4_31420093	2.7E-05	8.5E-03	5.8	6.9	A/T	289/20	***	LOC_Os04g52770	helix-loop-helix DNA-binding domain containing protein, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_31498999	8.0E-08	6.4E-05	9.8	15.1	G/C	290/17	***	LOC_Os04g52890	ATBAG1, putative, expressed
<i>Xoc</i>	MAI139	S4_31498999	6.2E-04	5.6E-01	4.9	6.2	G/C	226/12	*	LOC_Os04g52890	ATBAG1, putative, expressed
<i>Xoc</i>	BAI5	S4_31531412	8.7E-04	1.9E-01	3.7	-4.8	T/A	92/209	*	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed
<i>Xoc</i>	MAI67	S4_31531412	6.1E-04	4.9E-01	4.5	-1.3	T/A	84/177	*	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed
<i>Xoo</i>	BAI3	S4_31531412	1.8E-05	6.3E-03	6.1	-4.0	T/A	93/211	***	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed
<i>Xoo</i>	MAI70	S4_31531412	1.9E-04	1.7E-01	5.1	-3.3	T/A	88/198	*	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed
<i>Xoo</i>	MAI130	S4_31531412	4.0E-05	4.1E-02	6.8	-2.2	T/A	85/190	***	LOC_Os04g52940	SIT4 phosphatase-associated protein domain containing protein, expressed
<i>Xoc</i>	MAI46	S4_31553238	1.5E-04	2.9E-01	6.8	-4.4	T/C	194/45	*	LOC_Os04g52970	NBS-LRR disease resistance protein, putative, expressed
<i>Xoc</i>	MAI123	S4_31553238	4.3E-04	5.2E-01	6.2	-2.4	T/C	176/42	*	LOC_Os04g52970	NBS-LRR disease resistance protein, putative, expressed
<i>Xoc</i>	MAI46	S4_31553264	1.5E-04	2.9E-01	6.8	-4.4	T/C	194/45	*	LOC_Os04g52970	NBS-LRR disease resistance protein, putative, expressed
<i>Xoc</i>	MAI123	S4_31553264	4.3E-04	5.2E-01	6.2	-2.4	T/C	176/42	*	LOC_Os04g52970	NBS-LRR disease resistance protein, putative, expressed
<i>Xoc</i>	MAI46	S4_31559540	2.5E-04	2.9E-01	5.9	-3.7	A/C	190/67	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	MAI67	S4_31559540	8.7E-04	5.7E-01	4.9	-1.3	A/C	188/65	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	MAI46	S4_31559557	2.3E-04	2.9E-01	5.9	-3.7	G/T	190/66	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	MAI67	S4_31559557	8.3E-04	5.7E-01	5.0	-1.4	G/T	188/64	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	MAI46	S4_31559582	2.5E-04	2.9E-01	5.9	-3.7	T/C	190/67	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	MAI67	S4_31559582	8.7E-04	5.7E-01	4.9	-1.3	T/C	188/65	*	LOC_Os04g52980	expressed protein
<i>Xoc</i>	BAI5	S4_31669472	5.7E-08	4.9E-05	10.2	-7.7	A/G	140/160	***	LOC_Os04g53195	expressed protein
<i>Xoo</i>	MAI130	S4_31669472	9.2E-06	1.2E-02	7.8	-2.3	A/G	130/146	***	LOC_Os04g53195	expressed protein
<i>Xoc</i>	BAI5	S4_31670015	1.3E-06	6.2E-04	8.3	-7.1	T/G	149/146	***	LOC_Os04g53190	CPuORF12 - conserved peptide uORF-containing transcript, expressed
<i>Xoo</i>	MAI130	S4_31670015	1.3E-05	1.5E-02	7.7	-2.3	T/G	136/135	***	LOC_Os04g53190	CPuORF12 - conserved peptide uORF-containing transcript, expressed
<i>Xoc</i>	BAI5	S4_31716597	2.9E-17	2.1E-13	27.7	18.2	G/A	267/32	***	LOC_Os04g53240	autophagy-related protein, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI10	S4_31716597	3.8E-06	2.7E-02	8.1	4.3	G/A	239/26	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	MAI61	S4_31716597	6.0E-04	9.1E-01	5.4	3.0	G/A	223/26	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	MAI67	S4_31716597	3.6E-06	5.7E-03	8.4	2.6	G/A	229/29	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	MAI77	S4_31716597	1.4E-05	6.6E-02	7.3	3.7	G/A	232/27	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	MAI123	S4_31716597	2.8E-04	5.2E-01	5.2	3.0	G/A	219/25	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	MAI139	S4_31716597	8.3E-05	1.7E-01	6.8	5.1	G/A	206/25	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	BAI3	S4_31716597	6.8E-17	4.9E-13	25.1	11.6	G/A	270/31	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	CFBP1951	S4_31716597	8.2E-05	7.0E-02	6.0	1.4	G/A	229/29	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	MAI70	S4_31716597	3.4E-09	2.1E-05	12.9	7.9	G/A	251/30	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	MAI101	S4_31716597	2.6E-05	2.2E-02	7.3	5.3	G/A	221/26	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	MAI130	S4_31716597	2.3E-06	5.3E-03	8.5	3.7	G/A	242/29	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	MAI136	S4_31716597	2.2E-05	4.7E-02	7.1	4.3	G/A	225/29	***	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoo</i>	MAI145	S4_31716597	1.0E-04	6.0E-02	5.7	3.9	G/A	234/29	*	LOC_Os04g53240	autophagy-related protein, putative, expressed
<i>Xoc</i>	BAI5	S4_31721763	6.3E-04	1.5E-01	3.9	-5.9	C/A	237/63	*	LOC_Os04g53250	polyphenol oxidase protein, putative, expressed
<i>Xoc</i>	BAI5	S4_31728040	1.1E-14	2.3E-11	23.2	16.4	C/G	256/32	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI10	S4_31728040	2.7E-05	5.6E-02	7.6	3.9	C/G	230/26	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI67	S4_31728040	4.4E-06	6.3E-03	9.6	2.6	C/G	219/29	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI77	S4_31728040	1.1E-04	1.6E-01	5.9	3.2	C/G	217/28	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI123	S4_31728040	3.8E-04	5.2E-01	5.1	3.0	C/G	210/24	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI139	S4_31728040	3.2E-05	1.7E-01	7.8	5.2	C/G	194/27	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	BAI3	S4_31728040	1.1E-12	1.8E-09	19.5	9.7	C/G	260/31	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	CFBP1951	S4_31728040	5.3E-05	6.2E-02	6.4	1.4	C/G	219/29	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI70	S4_31728040	5.6E-08	1.0E-04	11.4	7.1	C/G	243/31	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI101	S4_31728040	1.7E-05	2.1E-02	7.9	5.4	C/G	211/27	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI130	S4_31728040	4.7E-06	6.7E-03	8.0	3.6	C/G	233/30	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI133	S4_31728040	1.9E-04	3.4E-01	5.8	2.2	C/G	206/29	*	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI136	S4_31728040	2.4E-05	4.7E-02	8.0	4.3	C/G	215/29	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI145	S4_31728040	5.1E-05	3.7E-02	6.2	4.0	C/G	222/30	***	LOC_Os04g53260	polyphenol oxidase, putative, expressed
<i>Xoc</i>	BAI5	S4_31751408	2.6E-14	4.7E-11	22.2	16.4	T/C	256/33	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI10	S4_31751408	4.3E-05	6.9E-02	7.3	3.8	T/C	230/27	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI46	S4_31751408	7.0E-04	5.4E-01	4.7	4.6	T/C	226/30	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI67	S4_31751408	1.3E-06	3.5E-03	9.4	2.6	T/C	223/31	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI77	S4_31751408	2.2E-05	6.6E-02	7.4	3.5	T/C	224/29	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	MAI139	S4_31751408	7.5E-05	1.7E-01	7.2	4.9	T/C	200/28	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	BAI3	S4_31751408	4.6E-14	9.6E-11	20.9	10.5	T/C	260/32	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	CFBP1951	S4_31751408	6.1E-05	6.6E-02	6.3	1.4	T/C	221/31	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI70	S4_31751408	2.9E-08	6.0E-05	12.2	7.2	T/C	240/32	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI101	S4_31751408	2.2E-05	2.1E-02	7.9	5.3	T/C	215/28	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI130	S4_31751408	3.3E-06	5.3E-03	9.2	3.6	T/C	234/31	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI133	S4_31751408	7.3E-04	3.4E-01	4.8	1.9	T/C	211/31	*	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI136	S4_31751408	2.6E-05	4.7E-02	8.4	4.2	T/C	219/31	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoo</i>	MAI145	S4_31751408	2.3E-05	2.2E-02	7.9	4.2	T/C	227/31	***	LOC_Os04g53300	polyphenol oxidase, putative, expressed
<i>Xoc</i>	BAI5	S4_31778051	2.3E-15	7.6E-12	26.0	18.1	C/T	253/28	***	LOC_Os04g53360	expressed protein
<i>Xoc</i>	MAI10	S4_31778051	9.3E-06	2.7E-02	7.8	4.4	C/T	228/23	***	LOC_Os04g53360	expressed protein
<i>Xoc</i>	MAI67	S4_31778051	1.1E-06	3.5E-03	9.7	2.9	C/T	217/26	***	LOC_Os04g53360	expressed protein
<i>Xoc</i>	MAI77	S4_31778051	5.4E-04	5.2E-01	4.6	3.0	C/T	218/25	*	LOC_Os04g53360	expressed protein
<i>Xoc</i>	MAI123	S4_31778051	6.6E-04	6.3E-01	4.8	3.0	C/T	208/22	*	LOC_Os04g53360	expressed protein
<i>Xoc</i>	MAI139	S4_31778051	1.1E-04	1.9E-01	7.8	5.2	C/T	196/23	*	LOC_Os04g53360	expressed protein
<i>Xoo</i>	BAI3	S4_31778051	6.9E-15	2.5E-11	24.7	11.5	C/T	256/27	***	LOC_Os04g53360	expressed protein
<i>Xoo</i>	CFBP1951	S4_31778051	8.5E-05	7.0E-02	6.2	1.5	C/T	218/26	*	LOC_Os04g53360	expressed protein
<i>Xoo</i>	MAI70	S4_31778051	7.3E-09	2.1E-05	13.8	7.9	C/T	241/28	***	LOC_Os04g53360	expressed protein
<i>Xoo</i>	MAI101	S4_31778051	2.1E-05	2.1E-02	7.7	5.4	C/T	211/25	***	LOC_Os04g53360	expressed protein
<i>Xoo</i>	MAI130	S4_31778051	3.0E-06	5.3E-03	8.8	3.8	C/T	232/27	***	LOC_Os04g53360	expressed protein
<i>Xoo</i>	MAI136	S4_31778051	7.0E-05	6.3E-02	6.8	4.3	C/T	217/26	*	LOC_Os04g53360	expressed protein
<i>Xoo</i>	MAI145	S4_31778051	4.4E-05	3.5E-02	7.5	4.4	C/T	222/26	***	LOC_Os04g53360	expressed protein
<i>Xoc</i>	BAI5	S4_31781274	9.0E-04	1.9E-01	3.6	-5.6	T/C	240/64	*	intergenic	

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_31782187	8.7E-04	1.9E-01	3.9	-5.6	A/G	228/62	*	intergenic	
<i>Xoc</i>	BAI5	S4_31786637	4.6E-04	1.2E-01	4.1	5.7	A/G	61/240	*	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoc</i>	BAI5	S4_31787320	1.7E-09	2.1E-06	12.9	-9.0	C/G	113/183	***	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoc</i>	MAI46	S4_31787320	3.3E-04	3.4E-01	5.2	-3.2	C/G	97/166	*	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoc</i>	MAI67	S4_31787320	1.0E-04	1.2E-01	6.0	-1.4	C/G	97/160	*	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoo</i>	BAI3	S4_31787320	4.1E-04	6.6E-02	4.2	-3.3	C/G	113/185	*	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoo</i>	MAI130	S4_31787320	2.5E-04	1.9E-01	5.5	-2.0	C/G	99/171	*	LOC_Os04g53370	acyltransferase, putative, expressed
<i>Xoc</i>	BAI5	S4_31800256	1.2E-04	3.2E-02	5.1	5.7	G/A	202/95	**	LOC_Os04g53380	expressed protein
<i>Xoo</i>	BAI3	S4_31800256	1.1E-05	4.4E-03	6.6	4.2	G/A	204/96	***	LOC_Os04g53380	expressed protein
<i>Xoc</i>	BAI5	S4_31801219	4.9E-17	2.3E-13	26.0	18.7	C/A	281/30	***	LOC_Os04g53380	expressed protein
<i>Xoc</i>	MAI10	S4_31801219	1.3E-05	3.2E-02	7.0	4.2	C/A	253/24	***	LOC_Os04g53380	expressed protein
<i>Xoc</i>	MAI67	S4_31801219	2.1E-06	3.7E-03	8.6	2.7	C/A	240/28	***	LOC_Os04g53380	expressed protein
<i>Xoc</i>	MAI77	S4_31801219	2.6E-05	6.6E-02	6.7	3.6	C/A	241/26	*	LOC_Os04g53380	expressed protein
<i>Xoc</i>	MAI123	S4_31801219	4.2E-04	5.2E-01	4.9	3.0	C/A	231/24	*	LOC_Os04g53380	expressed protein
<i>Xoc</i>	MAI139	S4_31801219	6.9E-05	1.7E-01	6.8	5.1	C/A	218/25	*	LOC_Os04g53380	expressed protein
<i>Xoo</i>	BAI3	S4_31801219	1.8E-16	8.4E-13	24.4	11.9	C/A	285/29	***	LOC_Os04g53380	expressed protein
<i>Xoo</i>	CFBP1951	S4_31801219	4.6E-05	5.9E-02	6.3	1.5	C/A	241/28	*	LOC_Os04g53380	expressed protein
<i>Xoo</i>	MAI70	S4_31801219	5.6E-09	2.1E-05	12.2	7.9	C/A	266/29	***	LOC_Os04g53380	expressed protein
<i>Xoo</i>	MAI101	S4_31801219	1.7E-05	2.1E-02	7.4	5.6	C/A	232/25	***	LOC_Os04g53380	expressed protein
<i>Xoo</i>	MAI130	S4_31801219	1.7E-06	5.3E-03	8.4	3.9	C/A	255/28	***	LOC_Os04g53380	expressed protein
<i>Xoo</i>	MAI136	S4_31801219	1.4E-05	4.7E-02	7.3	4.5	C/A	237/28	***	LOC_Os04g53380	expressed protein
<i>Xoo</i>	MAI145	S4_31801219	3.3E-05	3.0E-02	6.6	4.3	C/A	246/28	***	LOC_Os04g53380	expressed protein
<i>Xoc</i>	BAI5	S4_31803015	4.7E-09	5.2E-06	14.4	-8.9	G/A	93/167	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI46	S4_31803015	2.4E-04	2.9E-01	5.9	-3.5	G/A	82/150	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI67	S4_31803015	6.3E-04	4.9E-01	5.3	-1.3	G/A	82/144	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI77	S4_31803015	3.3E-04	3.7E-01	5.3	-2.1	G/A	83/145	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	BAI3	S4_31803015	6.1E-04	8.9E-02	4.7	-3.3	G/A	92/170	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI70	S4_31803015	9.3E-04	5.2E-01	4.4	-3.0	G/A	87/160	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI130	S4_31803015	6.4E-04	3.3E-01	4.9	-1.9	G/A	84/153	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	BAI5	S4_31803018	3.2E-15	7.6E-12	27.6	17.6	C/T	233/31	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI10	S4_31803018	8.6E-06	2.7E-02	8.3	4.3	C/T	211/25	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI46	S4_31803018	8.2E-04	5.7E-01	4.9	4.7	C/T	206/28	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI67	S4_31803018	1.4E-06	3.5E-03	10.5	2.7	C/T	199/29	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI77	S4_31803018	2.5E-05	6.6E-02	7.2	3.6	C/T	204/27	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI123	S4_31803018	1.8E-04	5.2E-01	6.1	3.2	C/T	191/25	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI139	S4_31803018	1.2E-04	1.9E-01	7.3	5.0	C/T	184/25	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	BAI3	S4_31803018	3.9E-14	9.6E-11	24.8	10.9	C/T	236/30	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	CFBP1951	S4_31803018	3.3E-04	2.3E-01	7.1	1.3	C/T	202/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI70	S4_31803018	8.5E-09	2.1E-05	13.5	7.8	C/T	220/30	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI101	S4_31803018	5.1E-05	3.3E-02	7.5	5.2	C/T	193/26	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI130	S4_31803018	6.1E-07	4.8E-03	10.3	4.0	C/T	212/29	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI136	S4_31803018	1.6E-04	1.1E-01	8.1	3.9	C/T	199/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI145	S4_31803018	4.4E-04	2.0E-01	5.8	3.6	C/T	207/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	BAI5	S4_31803029	3.0E-15	7.6E-12	27.7	17.6	G/A	231/31	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI10	S4_31803029	8.7E-06	2.7E-02	8.3	4.3	G/A	209/25	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI46	S4_31803029	9.0E-04	5.7E-01	4.8	4.7	G/A	204/28	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI67	S4_31803029	1.5E-06	3.5E-03	10.5	2.7	G/A	197/29	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI77	S4_31803029	2.9E-05	6.6E-02	7.1	3.6	G/A	202/27	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoc</i>	MAI123	S4_31803029	1.9E-04	5.2E-01	6.0	3.2	G/A	189/25	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI139	S4_31803029	1.3E-04	1.9E-01	7.2	5.0	G/A	182/25	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	BAI3	S4_31803029	4.0E-14	9.6E-11	24.9	10.9	G/A	234/30	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	CFBP1951	S4_31803029	3.2E-04	2.3E-01	7.2	1.3	G/A	200/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI70	S4_31803029	8.1E-09	2.1E-05	13.6	7.8	G/A	218/30	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI101	S4_31803029	4.8E-05	3.3E-02	7.5	5.3	G/A	191/26	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI130	S4_31803029	6.6E-07	4.8E-03	10.3	4.0	G/A	210/29	***	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI136	S4_31803029	1.7E-04	1.1E-01	8.2	3.9	G/A	197/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed
<i>Xoo</i>	MAI145	S4_31803029	4.8E-04	2.1E-01	5.7	3.6	G/A	205/29	*	LOC_Os04g53390	MrBTB2 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH-related domain, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_31812050	2.1E-08	2.1E-05	10.6	16.0	G/T	296/17	***	LOC_Os04g53410	MBTB7 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain, expressed
<i>Xoc</i>	MAI139	S4_31812050	5.9E-04	5.6E-01	5.0	6.2	G/T	232/12	*	LOC_Os04g53410	MBTB7 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain, expressed
<i>Xoc</i>	BAI5	S4_31819592	1.2E-17	1.7E-13	27.5	18.9	G/T	276/31	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI10	S4_31819592	5.2E-06	2.7E-02	7.7	4.4	G/T	249/25	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI46	S4_31819592	8.1E-04	5.7E-01	4.3	4.7	G/T	243/28	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI67	S4_31819592	9.6E-07	3.5E-03	9.3	2.7	G/T	236/29	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI77	S4_31819592	1.4E-05	6.6E-02	7.2	3.7	G/T	238/27	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI123	S4_31819592	2.6E-04	5.2E-01	5.3	3.1	G/T	227/25	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	MAI139	S4_31819592	3.4E-05	1.7E-01	7.4	5.3	G/T	214/26	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	BAI3	S4_31819592	4.6E-17	4.9E-13	25.4	12.0	G/T	280/30	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	CFBP1951	S4_31819592	3.5E-05	5.5E-02	6.5	1.5	G/T	237/29	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	MAI70	S4_31819592	6.0E-09	2.1E-05	12.4	7.8	G/T	262/30	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	MAI101	S4_31819592	1.3E-05	2.1E-02	7.6	5.6	G/T	228/26	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	MAI130	S4_31819592	1.6E-06	5.3E-03	8.8	3.8	G/T	251/29	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	MAI133	S4_31819592	8.2E-04	3.4E-01	4.5	2.0	G/T	222/29	*	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoo</i>	MAI136	S4_31819592	1.3E-05	4.7E-02	7.7	4.5	G/T	233/29	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI145	S4_31819592	1.4E-05	1.6E-02	7.2	4.4	G/T	242/29	***	LOC_Os04g53440	RNA recognition motif containing protein, putative, expressed
<i>Xoc</i>	BAI5	S4_31956274	5.9E-09	6.2E-06	13.4	11.6	C/T	246/35	***	LOC_Os04g53600	expressed protein
<i>Xoc</i>	MAI10	S4_31956274	6.4E-04	4.9E-01	4.7	3.0	C/T	220/29	*	LOC_Os04g53600	expressed protein
<i>Xoc</i>	MAI67	S4_31956274	6.3E-06	8.0E-03	8.2	2.4	C/T	209/33	***	LOC_Os04g53600	expressed protein
<i>Xoc</i>	MAI77	S4_31956274	3.1E-04	3.7E-01	5.5	2.9	C/T	211/30	*	LOC_Os04g53600	expressed protein
<i>Xoc</i>	MAI139	S4_31956274	7.3E-04	6.2E-01	5.0	4.2	C/T	192/27	*	LOC_Os04g53600	expressed protein
<i>Xoo</i>	BAI3	S4_31956274	1.2E-10	1.6E-07	15.9	8.3	C/T	248/35	***	LOC_Os04g53600	expressed protein
<i>Xoo</i>	CFBP1951	S4_31956274	5.7E-04	3.0E-01	5.0	1.2	C/T	210/32	*	LOC_Os04g53600	expressed protein
<i>Xoo</i>	MAI70	S4_31956274	3.5E-05	4.3E-02	6.9	5.2	C/T	234/33	***	LOC_Os04g53600	expressed protein
<i>Xoo</i>	MAI101	S4_31956274	1.9E-04	8.9E-02	5.9	4.4	C/T	202/31	*	LOC_Os04g53600	expressed protein
<i>Xoo</i>	MAI130	S4_31956274	8.8E-05	8.0E-02	6.5	3.0	C/T	224/32	*	LOC_Os04g53600	expressed protein
<i>Xoo</i>	MAI136	S4_31956274	3.0E-05	4.8E-02	7.7	4.1	C/T	206/33	***	LOC_Os04g53600	expressed protein
<i>Xoo</i>	MAI145	S4_31956274	6.8E-05	4.3E-02	6.6	3.8	C/T	214/33	***	LOC_Os04g53600	expressed protein
<i>Xoc</i>	BAI5	S4_31962475	1.5E-10	2.1E-07	14.3	11.8	G/A	270/42	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI10	S4_31962475	8.0E-05	1.2E-01	5.6	3.3	G/A	245/33	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI46	S4_31962475	5.8E-04	5.3E-01	4.6	4.3	G/A	240/35	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI67	S4_31962475	1.5E-06	3.5E-03	8.8	2.4	G/A	232/37	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI77	S4_31962475	7.7E-05	1.3E-01	5.9	3.0	G/A	234/35	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI123	S4_31962475	2.5E-04	5.2E-01	5.3	2.7	G/A	224/32	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	MAI139	S4_31962475	7.3E-05	1.7E-01	6.7	4.7	G/A	213/30	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	BAI3	S4_31962475	2.1E-11	3.1E-08	15.3	8.1	G/A	273/41	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	CFBP1951	S4_31962475	8.3E-05	7.0E-02	5.9	1.3	G/A	234/36	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI70	S4_31962475	4.3E-07	6.3E-04	9.2	6.0	G/A	258/38	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI101	S4_31962475	2.5E-05	2.2E-02	7.0	4.8	G/A	225/34	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI130	S4_31962475	1.8E-06	5.3E-03	8.6	3.4	G/A	248/36	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI133	S4_31962475	3.2E-04	3.4E-01	5.1	1.9	G/A	219/37	*	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI136	S4_31962475	5.8E-06	4.2E-02	7.9	4.2	G/A	229/36	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoo</i>	MAI145	S4_31962475	4.5E-05	3.5E-02	6.3	3.7	G/A	239/37	***	LOC_Os04g53612	APO, putative, expressed
<i>Xoc</i>	BAI5	S4_31981005	2.3E-12	3.7E-09	17.7	13.6	G/A	268/38	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI10	S4_31981005	3.7E-05	6.6E-02	6.2	3.6	G/A	243/31	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI46	S4_31981005	4.5E-04	4.4E-01	4.8	4.5	G/A	236/34	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI67	S4_31981005	1.8E-06	3.6E-03	8.8	2.4	G/A	228/36	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI77	S4_31981005	6.1E-05	1.2E-01	6.3	3.1	G/A	232/33	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI123	S4_31981005	2.4E-04	5.2E-01	5.4	2.8	G/A	221/32	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI139	S4_31981005	5.4E-05	1.7E-01	7.0	4.8	G/A	210/30	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	BAI3	S4_31981005	1.2E-13	2.2E-10	19.2	9.3	G/A	271/38	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	CFBP1951	S4_31981005	6.5E-05	6.6E-02	6.1	1.3	G/A	231/35	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI70	S4_31981005	2.5E-07	4.0E-04	9.6	6.3	G/A	255/36	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI101	S4_31981005	1.3E-05	2.1E-02	7.6	5.0	G/A	222/33	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI130	S4_31981005	2.6E-06	5.3E-03	8.6	3.4	G/A	244/35	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI133	S4_31981005	1.6E-04	3.4E-01	5.6	2.0	G/A	216/36	*	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI136	S4_31981005	1.2E-06	1.8E-02	9.2	4.5	G/A	226/36	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoo</i>	MAI145	S4_31981005	6.2E-05	4.1E-02	6.2	3.7	G/A	236/36	***	LOC_Os04g53660	transposon protein, putative, unclassified, expressed
<i>Xoc</i>	MAI46	S4_31992079	6.7E-04	5.4E-01	5.1	-4.2	T/C	200/38	*	LOC_Os04g53670	expressed protein
<i>Xoo</i>	MAI130	S4_32007187	3.0E-04	2.0E-01	4.6	2.9	A/G	28/261	*	LOC_Os04g53700	zinc finger protein, putative, expressed
<i>Xoo</i>	BAI3	S4_32134600	5.5E-04	8.7E-02	4.0	3.7	C/A	239/64	*	LOC_Os04g53920	leucoanthocyanidin reductase, putative, expressed
<i>Xoc</i>	BAI5	S4_32136574	4.8E-06	1.7E-03	7.6	13.7	T/C	260/15	***	intergenic	
<i>Xoo</i>	BAI3	S4_32142089	9.8E-04	1.3E-01	3.5	5.2	G/T	293/21	*	LOC_Os04g53940	hypothetical protein
<i>Xoc</i>	BAI5	S4_32181189	8.0E-04	1.8E-01	3.7	7.7	T/G	290/24	*	LOC_Os04g53998	kinase, putative, expressed
<i>Xoo</i>	BAI3	S4_32181189	5.7E-04	8.7E-02	3.8	5.2	T/G	293/23	*	LOC_Os04g53998	kinase, putative, expressed
<i>Xoo</i>	MAI70	S4_32181189	9.2E-04	5.2E-01	3.8	4.9	T/G	278/23	*	LOC_Os04g53998	kinase, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BAI5	S4_32189350	1.7E-07	9.7E-05	10.0	14.5	C/T	268/17	***	intergenic	
<i>Xoo</i>	MAI130	S4_32193486	6.6E-04	3.3E-01	4.1	2.7	A/G	28/260	*	LOC_Os04g54002	serine/threonine-protein kinase receptor precursor, putative, expressed
<i>Xoo</i>	MAI136	S4_32234992	6.3E-04	2.6E-01	4.9	3.7	A/G	230/25	*	LOC_Os04g54090	RALFL18 - Rapid Alkalinization Factor RALF family protein precursor, expressed
<i>Xoc</i>	BAI5	S4_32297823	7.5E-04	1.7E-01	3.7	-5.7	T/C	238/67	*	LOC_Os04g54230	wound induced protein, putative, expressed
<i>Xoc</i>	BAI5	S4_32367097	9.3E-04	1.9E-01	3.5	-5.6	C/G	241/67	*	LOC_Os04g54400	BTBN12 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hypocotyl 3 NPH3 and coiled-coil domains, expressed
<i>Xoc</i>	BAI5	S4_32379663	1.5E-06	6.7E-04	8.7	13.4	T/G	264/17	***	LOC_Os04g54420	protein of unknown function, DUF618 domain containing protein, expressed
<i>Xoc</i>	BAI5	S4_32546106	4.3E-06	1.6E-03	7.2	12.2	C/G	285/18	***	LOC_Os04g54720	expressed protein
<i>Xoc</i>	BAI5	S4_32546110	4.3E-06	1.6E-03	7.2	12.2	C/A	285/18	***	LOC_Os04g54720	expressed protein
<i>Xoc</i>	BAI5	S4_32591580	4.8E-04	1.2E-01	4.1	8.3	A/C	280/23	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	BAI3	S4_32591580	7.5E-04	1.0E-01	3.8	5.2	A/C	283/22	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	MAI70	S4_32591580	9.9E-04	5.3E-01	4.3	5.0	A/C	268/22	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoc</i>	BAI5	S4_32593050	7.6E-04	1.7E-01	3.7	7.8	C/T	290/24	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoc</i>	BAI5	S4_32593833	5.6E-04	1.4E-01	3.9	8.2	T/A	288/23	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	BAI3	S4_32593833	6.9E-04	9.7E-02	3.7	5.2	T/A	291/22	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	MAI70	S4_32593833	6.8E-04	4.3E-01	4.0	5.2	T/A	276/22	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoc</i>	BAI5	S4_32595542	4.7E-04	1.2E-01	4.0	8.3	C/T	290/23	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	BAI3	S4_32595542	2.8E-04	4.7E-02	4.2	5.6	C/T	293/22	**	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	MAI70	S4_32595542	9.4E-04	5.2E-01	3.7	5.0	C/T	278/22	*	LOC_Os04g54810	beta-D-xylosidase, putative, expressed
<i>Xoo</i>	MAI130	S4_32627084	2.9E-04	2.0E-01	5.0	2.1	A/G	217/66	*	LOC_Os04g54850	pectinesterase, putative, expressed
<i>Xoo</i>	MAI130	S4_33325361	5.1E-04	3.1E-01	4.2	2.0	T/C	73/208	*	LOC_Os04g55950	expressed protein
<i>Xoo</i>	MAI130	S4_33336957	8.8E-04	4.0E-01	4.2	1.9	T/G	74/201	*	intergenic	
<i>Xoc</i>	MAI77	S4_33555508	3.1E-04	3.7E-01	5.9	2.3	G/T	54/180	*	intergenic	
<i>Xoc</i>	MAI77	S4_33600912	6.1E-04	5.2E-01	4.5	2.1	G/A	58/204	*	intergenic	
<i>Xoc</i>	MAI61	S5_69377	6.6E-04	9.1E-01	4.7	-3.4	T/C	221/20	*	LOC_Os05g01040	serine/threonine-protein kinase, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	MAI61	S5_103237	6.8E-04	9.1E-01	4.6	2.2	C/T	53/200	*	LOC_Os05g01120	cytochrome P450, putative, expressed
<i>Xoo</i>	BAI3	S5_103237	4.3E-05	1.2E-02	5.7	-4.4	C/T	60/244	***	LOC_Os05g01120	cytochrome P450, putative, expressed
<i>Xoo</i>	BAI3	S5_227187	5.5E-09	6.1E-06	11.9	-8.1	A/C	34/276	***	LOC_Os05g01370	polygalacturonase inhibitor precursor, putative, expressed
<i>Xoc</i>	MAI61	S5_231622	3.0E-04	9.1E-01	5.1	-3.4	C/T	225/22	*	LOC_Os05g01380	polygalacturonase inhibitor precursor, putative, expressed
<i>Xoc</i>	MAI61	S5_251710	8.4E-04	9.1E-01	4.4	-3.3	G/A	228/20	*	LOC_Os05g01440	phosphoribosylformylglycinamide synthase, putative, expressed
<i>Xoo</i>	BAI3	S5_285834	4.0E-08	4.2E-05	10.3	-7.9	A/G	31/283	***	LOC_Os05g01480	ras-related protein, putative, expressed
<i>Xoo</i>	BAI3	S5_347328	1.5E-04	3.3E-02	4.9	-4.1	G/A	60/245	**	LOC_Os05g01580	integral membrane protein DUF6 containing protein, expressed
<i>Xoo</i>	BAI3	S5_353165	1.6E-09	1.9E-06	12.3	-8.2	T/C	36/275	***	LOC_Os05g01590	heat shock protein DnaJ, putative, expressed
<i>Xoo</i>	MAI133	S5_353165	9.8E-04	3.7E-01	4.3	-1.9	T/C	32/224	*	LOC_Os05g01590	heat shock protein DnaJ, putative, expressed
<i>Xoo</i>	BAI3	S5_440644	2.1E-06	1.2E-03	7.8	-6.6	A/G	34/266	***	LOC_Os05g01710	transcription initiation factor IIA gamma chain, putative, expressed
<i>Xoo</i>	BAI3	S5_453169	8.4E-08	8.0E-05	9.6	7.6	G/A	284/33	***	LOC_Os05g01750	TruB family pseudouridylate synthase, putative, expressed
<i>Xoo</i>	BAI3	S5_574926	2.1E-06	1.2E-03	7.6	-6.4	T/C	36/269	***	LOC_Os05g02010	expressed protein
<i>Xoo</i>	BAI3	S5_849335	2.5E-05	8.4E-03	5.9	-6.4	T/C	25/287	***	LOC_Os05g02480	expressed protein
<i>Xoo</i>	BAI3	S5_850180	1.1E-06	7.3E-04	8.0	-6.8	C/G	33/280	***	LOC_Os05g02480	expressed protein
<i>Xoo</i>	MAI133	S5_850180	7.9E-04	3.4E-01	4.4	-2.0	C/G	28/228	*	LOC_Os05g02480	expressed protein
<i>Xoo</i>	BAI3	S5_904372	1.9E-04	3.7E-02	4.6	-4.2	T/G	51/247	**	LOC_Os05g02590	transferase family protein, putative, expressed
<i>Xoo</i>	BAI3	S5_934093	1.3E-05	5.1E-03	7.5	-6.6	A/T	27/233	***	LOC_Os05g02650	expressed protein
<i>Xoo</i>	BAI3	S5_1200961	6.5E-05	1.7E-02	5.2	-5.4	A/G	35/280	***	LOC_Os05g03070	transporter, putative, expressed
<i>Xoo</i>	BAI3	S5_1200964	6.5E-05	1.7E-02	5.2	-5.4	C/G	35/282	***	LOC_Os05g03070	transporter, putative, expressed
<i>Xoo</i>	BAI3	S5_1200971	6.5E-05	1.7E-02	5.2	-5.4	T/G	35/282	***	LOC_Os05g03070	transporter, putative, expressed
<i>Xoo</i>	BAI3	S5_1224178	7.7E-05	1.9E-02	5.1	-5.3	A/G	34/282	***	LOC_Os05g03100	HECT-domain domain containing protein, expressed
<i>Xoo</i>	BAI3	S5_1258051	6.3E-04	9.0E-02	3.9	-3.3	G/T	69/242	*	LOC_Os05g03140	tetraspanin family protein, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	BAI3	S5_1320280	5.6E-04	8.7E-02	3.9	3.4	G/A	241/67	*	intergenic	
<i>Xoc</i>	MAI46	S5_1475022	1.2E-04	2.9E-01	5.8	-3.5	C/A	168/96	*	LOC_Os05g03480	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed
<i>Xoc</i>	MAI46	S5_1475065	9.0E-04	5.7E-01	4.6	-2.9	C/T	127/122	*	LOC_Os05g03480	acyl-coenzyme A dehydrogenase, mitochondrial precursor, putative, expressed
<i>Xoo</i>	CFBP1951	S5_3057869	5.1E-04	3.0E-01	5.3	-1.0	G/A	56/171	*	LOC_Os05g06120	ubiquitin conjugating enzyme protein, putative, expressed
<i>Xoo</i>	CFBP1951	S5_7731832	2.3E-04	1.8E-01	5.2	-1.6	C/T	242/18	*	LOC_Os05g13904	expressed protein
<i>Xoo</i>	MAI134	S5_21351387	1.5E-06	2.1E-02	10.3	-2.7	C/T	260/14	***	intergenic	
<i>Xoo</i>	MAI72	S5_29597255	6.3E-04	2.7E-01	4.5	1.3	G/T	171/83	*	LOC_Os05g51620	expressed protein
<i>Xoo</i>	MAI101	S6_5631365	6.2E-04	1.7E-01	4.6	-4.6	T/G	234/24	*	LOC_Os06g10780	AP2 domain containing protein, expressed
<i>Xoo</i>	MAI101	S6_5631366	6.2E-04	1.7E-01	4.6	-4.6	T/C	234/24	*	LOC_Os06g10780	AP2 domain containing protein, expressed
<i>Xoo</i>	MAI101	S6_5631369	5.9E-04	1.7E-01	4.6	-4.6	C/G	235/24	*	LOC_Os06g10780	AP2 domain containing protein, expressed
<i>Xoo</i>	MAI101	S6_5631372	5.9E-04	1.7E-01	4.6	-4.6	G/T	235/24	*	LOC_Os06g10780	AP2 domain containing protein, expressed
<i>Xoo</i>	MAI101	S6_5631375	5.9E-04	1.7E-01	4.6	-4.6	T/A	235/24	*	LOC_Os06g10780	AP2 domain containing protein, expressed
<i>Xoo</i>	MAI101	S6_5658039	2.5E-04	1.1E-01	5.2	-4.9	T/G	239/24	*	LOC_Os06g10850	lipase, putative, expressed
<i>Xoc</i>	MAI123	S6_28685790	7.5E-04	6.3E-01	5.1	-1.8	T/C	120/98	*	LOC_Os06g47320	T-complex protein, putative, expressed
<i>Xoc</i>	MAI46	S6_29789433	7.5E-05	2.9E-01	6.1	-7.1	A/C	251/17	*	LOC_Os06g49160	thylakoid lumenal 16.5 kDa protein, chloroplast precursor, putative, expressed
<i>Xoc</i>	MAI77	S6_29827098	7.6E-04	6.0E-01	4.2	-3.3	A/G	248/19	*	intergenic	
<i>Xoc</i>	MAI77	S6_29827171	8.6E-04	6.4E-01	4.2	-3.3	A/T	247/19	*	intergenic	
<i>Xoc</i>	MAI46	S6_29851557	2.0E-04	2.9E-01	5.4	-4.0	A/C	222/54	*	LOC_Os06g49260	OsWAK65 - OsWAK receptor-like protein kinase, expressed
<i>Xoc</i>	MAI46	S6_29892576	2.4E-04	2.9E-01	5.4	-4.0	T/C	208/53	*	LOC_Os06g49340	OsFBDUF35 - F-box and DUF domain containing protein, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
Xoo	CFBP1951	S7_5956894	4.9E-12	6.8E-08	20.6	-2.0	G/A	209/50	***	intergenic	
Xoo	CFBP1951	S7_5993972	6.6E-11	4.6E-07	17.9	-1.8	C/T	183/62	***	LOC_Os07g10940	exo70 exocyst complex subunit family protein, expressed
Xoo	CFBP1951	S7_5994097	7.4E-10	3.5E-06	15.5	-1.6	C/T	192/65	***	LOC_Os07g10940	exo70 exocyst complex subunit family protein, expressed
Xoo	CFBP1951	S7_7043661	6.7E-06	1.9E-02	7.9	-1.2	T/C	191/63	***	intergenic	
Xoo	CFBP1951	S7_7043696	1.9E-05	3.4E-02	7.1	-1.1	C/T	202/64	***	intergenic	
Xoo	CFBP1951	S7_7047227	4.1E-05	5.8E-02	7.0	-1.1	A/G	173/58	*	LOC_Os07g12380	hypothetical protein
Xoo	CFBP1951	S7_7047284	5.5E-04	3.0E-01	5.8	-0.9	G/A	175/59	*	LOC_Os07g12380	hypothetical protein
Xoo	CFBP1951	S7_7047325	5.5E-04	3.0E-01	5.8	-0.9	C/T	175/59	*	LOC_Os07g12380	hypothetical protein
Xoo	CFBP1951	S7_7047333	1.2E-05	2.4E-02	7.5	-1.2	T/C	201/63	***	LOC_Os07g12380	hypothetical protein
Xoo	CFBP1951	S7_7047343	1.2E-05	2.4E-02	7.5	-1.2	G/A	201/63	***	LOC_Os07g12380	hypothetical protein
Xoo	CFBP1951	S7_7182262	3.9E-04	2.4E-01	7.1	-1.2	G/A	204/32	*	LOC_Os07g12580	expressed protein
Xoo	CFBP1951	S7_7182273	3.9E-04	2.4E-01	7.1	-1.2	G/A	204/32	*	LOC_Os07g12580	expressed protein
Xoo	CFBP1951	S7_7186425	1.5E-06	5.1E-03	9.1	-1.3	C/G	199/64	***	LOC_Os07g12590	OsFBX225 - F-box domain containing protein, expressed
Xoc	MAI123	S7_18859878	7.3E-04	6.3E-01	4.9	-3.4	G/A	236/17	*	intergenic	
Xoc	MAI123	S7_18859880	7.3E-04	6.3E-01	4.9	-3.4	C/T	236/17	*	intergenic	
Xoo	MAI136	S7_23962559	3.0E-04	1.7E-01	5.4	-4.0	A/C	200/40	*	intergenic	
Xoo	MAI101	S7_24584432	2.6E-04	1.1E-01	5.9	-5.0	G/A	190/40	*	LOC_Os07g41080	hydrolase, alpha/beta fold family domain containing protein, expressed
Xoo	MAI72	S7_26755135	7.3E-04	2.7E-01	4.3	-1.2	A/T	179/95	*	LOC_Os07g44820	expressed protein
Xoo	MAI72	S7_26819778	4.7E-04	2.7E-01	4.7	-1.3	A/G	185/90	*	LOC_Os07g44970	XPA-binding protein 2, putative, expressed
Xoo	MAI72	S7_26916718	9.9E-05	1.9E-01	5.7	-1.4	A/G	177/91	*	LOC_Os07g45090	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor, putative, expressed
Xoo	MAI72	S7_26923436	1.2E-04	1.9E-01	5.6	-1.4	C/G	182/92	*	LOC_Os07g45100	endonuclease/exonuclease/phosphatase family domain containing protein, expressed
Xoo	MAI72	S7_27060318	7.6E-04	2.7E-01	4.3	-1.3	C/G	186/86	*	LOC_Os07g45370	expressed protein
Xoo	MAI72	S7_27060573	5.3E-04	2.7E-01	4.5	-1.3	A/G	187/86	*	LOC_Os07g45370	expressed protein
Xoo	MAI72	S7_27060806	6.0E-04	2.7E-01	4.5	-1.3	C/A	188/83	*	LOC_Os07g45370	expressed protein
Xoo	MAI72	S7_27135983	6.0E-04	2.7E-01	4.4	-1.3	A/T	185/88	*	LOC_Os07g45480	expressed protein
Xoo	MAI72	S7_27135987	6.0E-04	2.7E-01	4.4	-1.3	G/A	186/88	*	LOC_Os07g45480	expressed protein

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI72	S7_27142637	3.5E-04	2.7E-01	4.8	-1.4	A/T	185/78	*	LOC_Os07g45490	expressed protein
<i>Xoo</i>	MAI72	S7_27142664	3.5E-04	2.7E-01	4.8	-1.4	T/G	185/78	*	LOC_Os07g45490	expressed protein
<i>Xoo</i>	MAI72	S7_27142675	3.5E-04	2.7E-01	4.8	-1.4	T/A	185/78	*	LOC_Os07g45490	expressed protein
<i>Xoo</i>	MAI72	S7_27142677	3.5E-04	2.7E-01	4.8	-1.4	A/G	185/78	*	LOC_Os07g45490	expressed protein
<i>Xoo</i>	MAI72	S7_27479752	6.7E-04	2.7E-01	4.4	-1.3	G/A	186/88	*	LOC_Os07g46039	expressed protein
<i>Xoo</i>	MAI72	S7_27480009	8.2E-04	2.7E-01	4.2	-1.3	A/G	183/90	*	LOC_Os07g46039	expressed protein
<i>Xoo</i>	MAI72	S7_27480033	8.2E-04	2.7E-01	4.2	-1.3	A/G	183/90	*	LOC_Os07g46039	expressed protein
<i>Xoo</i>	MAI72	S7_27480041	8.2E-04	2.7E-01	4.2	-1.3	C/G	183/90	*	LOC_Os07g46039	expressed protein
<i>Xoo</i>	MAI72	S7_27590866	1.0E-03	3.0E-01	4.1	-1.2	C/T	189/89	*	LOC_Os07g46240	choline transporter-related, putative, expressed
<i>Xoo</i>	MAI72	S7_27619799	6.7E-04	2.7E-01	4.2	-1.2	A/G	185/97	*	LOC_Os07g46300	expressed protein
<i>Xoo</i>	MAI130	S7_28070395	2.4E-04	1.9E-01	5.9	-2.1	A/G	171/78	*	LOC_Os07g46970	sex determination protein tasselseed-2, putative, expressed
<i>Xoo</i>	MAI72	S7_28165250	8.6E-04	2.7E-01	4.3	-1.3	C/T	201/69	*	LOC_Os07g47100	transporter, monovalent cation:proton antiporter-2 family, putative, expressed
<i>Xoo</i>	MAI72	S7_28165258	8.6E-04	2.7E-01	4.3	-1.3	A/G	201/69	*	LOC_Os07g47100	transporter, monovalent cation:proton antiporter-2 family, putative, expressed
<i>Xoo</i>	MAI72	S7_28421931	8.2E-04	2.7E-01	4.3	-1.4	G/A	211/64	*	intergenic	
<i>Xoo</i>	MAI72	S7_28421964	8.2E-04	2.7E-01	4.3	-1.4	T/A	211/64	*	intergenic	
<i>Xoo</i>	MAI72	S7_28445131	5.5E-04	2.7E-01	4.4	-1.4	A/G	216/62	*	LOC_Os07g47560	expressed protein
<i>Xoo</i>	MAI72	S7_28829259	8.5E-04	2.7E-01	4.2	-1.4	A/C	214/62	*	LOC_Os07g48260	WRKY47, expressed
<i>Xoo</i>	MAI72	S7_28849458	6.3E-04	2.7E-01	4.6	-1.4	G/T	214/60	*	LOC_Os07g48280	expressed protein
<i>Xoo</i>	MAI130	S7_28904931	9.3E-04	4.1E-01	4.4	-1.7	A/T	149/104	*	LOC_Os07g48360	helicase conserved C-terminal domain containing protein, expressed
<i>Xoc</i>	BAI5	S8_2690001	3.3E-04	8.9E-02	4.5	5.1	A/C	78/210	*	intergenic	
<i>Xoo</i>	MAI101	S8_8259055	6.2E-04	1.7E-01	5.2	-4.1	C/A	184/45	*	LOC_Os08g13840	WRKY25, expressed
<i>Xoo</i>	BAI3	S9_12319855	9.7E-04	1.3E-01	3.5	-4.5	A/G	268/35	*	LOC_Os09g20460	VQ domain containing protein, putative, expressed
<i>Xoo</i>	BAI3	S9_19185317	3.7E-04	6.1E-02	4.4	-3.1	A/G	193/102	*	LOC_Os09g32140	expressed protein
<i>Xoo</i>	MAI134	S9_20394634	9.4E-04	9.1E-01	4.3	-1.3	C/G	251/30	*	intergenic	
<i>Xoc</i>	MAI10	S9_21084075	8.5E-04	5.8E-01	5.0	-3.4	C/T	211/21	*	LOC_Os09g36550	armadillo/beta-catenin repeat family protein, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
Xoo	MAI130	S10_11404753	8.2E-04	3.8E-01	4.7	1.8	T/C	101/152	*	LOC_Os10g22080	expressed protein
Xoo	MAI72	S10_19571781	7.1E-04	2.7E-01	4.3	-1.4	G/A	228/61	*	intergenic	
Xoo	MAI72	S10_19571798	4.5E-04	2.7E-01	4.6	-1.4	T/G	228/62	*	intergenic	
Xoo	MAI72	S10_19598933	8.9E-04	2.7E-01	4.1	-1.4	C/A	227/59	*	LOC_Os10g36626	expressed protein
Xoo	MAI72	S10_19599061	5.0E-04	2.7E-01	4.5	-1.4	C/G	223/63	*	LOC_Os10g36626	expressed protein
Xoo	MAI72	S10_19603128	1.5E-04	2.2E-01	5.5	-1.6	C/T	220/59	*	intergenic	
Xoo	MAI72	S10_19621750	4.5E-04	2.7E-01	4.6	-1.4	G/C	228/62	*	LOC_Os10g36690	dehydration response related protein, putative, expressed
Xoo	MAI72	S10_19676741	4.3E-05	1.5E-01	6.3	-1.6	G/T	228/62	*	LOC_Os10g36750	mitochondrial transcription termination factor-related, putative, expressed
Xoo	MAI72	S10_19676742	4.3E-05	1.5E-01	6.3	-1.6	C/T	228/62	*	LOC_Os10g36750	mitochondrial transcription termination factor-related, putative, expressed
Xoo	MAI72	S10_19677331	7.3E-05	1.8E-01	5.9	-1.6	G/T	229/61	*	LOC_Os10g36750	mitochondrial transcription termination factor-related, putative, expressed
Xoo	MAI72	S10_19690604	3.0E-05	1.5E-01	7.2	-1.8	C/T	196/56	*	LOC_Os10g36780	OsProCP4 - Putative Lysosomal Pro-x Carboxypeptidase homologue, expressed
Xoo	MAI72	S10_19754550	5.1E-05	1.5E-01	6.8	-1.7	G/A	213/55	*	LOC_Os10g36870	src homology-3 domain protein 3, putative, expressed
Xoo	MAI72	S10_19827002	1.2E-04	1.9E-01	6.0	-1.7	A/G	206/54	*	LOC_Os10g37020	transposon protein, putative, unclassified, expressed
Xoo	MAI72	S10_19847581	2.8E-04	2.7E-01	4.9	-1.4	G/T	227/63	*	LOC_Os10g37070	cytochrome P450, putative, expressed
Xoo	MAI93	S10_20158998	8.8E-04	1.0E+00	4.2	-3.8	G/A	185/86	*	LOC_Os10g37660	trehalase precursor, putative, expressed
Xoo	MAI93	S10_20275330	7.5E-04	1.0E+00	4.3	-3.8	C/T	192/84	*	intergenic	
Xoc	MAI123	S11_3907887	7.9E-04	6.3E-01	4.7	-1.9	T/C	149/70	*	LOC_Os11g07650	retrotransposon protein, putative, unclassified, expressed
Xoo	CFBP1951	S11_4854344	3.4E-04	2.3E-01	5.3	-1.5	C/T	221/24	*	intergenic	
Xoo	MAI136	S11_6923297	6.3E-05	6.3E-02	7.2	-3.0	T/C	186/65	*	intergenic	
Xoo	MAI136	S11_6940850	6.2E-04	2.6E-01	5.1	-2.8	G/A	188/52	*	LOC_Os11g12420	serpin domain containing protein, putative, expressed
Xoo	BAI3	S11_6970503	7.8E-04	1.0E-01	3.9	-3.0	T/C	163/134	*	LOC_Os11g12470	expressed protein
Xoo	MAI70	S11_6970503	3.6E-05	4.3E-02	6.3	-3.4	T/C	150/133	***	LOC_Os11g12470	expressed protein

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	MAI70	S11_6970755	3.5E-04	2.5E-01	5.3	-3.5	C/T	189/67	*	LOC_Os11g12470	expressed protein
<i>Xoo</i>	MAI130	S11_6970755	6.0E-04	3.3E-01	4.8	-2.1	C/T	181/62	*	LOC_Os11g12470	expressed protein
<i>Xoo</i>	MAI136	S11_6970755	8.1E-05	6.9E-02	8.4	-3.2	C/T	170/56	*	LOC_Os11g12470	expressed protein
<i>Xoo</i>	MAI70	S11_7102305	1.7E-04	1.7E-01	5.2	3.2	C/A	169/104	*		intergenic
<i>Xoo</i>	MAI101	S11_7102305	4.7E-04	1.5E-01	5.2	2.9	C/A	150/90	*		intergenic
<i>Xoo</i>	MAI70	S11_7104422	1.3E-04	1.4E-01	5.3	3.3	G/A	173/105	*	LOC_Os11g12620	receptor protein kinase CLAVATA1 precursor, putative, expressed
<i>Xoo</i>	MAI70	S11_7104857	1.6E-04	1.7E-01	5.1	3.2	T/G	173/110	*	LOC_Os11g12620	receptor protein kinase CLAVATA1 precursor, putative, expressed
<i>Xoo</i>	MAI101	S11_7104857	2.3E-04	1.0E-01	5.5	3.1	T/G	153/94	*	LOC_Os11g12620	receptor protein kinase CLAVATA1 precursor, putative, expressed
<i>Xoo</i>	MAI70	S11_7107785	2.1E-04	1.7E-01	5.0	3.2	T/G	171/104	*	LOC_Os11g12620	receptor protein kinase CLAVATA1 precursor, putative, expressed
<i>Xoo</i>	MAI72	S11_9150528	5.6E-04	2.7E-01	4.4	-1.2	A/C	133/138	*	LOC_Os11g16530	mal, putative, expressed
<i>Xoo</i>	MAI72	S11_9456372	4.1E-04	2.7E-01	4.7	-1.3	T/C	164/108	*	LOC_Os11g17060	expressed protein
<i>Xoo</i>	MAI72	S11_9456382	4.1E-04	2.7E-01	4.7	-1.3	G/A	164/108	*	LOC_Os11g17060	expressed protein
<i>Xoo</i>	MAI72	S11_9465629	8.0E-04	2.7E-01	4.2	-1.2	A/G	160/107	*	LOC_Os11g17070	expressed protein
<i>Xoo</i>	MAI72	S11_9465651	6.4E-04	2.7E-01	4.3	-1.2	G/A	160/108	*	LOC_Os11g17070	expressed protein
<i>Xoo</i>	MAI72	S11_9465660	6.4E-04	2.7E-01	4.3	-1.2	G/A	160/108	*	LOC_Os11g17070	expressed protein
<i>Xoo</i>	MAI72	S11_16864795	7.7E-04	2.7E-01	4.4	-1.2	C/G	127/124	*		intergenic
<i>Xoo</i>	MAI72	S11_17605358	4.9E-05	1.5E-01	6.8	-1.6	C/T	172/88	*	LOC_Os11g30320	expressed protein
<i>Xoc</i>	MAI67	S11_18071192	1.4E-04	1.6E-01	5.6	-1.4	A/G	166/88	*	LOC_Os11g31060	IQ calmodulin-binding and BAG domain containing protein, putative, expressed
<i>Xoo</i>	MAI133	S11_24397797	4.7E-04	3.4E-01	5.2	1.8	C/T	216/41	*	LOC_Os11g40790	expressed protein
<i>Xoo</i>	MAI70	S11_25082818	3.2E-04	2.4E-01	4.9	-6.5	T/C	255/15	*		intergenic
<i>Xoo</i>	MAI133	S11_25082818	1.9E-04	3.4E-01	5.9	-3.3	T/C	222/12	*		intergenic
<i>Xoo</i>	BAI3	S11_25522745	2.5E-04	4.3E-02	4.3	-6.7	C/T	302/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25522746	2.5E-04	4.3E-02	4.3	-6.7	C/G	302/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25522749	2.5E-04	4.3E-02	4.3	-6.7	G/C	302/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25522752	2.5E-04	4.3E-02	4.3	-6.7	C/G	302/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25522753	2.5E-04	4.3E-02	4.3	-6.7	C/A	302/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25522755	2.1E-04	4.0E-02	4.5	-6.8	G/C	299/17	**	LOC_Os11g42410	expressed protein
<i>Xoo</i>	BAI3	S11_25591134	2.6E-04	4.4E-02	4.4	-6.3	G/T	290/19	**	LOC_Os11g42490	retrotransposon protein, putative, unclassified, expressed
<i>Xoc</i>	BLS256	S11_26879946	8.2E-04	1.7E-01	4.7	-11.2	C/T	237/20	*	LOC_Os11g44430	protein kinase, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BLS256	S11_26950888	3.6E-05	4.2E-02	7.3	-12.3	A/G	227/27	***	LOC_Os11g44570	expressed protein
<i>Xoo</i>	BAI3	S11_26950888	2.5E-04	4.3E-02	4.6	-5.4	A/G	277/33	**	LOC_Os11g44570	expressed protein
<i>Xoo</i>	MAI101	S11_26950888	6.0E-04	1.7E-01	5.0	-4.6	A/G	229/26	*	LOC_Os11g44570	expressed protein
<i>Xoo</i>	MAI136	S11_26950888	7.5E-04	2.9E-01	5.0	-3.7	A/G	233/27	*	LOC_Os11g44570	expressed protein
<i>Xoc</i>	BLS256	S11_27033636	2.0E-05	3.6E-02	7.8	-12.9	A/G	217/27	***	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoo</i>	BAI3	S11_27033636	1.9E-04	3.7E-02	5.0	-5.6	A/G	263/33	**	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoo</i>	MAI145	S11_27033636	9.6E-04	2.9E-01	4.3	-3.5	A/G	232/29	*	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoc</i>	BLS256	S11_27033687	1.7E-05	3.6E-02	7.9	-12.8	A/G	226/27	***	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoo</i>	BAI3	S11_27033687	7.3E-05	1.8E-02	5.4	-5.8	A/G	272/34	***	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoo</i>	MAI101	S11_27033687	3.9E-04	1.4E-01	5.5	-4.6	A/G	228/28	*	LOC_Os11g44700	calmodulin binding protein, putative, expressed
<i>Xoc</i>	BLS256	S11_27181429	1.3E-05	3.6E-02	7.6	-12.6	C/G	226/30	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	BAI3	S11_27181429	9.4E-06	4.1E-03	6.6	-6.4	C/G	275/37	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	MAI101	S11_27181429	3.8E-05	3.1E-02	7.0	-5.3	C/G	228/30	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	MAI136	S11_27181429	4.9E-05	6.0E-02	6.5	-4.2	C/G	232/31	*	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	MAI145	S11_27181429	2.0E-04	1.1E-01	5.2	-3.8	C/G	242/32	*	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoc</i>	BLS256	S11_27181436	8.5E-05	6.7E-02	6.1	-11.2	A/G	225/31	*	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	BAI3	S11_27181436	1.6E-06	1.0E-03	7.9	-6.8	A/G	272/38	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
<i>Xoo</i>	MAI101	S11_27181436	2.0E-05	2.1E-02	7.7	-5.4	A/G	227/31	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
Xoo	MAI136	S11_27181436	1.7E-05	4.7E-02	7.2	-4.4	A/G	231/32	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
Xoo	MAI145	S11_27181436	1.5E-05	1.6E-02	7.0	-4.4	A/G	241/33	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
Xoo	BAI3	S11_27183806	5.2E-05	1.4E-02	5.8	-5.8	A/G	250/37	***	LOC_Os11g44910	DEAD-box ATP-dependent RNA helicase, putative, expressed
Xoo	BAI3	S11_27192125	7.7E-05	1.9E-02	5.9	-5.8	G/A	260/34	***	LOC_Os11g44920	expressed protein
Xoo	MAI133	S11_27192125	7.7E-04	3.4E-01	4.9	-2.0	G/A	213/29	*	LOC_Os11g44920	expressed protein
Xoo	MAI136	S11_27192125	5.0E-04	2.4E-01	4.9	-3.7	G/A	222/29	*	LOC_Os11g44920	expressed protein
Xoo	MAI145	S11_27192125	4.1E-04	2.0E-01	4.8	-3.7	G/A	232/30	*	LOC_Os11g44920	expressed protein
Xoc	BLS256	S11_27197214	2.2E-04	8.8E-02	6.3	-10.9	T/C	192/29	*	intergenic	
Xoo	BAI3	S11_27197214	1.6E-05	5.5E-03	7.0	-6.4	T/C	236/36	***	intergenic	
Xoo	MAI101	S11_27197214	4.4E-05	3.2E-02	7.4	-5.3	T/C	194/29	***	intergenic	
Xoo	MAI136	S11_27197214	4.1E-04	2.2E-01	5.6	-3.7	T/C	197/30	*	intergenic	
Xoo	MAI145	S11_27197214	4.5E-04	2.0E-01	5.3	-3.7	T/C	205/31	*	intergenic	
Xoc	BLS256	S11_27197220	2.2E-04	8.8E-02	6.3	-10.9	T/C	192/29	*	intergenic	
Xoo	BAI3	S11_27197220	1.6E-05	5.5E-03	7.0	-6.4	T/C	236/36	***	intergenic	
Xoo	MAI101	S11_27197220	4.4E-05	3.2E-02	7.4	-5.3	T/C	194/29	***	intergenic	
Xoo	MAI136	S11_27197220	4.1E-04	2.2E-01	5.6	-3.7	T/C	197/30	*	intergenic	
Xoo	MAI145	S11_27197220	4.5E-04	2.0E-01	5.3	-3.7	T/C	205/31	*	intergenic	
Xoc	BLS256	S11_27205864	1.6E-04	8.6E-02	6.0	-10.8	T/G	227/30	*	LOC_Os11g44950	glycosyl hydrolase family 3 protein, putative, expressed
Xoo	BAI3	S11_27205864	1.6E-05	5.5E-03	6.3	-6.1	T/G	275/38	***	LOC_Os11g44950	glycosyl hydrolase family 3 protein, putative, expressed
Xoo	MAI101	S11_27205864	3.4E-04	1.4E-01	5.4	-4.5	T/G	228/31	*	LOC_Os11g44950	glycosyl hydrolase family 3 protein, putative, expressed
Xoo	MAI136	S11_27205864	2.5E-04	1.5E-01	5.6	-3.7	T/G	232/32	*	LOC_Os11g44950	glycosyl hydrolase family 3 protein, putative, expressed
Xoc	BLS256	S11_27393912	1.7E-04	8.6E-02	5.9	-10.6	T/C	226/31	*	intergenic	
Xoo	BAI3	S11_27393912	8.2E-06	3.7E-03	6.8	-6.2	T/C	274/39	***	intergenic	
Xoo	MAI101	S11_27393912	2.9E-04	1.2E-01	5.5	-4.4	T/C	227/32	*	intergenic	
Xoo	MAI136	S11_27393912	6.2E-04	2.6E-01	4.8	-3.4	T/C	231/33	*	intergenic	
Xoo	BAI3	S11_27412501	1.6E-04	3.5E-02	5.7	-5.7	G/C	236/31	**	LOC_Os11g45295	retrotransposon protein, putative, unclassified, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	BAI3	S11_27412530	1.6E-04	3.5E-02	5.7	-5.7	T/C	236/31	**	LOC_Os11g45295	retrotransposon protein, putative, unclassified, expressed
<i>Xoc</i>	BLS256	S11_27442768	2.3E-04	9.0E-02	6.1	-12.6	C/A	204/20	*	intergenic	
<i>Xoc</i>	BLS256	S11_27442782	9.7E-07	1.4E-02	11.1	-14.4	A/G	195/29	***	intergenic	
<i>Xoo</i>	BAI3	S11_27442782	1.0E-04	2.3E-02	6.1	-5.7	A/G	238/35	**	intergenic	
<i>Xoo</i>	MAI101	S11_27442782	5.9E-05	3.7E-02	8.6	-5.3	A/G	193/27	***	intergenic	
<i>Xoo</i>	MAI133	S11_27442782	6.7E-04	3.4E-01	5.4	-2.0	A/G	194/29	*	intergenic	
<i>Xoo</i>	MAI145	S11_27442782	5.3E-04	2.1E-01	5.6	-3.7	A/G	208/30	*	intergenic	
<i>Xoc</i>	BLS256	S11_27451641	8.2E-05	6.7E-02	6.6	-11.7	C/G	221/28	*	LOC_Os11g45380	zinc finger family protein, putative, expressed
<i>Xoo</i>	BAI3	S11_27451641	9.6E-05	2.2E-02	5.4	-5.8	C/G	268/34	***	LOC_Os11g45380	zinc finger family protein, putative, expressed
<i>Xoo</i>	MAI101	S11_27451641	8.2E-05	4.9E-02	6.4	-5.2	C/G	224/27	***	LOC_Os11g45380	zinc finger family protein, putative, expressed
<i>Xoo</i>	MAI133	S11_27451641	3.8E-04	3.4E-01	5.2	-2.1	C/G	220/28	*	LOC_Os11g45380	zinc finger family protein, putative, expressed
<i>Xoo</i>	MAI145	S11_27451641	5.6E-04	2.2E-01	4.6	-3.7	C/G	237/29	*	LOC_Os11g45380	zinc finger family protein, putative, expressed
<i>Xoo</i>	BAI3	S11_27464711	2.3E-04	4.3E-02	4.9	-5.2	T/C	254/36	**	intergenic	
<i>Xoc</i>	BLS256	S11_27464784	2.1E-04	8.8E-02	5.6	-11.1	T/C	216/27	*	intergenic	
<i>Xoo</i>	BAI3	S11_27464784	3.2E-05	9.7E-03	6.3	-6.1	T/C	257/34	***	intergenic	
<i>Xoo</i>	MAI101	S11_27464784	1.4E-04	7.7E-02	6.2	-5.0	T/C	218/27	*	intergenic	
<i>Xoo</i>	MAI136	S11_27464784	4.8E-04	2.4E-01	5.2	-3.7	T/C	218/28	*	intergenic	
<i>Xoc</i>	BLS256	S11_27468322	1.8E-04	8.6E-02	6.0	-10.7	A/G	222/30	*	LOC_Os11g45390	von Willebrand factor type A domain containing protein, putative, expressed
<i>Xoo</i>	BAI3	S11_27468322	5.2E-05	1.4E-02	5.8	-5.8	A/G	269/37	***	LOC_Os11g45390	von Willebrand factor type A domain containing protein, putative, expressed
<i>Xoo</i>	MAI101	S11_27468322	8.9E-05	5.2E-02	6.3	-4.9	A/G	224/31	*	LOC_Os11g45390	von Willebrand factor type A domain containing protein, putative, expressed
<i>Xoo</i>	MAI145	S11_27468322	8.3E-04	2.7E-01	4.3	-3.4	A/G	240/32	*	LOC_Os11g45390	von Willebrand factor type A domain containing protein, putative, expressed
<i>Xoc</i>	BLS256	S11_27483001	8.9E-05	6.7E-02	6.4	-11.4	A/G	227/29	*	intergenic	
<i>Xoo</i>	BAI3	S11_27483001	3.6E-05	1.1E-02	5.8	-6.0	A/G	276/36	***	intergenic	

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
Xoo	MAI101	S11_27483001	1.7E-04	8.7E-02	5.8	-4.9	A/G	229/29	*	intergenic	
Xoo	MAI136	S11_27483001	5.4E-04	2.5E-01	5.1	-3.6	A/G	233/30	*	intergenic	
Xoo	MAI145	S11_27483001	8.6E-04	2.7E-01	4.4	-3.5	A/G	243/31	*	intergenic	
Xoc	BLS256	S11_27496126	2.0E-04	8.8E-02	5.5	-10.8	G/A	225/29	*	LOC_Os11g45410	expressed protein
Xoo	BAI3	S11_27496126	1.3E-04	2.9E-02	5.1	-5.4	G/A	270/37	**	LOC_Os11g45410	expressed protein
Xoc	BLS256	S11_27496991	1.3E-04	8.1E-02	6.2	-11.2	G/A	226/29	*	LOC_Os11g45410	expressed protein
Xoo	BAI3	S11_27496991	3.4E-05	1.0E-02	5.9	-6.1	G/A	275/36	***	LOC_Os11g45410	expressed protein
Xoo	MAI101	S11_27496991	1.4E-04	7.7E-02	6.1	-4.9	G/A	228/29	*	LOC_Os11g45410	expressed protein
Xoo	MAI136	S11_27496991	6.4E-04	2.6E-01	4.8	-3.6	G/A	232/30	*	LOC_Os11g45410	expressed protein
Xoo	MAI145	S11_27496991	8.0E-04	2.6E-01	4.4	-3.5	G/A	242/31	*	LOC_Os11g45410	expressed protein
Xoc	BLS256	S11_27574157	6.9E-04	1.7E-01	4.7	-10.7	A/T	232/23	*	LOC_Os11g45540	TKL_IRAK_DUF26-lh.11 - DUF26 kinases have homology to DUF26 containing loci, expressed
Xoc	BLS256	S11_27603799	8.5E-04	1.7E-01	4.6	-9.1	A/C	222/32	*	LOC_Os11g45620	rust-resistance protein Lr21, putative, expressed
Xoo	BAI3	S11_27603799	6.7E-05	1.7E-02	5.5	-5.4	A/C	270/40	***	LOC_Os11g45620	rust-resistance protein Lr21, putative, expressed
Xoo	MAI136	S11_27603799	7.9E-04	3.0E-01	4.8	-3.3	A/C	227/34	*	LOC_Os11g45620	rust-resistance protein Lr21, putative, expressed
Xoo	MAI145	S11_27603799	5.8E-04	2.2E-01	4.6	-3.4	A/C	238/35	*	LOC_Os11g45620	rust-resistance protein Lr21, putative, expressed
Xoc	BLS256	S11_27672705	5.3E-04	1.4E-01	5.3	-9.8	C/T	208/32	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	BAI3	S11_27672705	3.8E-06	1.8E-03	7.9	-6.6	C/T	253/40	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI101	S11_27672705	2.0E-05	2.1E-02	8.1	-5.3	C/T	208/32	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI133	S11_27672705	6.2E-04	3.4E-01	5.1	-1.9	C/T	206/33	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI145	S11_27672705	1.6E-05	1.6E-02	7.6	-4.3	C/T	221/35	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoc	BLS256	S11_27672709	5.3E-04	1.4E-01	5.3	-9.8	A/G	208/32	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	BAI3	S11_27672709	3.8E-06	1.8E-03	7.9	-6.6	A/G	253/40	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	ALLs with Effect allele/Null	Significance correspondance	Locus	Annotation
Xoo	MAI101	S11_27672709	2.0E-05	2.1E-02	8.1	-5.3	A/G	208/32	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI133	S11_27672709	6.2E-04	3.4E-01	5.1	-1.9	A/G	206/33	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI145	S11_27672709	1.6E-05	1.6E-02	7.6	-4.3	A/G	221/35	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoc	BLS256	S11_27672719	5.3E-04	1.4E-01	5.3	-9.8	T/C	208/32	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	BAI3	S11_27672719	3.8E-06	1.8E-03	7.9	-6.6	T/C	253/40	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI101	S11_27672719	2.0E-05	2.1E-02	8.1	-5.3	T/C	208/32	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI133	S11_27672719	6.2E-04	3.4E-01	5.1	-1.9	T/C	206/33	*	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	MAI145	S11_27672719	1.6E-05	1.6E-02	7.6	-4.3	T/C	221/35	***	LOC_Os11g45740	MYB family transcription factor, putative, expressed
Xoo	BAI3	S11_28483934	1.0E-05	4.2E-03	7.0	-8.2	A/C	264/16	***	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI101	S11_28483934	2.0E-04	9.4E-02	5.8	-6.1	A/C	219/15	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI133	S11_28483934	5.1E-04	3.4E-01	5.3	-3.0	A/C	218/13	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI136	S11_28483934	4.4E-05	6.0E-02	8.1	-5.8	A/C	224/14	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI145	S11_28483934	1.6E-05	1.6E-02	7.9	-5.9	A/C	232/15	***	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	BAI3	S11_28483987	1.5E-06	9.9E-04	8.5	-8.5	C/T	274/17	***	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI101	S11_28483987	4.0E-04	1.4E-01	5.1	-5.6	C/T	229/16	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI133	S11_28483987	8.8E-04	3.5E-01	4.7	-2.7	C/T	230/14	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI136	S11_28483987	1.1E-04	8.6E-02	6.2	-5.3	C/T	236/15	*	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoo	MAI145	S11_28483987	6.2E-05	4.1E-02	6.2	-5.3	C/T	243/16	***	LOC_Os11g47350	beta-D-xylosidase, putative, expressed
Xoc	BLS256	S11_28652242	2.3E-04	9.0E-02	5.6	-10.7	T/C	224/29	*	intergenic	
Xoo	BAI3	S11_28652242	3.4E-07	2.9E-04	9.1	-7.5	T/C	272/36	***	intergenic	
Xoo	MAI70	S11_28652242	5.5E-04	3.8E-01	4.2	-4.6	T/C	260/32	*	intergenic	
Xoo	MAI101	S11_28652242	5.6E-06	2.1E-02	8.8	-5.9	T/C	227/29	***	intergenic	
Xoo	MAI133	S11_28652242	6.5E-05	3.4E-01	6.5	-2.3	T/C	222/30	*	intergenic	
Xoo	MAI136	S11_28652242	5.0E-05	6.0E-02	7.0	-4.3	T/C	230/30	*	intergenic	
Xoo	MAI145	S11_28652242	1.8E-06	8.4E-03	8.9	-4.9	T/C	240/32	***	intergenic	

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoc</i>	BLS256	S11_28652283	9.9E-04	1.9E-01	4.5	-9.3	A/C	225/30	*	intergenic	
<i>Xoo</i>	BAI3	S11_28652283	8.9E-08	8.0E-05	9.9	-7.6	A/C	274/37	***	intergenic	
<i>Xoo</i>	MAI70	S11_28652283	2.1E-04	1.7E-01	4.7	-4.8	A/C	261/33	*	intergenic	
<i>Xoo</i>	MAI101	S11_28652283	7.9E-06	2.1E-02	8.4	-5.7	A/C	227/30	***	intergenic	
<i>Xoo</i>	MAI133	S11_28652283	1.7E-04	3.4E-01	5.8	-2.2	A/C	222/31	*	intergenic	
<i>Xoo</i>	MAI136	S11_28652283	1.1E-04	8.6E-02	6.3	-4.0	A/C	232/31	*	intergenic	
<i>Xoo</i>	MAI145	S11_28652283	5.7E-07	8.3E-03	9.7	-5.1	A/C	240/33	***	intergenic	
<i>Xoo</i>	MAI145	S11_28656770	1.5E-05	1.6E-02	7.7	-5.8	G/A	238/16	***	intergenic	
<i>Xoc</i>	BLS256	S11_28697227	4.4E-04	1.3E-01	5.1	-9.9	A/G	229/31	*	intergenic	
<i>Xoo</i>	BAI3	S11_28697227	8.0E-07	5.8E-04	8.3	-7.1	A/G	277/38	***	intergenic	
<i>Xoo</i>	MAI101	S11_28697227	1.2E-05	2.1E-02	8.0	-5.5	A/G	230/31	***	intergenic	
<i>Xoo</i>	MAI133	S11_28697227	4.4E-04	3.4E-01	4.9	-2.0	A/G	227/32	*	intergenic	
<i>Xoo</i>	MAI136	S11_28697227	5.3E-04	2.5E-01	4.9	-3.5	A/G	234/32	*	intergenic	
<i>Xoo</i>	MAI145	S11_28697227	4.9E-06	1.4E-02	8.0	-4.6	A/G	243/34	***	intergenic	
<i>Xoc</i>	BLS256	S11_28697250	3.0E-04	1.0E-01	5.4	-10.5	G/C	228/29	*	intergenic	
<i>Xoo</i>	BAI3	S11_28697250	5.1E-07	4.1E-04	8.8	-7.3	G/C	277/36	***	intergenic	
<i>Xoo</i>	MAI101	S11_28697250	1.7E-05	2.1E-02	7.9	-5.5	G/C	230/29	***	intergenic	
<i>Xoo</i>	MAI133	S11_28697250	7.6E-04	3.4E-01	4.6	-2.0	G/C	226/30	*	intergenic	
<i>Xoo</i>	MAI136	S11_28697250	1.5E-04	1.1E-01	5.9	-4.0	G/C	234/30	*	intergenic	
<i>Xoo</i>	MAI145	S11_28697250	3.7E-06	1.4E-02	8.4	-4.8	G/C	243/32	***	intergenic	
<i>Xoc</i>	BLS256	S11_28775260	7.8E-04	1.7E-01	4.8	-9.0	T/C	195/35	*	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	BAI3	S11_28775260	1.9E-06	1.1E-03	8.3	-6.5	T/C	241/42	***	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	MAI70	S11_28775260	6.0E-04	3.9E-01	5.0	-4.2	T/C	229/38	*	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	MAI101	S11_28775260	5.9E-06	2.1E-02	10.1	-5.4	T/C	199/35	***	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	MAI133	S11_28775260	3.3E-04	3.4E-01	5.7	-2.0	T/C	197/35	*	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	MAI136	S11_28775260	7.0E-05	6.3E-02	8.5	-3.9	T/C	200/36	*	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	MAI145	S11_28775260	1.4E-06	8.4E-03	10.6	-4.7	T/C	211/38	***	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	BAI3	S11_28777668	8.2E-05	1.9E-02	6.1	-7.3	T/C	250/16	***	LOC_Os11g47650	trp repressor/replication initiator, putative, expressed
<i>Xoo</i>	BAI3	S11_28784287	2.3E-04	4.3E-02	4.5	-6.6	C/T	293/17	**	LOC_Os11g47690	zinc finger, C3HC4 type domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28784296	1.9E-04	3.7E-02	4.7	-6.7	G/A	292/17	**	LOC_Os11g47690	zinc finger, C3HC4 type domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28794135	7.0E-04	9.7E-02	3.7	-5.9	G/T	302/17	*	LOC_Os11g47730	expressed protein
<i>Xoo</i>	MAI145	S11_28794135	4.5E-04	2.0E-01	4.4	-4.6	G/T	265/16	*	LOC_Os11g47730	expressed protein
<i>Xoo</i>	BAI3	S11_28815283	1.9E-05	6.3E-03	6.8	-8.2	C/T	278/16	***	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoo</i>	MAI136	S11_28815283	4.8E-04	2.4E-01	5.3	-5.0	C/T	235/14	*	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoo</i>	MAI145	S11_28815283	5.8E-04	2.2E-01	4.9	-4.7	C/T	244/15	*	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoc</i>	BLS256	S11_28815394	8.6E-04	1.7E-01	5.0	-13.5	G/A	223/12	*	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoo</i>	BAI3	S11_28815394	1.1E-05	4.4E-03	7.3	-8.1	G/A	269/17	***	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoo</i>	MAI101	S11_28815394	3.7E-04	1.4E-01	5.9	-5.6	G/A	224/16	*	LOC_Os11g47780	pollen signalling protein with adenylyl cyclase activity, putative, expressed
<i>Xoo</i>	BAI3	S11_28852557	1.0E-05	4.3E-03	6.3	-7.7	T/G	302/18	***	LOC_Os11g47830	RNA recognition motif containing protein, expressed
<i>Xoo</i>	MAI101	S11_28852557	8.4E-04	2.3E-01	4.3	-5.1	T/G	249/17	*	LOC_Os11g47830	RNA recognition motif containing protein, expressed
<i>Xoo</i>	MAI145	S11_28852557	9.1E-04	2.8E-01	4.0	-4.2	T/G	265/17	*	LOC_Os11g47830	RNA recognition motif containing protein, expressed
<i>Xoo</i>	MAI133	S11_28865011	3.8E-04	3.4E-01	5.2	-1.5	A/C	176/73	*	LOC_Os11g47860	expressed protein
<i>Xoc</i>	BLS256	S11_28865030	2.5E-04	9.0E-02	5.3	-9.8	C/G	221/34	*	LOC_Os11g47860	expressed protein
<i>Xoo</i>	BAI3	S11_28865030	2.8E-06	1.5E-03	7.5	-6.4	C/G	269/41	***	LOC_Os11g47860	expressed protein
<i>Xoo</i>	MAI101	S11_28865030	1.7E-04	8.7E-02	5.9	-4.4	C/G	222/35	*	LOC_Os11g47860	expressed protein
<i>Xoo</i>	MAI136	S11_28865030	2.2E-04	1.4E-01	5.3	-3.5	C/G	227/36	*	LOC_Os11g47860	expressed protein
<i>Xoo</i>	MAI145	S11_28865030	9.4E-06	1.6E-02	7.4	-4.3	C/G	236/36	***	LOC_Os11g47860	expressed protein
<i>Xoo</i>	BAI3	S11_28870400	1.7E-04	3.6E-02	5.4	-6.5	C/T	246/18	**	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr_Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	BAI3	S11_28870403	2.4E-04	4.3E-02	5.3	-4.8	T/C	219/41	**	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI145	S11_28870403	6.4E-04	2.3E-01	5.2	-3.3	T/C	190/37	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28870482	6.6E-07	5.0E-04	9.7	-7.0	A/G	225/39	***	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI101	S11_28870482	4.1E-04	1.4E-01	6.9	-4.4	A/G	182/32	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI145	S11_28870482	3.9E-05	3.3E-02	8.2	-4.1	A/G	194/35	***	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28870897	5.1E-05	1.4E-02	5.8	-5.4	A/C	254/41	***	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI145	S11_28870897	3.2E-04	1.6E-01	5.0	-3.5	A/C	222/36	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoc</i>	BLS256	S11_28870941	2.5E-04	9.0E-02	5.7	-10.1	G/T	206/33	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28870941	2.7E-05	8.5E-03	6.3	-5.8	G/T	253/41	***	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI101	S11_28870941	4.8E-04	1.5E-01	5.2	-4.2	G/T	210/34	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI136	S11_28870941	5.7E-05	6.3E-02	7.9	-4.0	G/T	213/34	*	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	MAI145	S11_28870941	1.4E-05	1.6E-02	7.4	-4.3	G/T	222/36	***	LOC_Os11g47870	GRAS family transcription factor domain containing protein, expressed
<i>Xoo</i>	BAI3	S11_28895438	2.5E-04	4.3E-02	4.3	-6.2	C/A	299/18	**	LOC_Os11g47910	SCARECROW, putative, expressed
<i>Xoo</i>	MAI145	S11_28895438	7.7E-04	2.6E-01	4.1	-4.3	C/A	262/17	*	LOC_Os11g47910	SCARECROW, putative, expressed
<i>Xoo</i>	MAI133	S11_28896289	6.8E-04	3.4E-01	5.8	-1.5	A/G	153/61	*	LOC_Os11g47910	SCARECROW, putative, expressed
<i>Xoo</i>	MAI133	S11_28904361	9.0E-04	3.5E-01	4.6	-1.4	T/C	179/67	*	LOC_Os11g47930	alpha-hemolysin, putative, expressed
<i>Xoc</i>	BLS256	S11_28920280	7.5E-05	6.7E-02	7.2	-10.8	T/A	197/32	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	BAI3	S11_28920280	7.6E-04	1.0E-01	4.0	-4.5	T/A	244/37	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI101	S11_28920280	3.7E-04	1.4E-01	6.1	-4.2	T/A	201/33	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI133	S11_28920280	8.2E-04	3.4E-01	4.7	-2.0	T/A	199/30	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI145	S11_28920280	8.5E-05	5.1E-02	7.4	-3.9	T/A	212/33	*	LOC_Os11g47944	thaumatin, putative, expressed

Continuation Table S2.5.

Pathovar	Strain	Marker (Chr Pos)	P-value	q-value	R ²	Effect estimate	Effect allele/Null	AILs with Effect allele/Null	Significance correspondance	Locus	Annotation
<i>Xoo</i>	BAI3	S11_28920303	8.8E-04	1.2E-01	3.8	-5.9	C/A	267/17	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI145	S11_28920303	6.6E-04	2.3E-01	5.4	-4.4	C/A	231/17	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	BAI3	S11_28920325	6.0E-04	8.9E-02	3.8	-6.0	C/G	295/17	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI145	S11_28920325	5.0E-04	2.1E-01	4.5	-4.6	C/G	259/16	*	LOC_Os11g47944	thaumatin, putative, expressed
<i>Xoo</i>	MAI133	S11_28938622	3.0E-04	3.4E-01	6.4	-3.1	G/A	212/13	*	LOC_Os11g47980	expressed protein
<i>Xoo</i>	BAI3	S11_28977691	5.4E-06	2.5E-03	7.3	-6.0	T/C	264/42	***	intergenic	
<i>Xoo</i>	MAI145	S11_28977691	1.2E-04	6.5E-02	5.7	-3.7	T/C	232/37	*	intergenic	
<i>Xoo</i>	BAI3	S12_2195904	8.2E-04	1.1E-01	4.0	2.9	T/C	137/156	*	LOC_Os12g05040	heavy-metal-associated domain- containing protein, putative, expressed
<i>Xoo</i>	BAI3	S12_2203648	5.2E-04	8.3E-02	4.1	2.8	G/A	172/115	*	intergenic	

Table S2.6. QTL detection for resistance to African *Xoc* and *Xoo* in indica MAGIC S4 subset (P -value < 0.001), organized by chromosome. Wald statistic for test that no parents have effects on trait (Wald, 7 df). Parental source of resistance determined by founder effects estimates relative to Sambha Mahsuri + Sub1. Stars in significance correspondence panel indicate level of significance of GWAS (*) P value < 0.001 and q -value > 0.05.

Pathovar	Strain	Chr	QTL name	QTL position			Supporting interval		Interval size		Wald	p-value	Predicted parental source of resistance	Corroboration GWA
				(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				
<i>Xoo</i>	BAI3	1		124.4	S1_31010757	S1_31182879	S1_28664444	S1_32112121	13.8	3,448	27.8	2.E-04	FED, IR45, IR46	
<i>Xoc</i>	MAI3	2	qXO-2-2	141.6	S2_35477326	S2_35580048	S2_35342151	S2_35891034	2.2	549	25.3	7.E-04	FED, PSBRc158	
<i>Xoo</i>	BAI3	3		55.0	S3_13969997	S3_14144630	S3_12659394	S3_14658353	8.0	1,999	32.3	4.E-05	FED, SHZ-2	
<i>Xoc</i>	MAI3	3		133.0	S3_33208259	S3_33647311	S3_32013647	S3_34825996	11.2	2,812	24.3	1.E-03	FED, IR45, IR46, PSBRc82, SHZ-2	
<i>Xoc</i>	MAI3	4		122.2	S4_30383295	S4_30738888	S4_30030316	S4_31803018	7.1	1,773	30.0	1.E-04	IR45, IR46, SHZ-2	
<i>Xoc</i>	BAI5	4	qXO-4-2	123.6	S4_30738922	S4_31079998	S4_30383295	S4_31882603	6.0	1,499	48.4	3.E-08	FED, IR46, SHZ-2	*
<i>Xoo</i>	BAI3	4		126.1	S4_31666827	S4_31716597	S4_30383295	S4_31992079	6.4	1,609	56.1	9.E-10	IR46, PSBRc82	*
<i>Xoo</i>	BAI3	5		4.0	S5_1065077	S5_1073143	S5_761076	S5_1258099	2.0	497	47.4	5.E-08	PSBRc82	*
<i>Xoc</i>	BAI5	5		9.0	S5_2312513	S5_2821285	S5_2062346	S5_4184550	8.5	2,122	27.1	3.E-04	All	
<i>Xoc</i>	MAI3	7		1.0	S7_1000810	S7_1032993	S7_756131	S7_1433062	2.7	677	35.1	1.E-05	All	
<i>Xoc</i>	BAI5	8		20.9	S8_5373265	S8_5418149	S8_4491493	S8_6277593	7.1	1,786	30.8	7.E-05	All except SHZ-2	*
<i>Xoo</i>	BAI3	8		89.8	S8_21378692	S8_22606500	S8_20188025	S8_24097520	15.6	3,909	27.2	3.E-04	IR45, IR46	
<i>Xoo</i>	MAI1	9		48.6	S9_12636353	S9_14163560	S9_12086978	S9_14163560	8.3	2,077	24.4	1.E-03	IR46	*
<i>Xoo</i>	BAI3	9		83.0	S9_21176469	S9_21243301	S9_20977131	S9_21546286	2.3	569	33.0	3.E-05	IR46	*
<i>Xoc</i>	BAI5	10		76.0	S10_19063585	S10_19107872	S10_18851296	S10_19354685	2.0	503	25.0	8.E-04	IR45	
<i>Xoo</i>	BAI3	10		89.7	S10_21573347	S10_22502006	S10_20993968	S10_22911489	7.7	1,918	30.0	9.E-05	FED, IR77, PSBRc158, PSBRc82	
<i>Xoc</i>	BAI5	11		95.9	S11_23983620	S11_24295017	S11_23558018	S11_24809810	5.0	1,252	31.1	6.E-05	All except FED	
<i>Xoc</i>	MAI3	11	qXO-11-2	112.5	S11_28116388	S11_28483934	S11_27573854	S11_28988578	5.7	1,415	37.0	5.E-06	All except IR77	*
<i>Xoo</i>	BAI3	11		114.6	S11_28483987	S11_28652283	S11_27573854	S11_28988578	5.7	1,415	41.8	6.E-07	FED, IR45, IR46, PSBRc158, SHZ-2	*

Table S2.7. QTL detection for resistance to African and Asian *Xoc* and *Xoo* in indica MAGIC S8 subset (P -value < 0.001), organized by chromosome. Wald statistic for test that no parents have effects on trait (Wald, 7 df). Parental source of resistance determined by founder effects estimates relative to Sambha Mahsuri + Sub1; nd = non-determined. Stars in corroboration GWA panel indicate level of significance of GWAS markers as follows: (*) P -value < 0.001 and q -value > 0.05; (***) P -value < 0.0001 and q -value < 0.05. Known resistance column refers to previously identified QTL and single resistance genes (denoted by the prefix *Xa* or *Xo*).

Pathovar	Strain	Chr	QTL	QTL position		Supporting interval		Interval size		Wald	P -value	Phenotypic variance (%)	Predicted parental source of resistance	Corroboration GWAS	Known resistance loci to	
				(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM) (Kb)						African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
<i>Xoo</i>	MAI72	1	qXO-1-1	5.2	S1_1335951	S1_1336798	S1_1264553	S1_1511717	1.0	247	33.9	1.8E-05	8.4	nd		
<i>Xoo</i>	MAI130	1		5.4	S1_1365841	S1_1375634	S1_1336959	S1_1516299	0.7	179	47.8	4.0E-08	12.1	nd		
<i>Xoc</i>	MAI123	1		5.9	S1_1401021	S1_1500023	S1_1365711	S1_1550887	0.7	185	30.7	7.1E-05	8.2	nd		
<i>Xoo</i>	MAI134	1		44.9	S1_11258688	S1_11272858	S1_11078476	S1_11531550	1.8	453	30.2	8.6E-05	7.3	PSBRc158		qABB-1
<i>Xoo</i>	MAI134	1		56.3	S1_14102698	S1_14174257	S1_13542393	S1_14346639	3.2	804	28.8	1.6E-04	6.9	PSBRc158		qABB-1
<i>Xoc</i>	BAI5	2		17.6	S2_4440042	S2_4553565	S2_4150417	S2_4868450	2.9	718	27.1	3.2E-04	5.9	FED, IR45, IR46		
<i>Xoc</i>	MAI46	2		19.9	S2_5030179	S2_5044670	S2_4950345	S2_5044670	0.4	94	27.8	2.4E-04	6.8	IR46, SHZ-2		
<i>Xoo</i>	MAI134	2		26.6	S2_6651629	S2_6706358	S2_6246858	S2_6778045	2.1	531	27.8	2.4E-04	6.6	IR45		
<i>Xoc</i>	MAI61	2		92.2	S2_22897004	S2_23098527	S2_22249726	S2_23384851	4.5	1135	25.5	6.1E-04	6.5	IR45, IR46, IR77, PSBRc82, SHZ-2		Qbr2a
<i>Xoc</i>	MAI77	2	qXO-2-1	96.3	S2_24122049	S2_24133875	S2_24021185	S2_24165677	0.6	144	33.9	1.8E-05	8.8	IR45, IR46, IR77	SNPs near interval (*)	Qbr2a
<i>Xoc</i>	MAI46	2		96.9	S2_24278085	S2_24278919	S2_24210631	S2_24387205	0.7	177	33.7	2.0E-05	8.6	IR45, IR77, PSBRc82, SHZ-2	*	Qbr2a
<i>Xoc</i>	MAI139	2		100.9	S2_25272641	S2_25273930	S2_25212962	S2_25305176	0.4	92	41.0	8.0E-07	12.0	IR45, IR46, IR77, SHZ-2	SNPs near interval (*)	
<i>Xoc</i>	MAI10	2		101.1	S2_25332318	S2_25351909	S2_23819009	S2_27466604	14.6	3648	30.3	8.3E-05	7.5	FED, IR77, SHZ-2	*	Qbr2a
<i>Xoc</i>	BLS256	2		103.3	S2_25869421	S2_25885474	S2_25698342	S2_26335825	2.5	637	44.5	1.7E-07	12.3	All except PSBRc158	***	
<i>Xoc</i>	MAI61	2		104.2	S2_26097152	S2_26101866	S2_25510717	S2_26467059	3.8	956	26.9	3.5E-04	6.9	FED, IR45, IR46, IR77	*	
<i>Xoc</i>	BAI5	2		104.3	S2_26101866	S2_26113224	S2_25698342	S2_26375084	2.7	677	31.8	4.5E-05	7.1	FED, IR77, SHZ-2	*	
<i>Xoo</i>	MAI130	2		107.8	S2_26854556	S2_26993900	S2_26854556	S2_27203917	1.4	349	31.8	4.5E-05	7.7	nd		
<i>Xoo</i>	MAI101	2		115.0	S2_28802779	S2_28808167	S2_28788926	S2_28828402	0.2	39	27.7	2.5E-04	7.1	IR45, IR46, IR77		
<i>Xoc</i>	MAI139	2	qXO-2-2	141.1	S2_35289602	S2_35313442	S2_35068072	S2_35589943	2.1	522	26.5	4.2E-04	7.2	nd		AQBT001, qBbr2b
<i>Xoo</i>	MAI130	2		142.4	S2_35642187	S2_35659739	S2_35140697	S2_35891362	3.0	751	28.2	2.1E-04	6.7	SHZ-2	*	AQBT001, qBbr2b, <i>Xa24(t)</i>
<i>Xoo</i>	MAI101	2		142.9	S2_35772697	S2_35781025	S2_35642187	S2_35891364	1.0	249	33.6	2.1E-05	9.0	nd		AQBT001, <i>Xa24(t)</i>
<i>Xoo</i>	MAI134	3		6.4	S3_1796192	S3_1818201	S3_1270943	S3_2093081	3.3	822	34.4	1.4E-05	8.5	nd		AQBT002
<i>Xoo</i>	MAI93	3		58.1	S3_14739507	S3_14760067	S3_10841565	S3_15864307	20.1	5023	28.3	1.9E-04	11.4	FED		qBB3-1 (AQW002)
<i>Xoo</i>	MAI72	3		81.7	S3_20646866	S3_20691702	S3_20568320	S3_20691702	0.5	123	26.8	3.6E-04	6.3	All		

Continuation Table S2.7.

Pathovar	Strain	Chr	QTL	QTL position		Supporting interval		Interval size		Wald	P-value	Phenotypic variance (%)	Predicted parental source of resistance	Corroboration GWAS	Known resistance loci to	
				(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM) (Kb)						African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
<i>Xoc</i>	MAI10	4		52.3	S4_13164480	S4_13173499	S4_13000541	S4_14723818	6.9	1723	26.6	4.0E-04	6.3	All except PSBRc82		qBbr4a
<i>Xoc</i>	MAI61	4		77.0	S4_19349782	S4_19375312	S4_19233155	S4_19711091	1.9	478	25.7	5.6E-04	6.5	nd		
<i>Xoo</i>	MAI145	4		79.7	S4_20042539	S4_20065837	S4_20027337	S4_20090957	0.3	64	30.9	6.5E-05	7.7	IR45, IR46, IR77, PSBRc82		
<i>Xoc</i>	MAI10	4		80.4	S4_20195543	S4_20213857	S4_20167660	S4_20246699	0.3	79	49.0	2.3E-08	12.7	nd		
<i>Xoo</i>	MAI136	4		81.1	S4_20382464	S4_20389318	S4_20381546	S4_20394209	0.1	13	32.2	3.8E-05	8.4	IR45, IR77, PSBRc82, SHZ-2		
<i>Xoo</i>	CFBP1951	4		83.1	S4_20892614	S4_20904803	S4_20863240	S4_20927918	0.3	65	28.2	2.0E-04	7.0	nd		
<i>Xoc</i>	MAI67	4		85.4	S4_21464884	S4_21470998	S4_21448290	S4_21498207	0.2	50	35.1	1.1E-05	9.1	IR46		qBbr4b
<i>Xoo</i>	MAI72	4		99.0	S4_24504517	S4_24863454	S4_24071697	S4_26519264	9.8	2448	26.8	3.6E-04	6.3	SHZ-2		qBbr4b, qBB-4
<i>Xoo</i>	CFBP1951	4		117.7	S4_29505127	S4_29526391	S4_29247633	S4_29883989	2.5	636	29.0	1.4E-04	7.3	nd		
<i>Xoc</i>	MAI46	4		123.9	S4_31080257	S4_31127321	S4_30862506	S4_31205433	1.4	343	29.3	1.3E-04	7.3	IR46, SHZ-2		
<i>Xoo</i>	MAI145	4		125.8	S4_31553264	S4_31559540	S4_30862506	S4_31803141	3.8	941	28.4	1.9E-04	7.0	FED, IR46	***	<i>Xo1</i> <i>Xa1</i> , <i>Xa2</i> , <i>Xa31(t)</i> , <i>Xa38</i>
<i>Xoo</i>	CFBP1951	4		126.5	S4_31728040	S4_31728342	S4_31721763	S4_31782187	0.2	60	38.0	3.0E-06	10.0	nd	*	<i>Xo1</i> <i>Xa2</i>
<i>Xoc</i>	MAI10	4		126.8	S4_31803168	S4_31812015	S4_31531452	S4_31872983	1.4	342	25.2	7.0E-04	7.7	IR46, SHZ-2	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoc</i>	MAI67	4		126.8	S4_31803168	S4_31812015	S4_31449324	S4_32064419	2.5	615	27.9	2.3E-04	8.5	IR46	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa31(t)</i>
<i>Xoo</i>	BAI3	4		126.8	S4_31803168	S4_31812015	S4_31506827	S4_31900997	1.6	394	90.3	1.1E-16	20.8	FED, IR46, SHZ-2	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoo</i>	MAI70	4		126.8	S4_31803168	S4_31812015	S4_31506827	S4_31872983	1.5	366	45.9	9.1E-08	11.8	FED, IR45, IR46, SHZ-2	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoc</i>	MAI139	4	qXO-4-1	126.8	S4_31803168	S4_31812015	S4_31553238	S4_32134600	2.3	581	40.2	1.2E-06	11.7	IR45, IR46, IR77, PSBRc82, !	*	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoc</i>	BAI5	4		126.8	S4_31819592	S4_31872983	S4_31786637	S4_31872983	0.3	86	216.9	3.0E-43	39.5	IR46, SHZ-2	***	<i>Xo1</i> AQBTO08, <i>Xa2</i>
<i>Xoc</i>	MAI77	4		126.8	S4_31819592	S4_31872983	S4_31803141	S4_31956274	0.6	153	34.9	1.2E-05	9.1	IR46, SHZ-2	*	<i>Xo1</i> AQBTO08, <i>Xa2</i>
<i>Xoo</i>	MAI130	4		127.2	S4_31873066	S4_31900997	S4_31531452	S4_32134600	2.4	603	47.3	5.0E-08	12.0	IR46	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoo</i>	MAI101	4		127.5	S4_31992079	S4_32007187	S4_31559582	S4_32134600	2.3	575	31.7	4.6E-05	8.4	FED, IR46, IR77, SHZ-2	***	<i>Xo1</i> AQBTO08, <i>Xa1</i> , <i>Xa2</i> , <i>Xa38</i>
<i>Xoo</i>	MAI136	4		127.7	S4_32037850	S4_32064419	S4_31819592	S4_32134600	1.3	315	31.6	4.7E-05	8.22	All except PSBRc158	***	<i>Xo1</i> AQBTO08, <i>Xa2</i>
<i>Xoc</i>	MAI46	4		133.3	S4_33428983	S4_33431106	S4_32681859	S4_33498618	3.3	817	27.0	3.3E-04	7.7	FED, IR45, SHZ-2		<i>Xa2</i>
<i>Xoc</i>	MAI61	5	qXO-5-1	0.1	S5_69530	S5_87749	S5_37878	S5_162688	0.5	125	25.9	5.2E-04	6.6	IR45, IR46, IR77, SHZ-2	*	
<i>Xoo</i>	BAI3	5		1.3	S5_347328	S5_353165	S5_37878	S5_453169	1.7	415	45.2	1.3E-07	10.5	IR45, PSBRc82, SHZ-2	***	qBLSr5a, qBbr5, <i>xa5</i>
<i>Xoc</i>	MAI46	5	qXO-5-2	5.9	S5_1494420	S5_1503830	S5_1200971	S5_1729230	2.1	528	25.9	5.2E-04	6.2	IR45, IR46, IR77, PSBRc158, *		
<i>Xoc</i>	MAI61	5		8.0	S5_2027760	S5_2046183	S5_1027632	S5_2167880	4.6	1140	24.8	8.2E-04	6.2	All except PSBRc158		
<i>Xoo</i>	CFBP1951	5		26.6	S5_6637584	S5_6678610	S5_6637583	S5_6722685	0.3	85	27.0	3.3E-04	6.7	FED	SNPs near interval (*)	
<i>Xoo</i>	MAI134	5		84.9	S5_21255253	S5_21351387	S5_20924798	S5_21471465	2.2	547	36.0	7.2E-06	9.0	nd	***	qBB-5-2
<i>Xoc</i>	BLS256	5	qXO-5-3	90.7	S5_22720353	S5_22750867	S5_21141624	S5_24383716	13.0	3242	25.8	5.6E-04	6.6	FED, IR46, PSBRc82, SHZ-2		qBB5, qBB-5-2, AQW004, qBBR5

Continuation Table S2.7.

Pathovar	Strain	Chr	QTL	QTL position		Supporting interval		Interval size		Wald	P-value	Phenotypic variance (%)	Predicted parental source of resistance	Corroboration GWAS	Known resistance loci to	
				(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM) (Kb)						African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
<i>Xoo</i>	MAI101	6		100.0	S6_25124153	S6_25144615	S6_24427437	S6_25422894	4.0 995	28.4	1.9E-04	7.4	IR45, IR46, PSBRc158, SHZ-2			
<i>Xoo</i>	MAI136	7	qBB-7-1	20.11	S7_5097414	S7_5129087	S7_3622979	S7_6502570	11.5 2880	31.9	4.2E-05	8.31	FED		qABB-7	<i>xa8</i>
<i>Xoo</i>	CFBP1951	7		23.57	S7_5956894	S7_5993972	S7_5956894	S7_6502570	2.2 546	65.5	1.2E-11	17.3	nd	***	qABB-7	
<i>Xoo</i>	CFBP1951	7		81.62	S7_20506279	S7_20525028	S7_20393784	S7_20525704	0.5 132	27.9	2.3E-04	7.0	FED			
<i>Xoo</i>	MAI72	7	qXO-7-2	109.9	S7_27578266	S7_27585272	S7_27479742	S7_27619799	0.6 140	31.2	5.7E-05	7.6	nd	*		
<i>Xoc</i>	MAI61	7		112.3	S7_28165258	S7_28179129	S7_27614620	S7_28469553	3.4 855	36.0	7.3E-06	9.7	FED, IR77			
<i>Xoo</i>	MAI101	8		4.2	S8_1074851	S8_1090318	S8_760745	S8_1758774	4.0 998	25.4	6.5E-04	6.4	IR45, IR46, PSBRc82			
<i>Xoc</i>	MAI139	8		20.7	S8_5140943	S8_5217372	S8_4153941	S8_5318021	4.7 1164	29.2	1.3E-04	8.1	IR45, IR46, IR77, PSBRc82, SHZ-2			
<i>Xoo</i>	CFBP1951	8		98.7	S8_24733521	S8_24833706	S8_24640146	S8_24947837	1.2 308	37.8	3.3E-06	9.9	IR77			qBbr8b
<i>Xoc</i>	MAI123	8	qBLS-8-1	102.6	S8_25638183	S8_25700349	S8_25638183	S8_25937369	1.2 299	26.2	4.6E-04	6.8	IR45			qBbr8b
<i>Xoc</i>	MAI77	8		102.7	S8_25700349	S8_25729831	S8_25638183	S8_26014015	1.5 376	30.0	9.4E-05	7.6	IR45			qBbr8b
<i>Xoo</i>	MAI70	9		34.1	S9_9220532	S9_9340981	S9_9220532	S9_9344787	0.5 124	35.4	9.5E-06	9.4	IR46, PSBRc82, PSBRc158, SHZ-2			
<i>Xoo</i>	CFBP1951	9		41.9	S9_11299373	S9_11318792	S9_11230720	S9_11318792	0.4 88	53.4	3.0E-09	14.2	nd			
<i>Xoc</i>	MAI123	9		47.3	S9_12629477	S9_12636353	S9_12628300	S9_12699426	0.3 71	29.6	1.1E-04	7.9	IR46			
<i>Xoo</i>	MAI145	9		82.4	S9_21390442	S9_21418696	S9_21317041	S9_21501670	0.7 185	28.0	2.2E-04	6.9	IR45			
<i>Xoo</i>	MAI136	10		36.4	S10_8918195	S10_9170996	S10_7551300	S10_10628934	12.3 3078	25.1	7.2E-04	6.2	FED, SHZ-2			qBbr10, QBbr10, qBBR10
<i>Xoc</i>	BAI5	10		46.2	S10_11626385	S10_11634014	S10_11575914	S10_11743048	0.7 167	28.4	1.9E-04	6.2	IR45, IR46, SHZ-2			
<i>Xoo</i>	CFBP1951	10		59.6	S10_14985398	S10_15006373	S10_14926494	S10_15168059	1.0 242	35.2	1.0E-05	9.1	nd			
<i>Xoc</i>	MAI10	10	qXO-10-1	79.6	S10_19975243	S10_20082337	S10_19903199	S10_20082337	0.7 179	28.8	1.6E-04	7.0	IR45, IR77		qABB-10	
<i>Xoc</i>	MAI46	10		79.6	S10_19975243	S10_20082337	S10_19916740	S10_20082337	0.7 166	40.9	8.6E-07	10.6	IR45		qABB-10	
<i>Xoo</i>	CFBP1951	10		80.8	S10_20275339	S10_20983368	S10_19975243	S10_20983368	4.0 1008	56.0	9.4E-10	14.9	nd		qABB-10	
<i>Xoo</i>	MAI101	10		88.1	S10_21966227	S10_22098921	S10_21786349	S10_22502019	2.9 716	36.7	5.4E-06	9.9	IR45, IR46, IR77, PSBRc82		qABB-10	

Continuation Table S2.7

Pathovar	Strain	Chr	QTL	QTL position		Supporting interval		Interval size (cM)	Wald	P-value	Phenotypic variance (%)	Predicted parental source of resistance	Corroboration GWAS	Known resistance loci to			
				(cM)	Left Mrk	Right Mrk	Left Mrk							Right Mrk	(Kb)	African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
<i>Xoo</i>	BAI3	11	qBB-11.1	28.0	S11_7012013	S11_7013171	S11_6647060	S11_7438223	3.2	791	27.0	3.4E-04	5.8	FED, IR77, PSBrc158, SHZ-2 *			
<i>Xoo</i>	MAI70	11		28.9	S11_7221827	S11_7244498	S11_6647060	S11_7616946	3.9	970	26.2	4.7E-04	5.9	FED, IR77	***		
<i>Xoc</i>	BLS256	11	qXO-11.2	107.5	S11_26879946	S11_26950070	S11_26393474	S11_27412501	4.1	1019	36.4	6.2E-06	9.9	All	***	qABB-11	QBbr11, Xa22, Xa35(t)
<i>Xoo</i>	MAI72	11		108.1	S11_27015438	S11_27033636	S11_26981276	S11_27205864	0.9	225	33.3	2.3E-05	8.2	All		qABB-11	QBbr11, Xa22, Xa35(t)
<i>Xoo</i>	MAI101	11		108.7	S11_27169283	S11_27176255	S11_26981276	S11_27205864	0.9	225	39.1	1.9E-06	10.7	All	***	qABB-11	QBbr11, Xa22, Xa35(t)
<i>Xoo</i>	CFBP1951	11		109.6	S11_27393912	S11_27412501	S11_27192125	S11_27574157	1.5	382	25.8	5.4E-04	6.3	All except IR46		qABB-11	QBbr11, Xa22, Xa35(t)
<i>Xoo</i>	MAI145	11		112.5	S11_28121355	S11_28483934	S11_27831677	S11_28697250	3.5	866	52.0	5.9E-09	13.6	All	***	qABB-11	Xa3/Xa26, Xa4, Xa22, Xa32(t), Xa35(t), Xa36(t), Xa40
<i>Xoo</i>	BAI3	11		114.6	S11_28656770	S11_28697227	S11_27831677	S11_28733787	3.6	902	56.1	9.1E-10	13.2	All	***	qABB-11	Xa3/Xa26, Xa4, Xa22, Xa32(t), Xa35(t), Xa36(t), Xa40
<i>Xoo</i>	MAI70	11		114.6	S11_28656770	S11_28697227	S11_27817978	S11_28733787	3.7	916	28.4	1.9E-04	6.5	All except SHZ-2	*	qABB-11	Xa3/Xa26, Xa4, Xa22, Xa32(t), Xa35(t), Xa36(t), Xa40
<i>Xoo</i>	MAI133	11		114.6	S11_28656770	S11_28697227	S11_27831677	S11_28977691	4.6	1146	25.1	7.3E-04	6.4	All except SHZ-2	*	qABB-11	AQB7023, Xa3/Xa26, Xa4, Xa22, Xa32(t), Xa35(t), Xa36(t), Xa40
<i>Xoo</i>	MAI136	11	114.6	S11_28656770	S11_28697227	S11_28010037	S11_28697250	2.7	687	32.1	3.8E-05	8.4	All	***	qABB-11	Xa3/Xa26, Xa4, Xa22, Xa32(t), Xa35(t), Xa36(t), Xa40	
<i>Xoc</i>	MAI77	12	qXO-12.1	0.9	S12_356349	S12_358464	S12_290036	S12_413400	0.5	123	25.0	7.5E-04	6.1	IR46, SHZ-2			
<i>Xoc</i>	MAI46	12		28.2	S12_7181057	S12_7185266	S12_7181057	S12_7186890	0.02	6	54.4	2.0E-09	14.2	All except FED			qBB-12
<i>Xoo</i>	MAI70	12		70.7	S12_17786177	S12_17902596	S12_17780296	S12_17902596	0.5	122	24.8	8.1E-04	5.5	IR77, SHZ-2			AQB7029
<i>Xoc</i>	MAI67	12		71.7	S12_18039016	S12_18060761	S12_18021980	S12_18084463	0.2	62	26.2	4.6E-04	6.4	IR77			AQB7029
<i>Xoc</i>	MAI10	12		71.8	S12_18060777	S12_18084420	S12_18021980	S12_18274373	1.0	252	30.8	6.8E-05	7.6	nd			AQB7029
<i>Xoc</i>	MAI46	12		71.8	S12_18060777	S12_18084420	S12_18021980	S12_18084463	0.2	62	30.7	7.2E-05	7.6	IR46, PSBrc82, SHZ-2			AQB7029
<i>Xoc</i>	MAI61	12		100.1	S12_24462484	S12_25156802	S12_24462484	S12_25613282	4.6	1151	28.5	1.8E-04	7.4	nd			

Table S2.8. Comparison of QTL estimates for indica MAGIC S4 and S8 subsets for *Xoc* BAI5 and *Xoo* BAI3. Stars in corroboration GWA panel indicate level of significance of GWAS markers as follows: (*) *P*-value < 0.001; (***) *P*-value < 0.0001 and q-value < 0.05.

MAGIC subset	Strain	Chr	QTL position			Supporting interval		Interval size		Wald	<i>P</i> -value	N° predicted genes	Corroboration GWAS
			(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				
S4	<i>Xoc</i> BAI5	4	123.6	S4_30738922	S4_31079998	S4_30383295	S4_31882603	6.0	1,499	48.4	2.9E-08	223	*
S8	<i>Xoc</i> BAI5	4	126.8	S4_31819592	S4_31872983	S4_31786637	S4_31872983	0.3	86	216.9	3.0E-43	14	***
S4	<i>Xoo</i> BAI3	4	126.1	S4_31666827	S4_31716597	S4_30383295	S4_31992079	6.4	1,609	56.1	8.9E-10	239	*
S8	<i>Xoo</i> BAI3	4	126.8	S4_31803168	S4_31812015	S4_31506827	S4_31900997	1.6	394	90	1.1E-16	58	***
S4	<i>Xoo</i> BAI3	5	4.0	S5_1065077	S5_1073143	S5_761076	S5_1258099	2.0	497	47.4	4.8E-08	77	*
S8	<i>Xoo</i> BAI3	5	1.3	S5_347328	S5_353165	S5_37878	S5_453169	1.7	415	45	1.3E-07	74	***
S4	<i>Xoc</i> BAI5	10	76.0	S10_19063585	S10_19107872	S10_18851296	S10_19354685	2.0	503	25.0	7.7E-04	86	
S8	<i>Xoc</i> BAI5	10	46.23	S10_11626385	S10_11634014	S10_11575914	S10_11743048	0.7	167	28.4	1.9E-04	17	
S4	<i>Xoo</i> BAI3	11	114.6	S11_28483987	S11_28652283	S11_27573854	S11_28988578	5.7	1,415	41.8	5.8E-07	214	*
S8	<i>Xoo</i> BAI3	11	114.6	S11_28656770	S11_28697227	S11_27831677	S11_28733787	3.6	902	56	9.1E-10	118	***

Table S2.9. QTL effective against multiple *X. oryzae* strains found in this study. Individual IM results (Table S7) were combined using the widest interval shared by the different *X. oryzae* strains to show common regions associated with resistance. Wald statistic for test that no parents have effects on trait (Wald, 7 df). Stars next to strains name indicate level of significance of GWAS markers as follows: (*) *P*-value < 0.001, (***) *P*-value < 0.0001 and q-value < 0.05.

Chr	QTL	Pathovar	QTL position			Supporting interval		Interval size		IM strains	Additional strains (only GWAS)	No. strains	Known resistance to	
			(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
1	qXO-1-1	both	5.2-5.9	S1_1335951	S1_1500023	S1_1264553	S1_1550887	1.1	286	<i>Xoc</i> MAI123, <i>Xoo</i> MAI72, MAI130	none	3		
2	qXO-2-1	both	96.3-107.8	S2_24122049	S2_26993900	S2_23819009	S2_27466604	14.6	3,648	<i>Xoc</i> BAI5*, BLS256***, MAI10*, MAI46*, MAI61*, MAI77, MAI139 <i>Xoo</i> MAI130	<i>Xoc</i> MAI67*, MAI123* <i>Xoo</i> BAI3*, MAI134*	12		Qbr2a
2	qXO-2-2	both	141.1-142.9	S2_35289602	S2_35781025	S2_35068072	S2_35891364	3.3	823	<i>Xoc</i> MAI139 <i>Xoo</i> MAI101, MAI130*	none	3		AQBT001, qBbr2b, <i>Xa24(t)</i>
4	qXO-4-1	both	125.8-127.7	S4_31553264	S4_32064419	S4_30862506	S4_32134600	5.1	1,272	<i>Xoc</i> BAI5***, MAI10***, MAI67***, MAI77*, MAI139* <i>Xoo</i> BAI3***, CFBP1951*, MAI70***, MAI101***, MAI130***, MAI136***, MAI145***	<i>Xoc</i> BLS256*, MAI46*, MAI61*, MAI123* <i>Xoo</i> MAI133*	16	<i>Xo1</i> <i>Xo1</i>	AQBT008, <i>Xa1</i> , <i>Xa2</i> , <i>Xa31(t)</i> , <i>Xa38</i>
5	qXO-5-1	both	0.1-1.3	S5_69530	S5_353165	S5_37878	S5_453169	1.7	415	<i>Xoc</i> MAI61*, <i>Xoo</i> BAI3***	<i>Xoo</i> MAI133*	3		qBLSr5a, qBbr5, <i>xa5</i>
5	qXO-5-2	both	5.9-8.0	S5_1494420	S5_2046183	S5_1027632	S5_2167880	4.6	1,140	<i>Xoc</i> MAI46*, MAI61	<i>Xoo</i> BAI3*, MAI134***	4		
5	qXO-5-3	both	84.9-90.7	S5_21255253	S5_22750867	S5_20924798	S5_24383716	5.8	3,459	<i>Xoc</i> BLS256, <i>Xoo</i> MAI134***		2		qBB-5-2, qBB5, qBB-5-2, AQW004, qBBR5

Continuation Table S2.9.

Chr	QTL	Pathovar	QTL position			Supporting interval		Interval size		IM strains	Additional strains (only GWAS)	No. strains	Known Resistance to	
			(cM)	Left Mrk	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				African <i>X. oryzae</i> strains	Asian <i>X. oryzae</i> strains
7	qBB-7-1	<i>Xoo</i>	20.1-23.6	S7_5097414	S7_5993972	S7_3622979	S7_6502570	11.5	2,880	<i>Xoo</i> CFBP1951***, MAI136*	none	2	qABB-7 (races A2, A3)	<i>xa8</i>
7	qXO-7-2	both	109.9-112.3	S7_27578266	S7_28179129	S7_27479742	S7_28469553	4.0	990	<i>Xoc</i> MAI61, <i>Xoo</i> MAI72*	<i>Xoo</i> MAI130*	3		
8	qBLS-8-1	<i>Xoc</i>	102.6-102.7	S8_25638183	S8_25729831	S8_25638183	S8_26014015	1.5	376	<i>Xoc</i> MAI77, MAI123	none	2		
10	qXO-10-1	both	79.6-80.8	S10_19975243	S10_20983368	S10_19903199	S10_20983368	4.3	1,080	<i>Xoc</i> MAI10, MAI46 <i>Xoo</i> CFBP1951	<i>Xoo</i> MAI72*, MAI93*	5	qABB-10 (race A1)	
11	qBB-11-1	<i>Xoo</i>	28.0-28.9	S11_7012013	S11_7244498	S11_6647060	S11_7616946	3.9	970	<i>Xoo</i> BAI3*, MAI70***	<i>Xoo</i> MAI101*, MAI130*, MAI136*	5		
11	qXO-11-2	both	107.5-114.6	S11_26879946	S11_28697227	S11_26393474	S11_28977691	10.3	2,584	<i>Xoc</i> BLS256*** <i>Xoo</i> BAI3***, CFBP1951, MAI70*, MAI72, MAI101***, MAI133*,	none	9	qABB-11 (races A1, A2, A3)	QBbr11, AQBTO23, <i>Xa3/Xa26</i> , <i>Xa4</i> , <i>Xa22</i> , <i>Xa32(t)</i> , <i>Xa35(t)</i> , <i>Xa36(t)</i> , <i>Xa40</i>
12	qXO-12-1	both	70.7-71.8	S12_17786177	S12_18084420	S12_17780296	S12_18274373	2.0	494	<i>Xoc</i> MAI10, MAI46, MAI67 <i>Xoo</i> MAI70	none	4		AQBTO29

Table S2.10. Significantly associated SNP for resistance to multiple *X. oryzae* strains on chromosome 2, detected by GWAS in the indica MAGIC S8 subset. The locus ID for each SNP was predicted from the MSU7 rice reference annotation. Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes. Founders are indicated with letters as follows: A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1. A colored box on the donor column indicates that founder carries the R allele. A colored box on the *X. oryzae* strains columns indicates that the SNP was found to be significantly associated with resistance to that particular strain (P -value < 0.001).

	LD block	SNP	Locus	SNP allele		Donor of R allele						Pathovar	N° strains	<i>Xoc</i>							<i>Xoo</i>														
				R	S											BA15	BL256	MA110	MA146	MA161	MA167	MA177	MA1123	MA1139	BA18	CFBP1951	MA170	MA172	MA193	MA1101	MA1130	MA1133	MA1134	MA1136	MA1145
qXO-2-1	1	S2_24509874	intergenic	A	G								<i>Xoc</i>	2																					
		S2_24527947	LOC_Os02g40454	G	A									<i>Xoc</i>	2																				
	2	S2_24691050	LOC_Os02g40730	A	G								<i>Xoc</i>	2																					
		S2_24692377	LOC_Os02g40730	G	T								<i>Xoc</i>	2																					
	4	S2_24848131	intergenic	A	T								<i>Xoc</i>	2																					
		S2_24877663	intergenic	T	A								<i>Xoc</i>	2																					
	5	S2_24937103	intergenic	G	A								<i>Xoc</i>	2																					
	8	S2_25618890	LOC_Os02g42590	A	G								<i>Xoc</i>	2																					
		S2_25639335	LOC_Os02g42620	A	T								<i>Xoc</i>	2																					
		S2_25639338	LOC_Os02g42620	G	A								<i>Xoc</i>	2																					
		S2_25639568	LOC_Os02g42620	T	C								<i>Xoc</i>	2																					
		S2_25803692	LOC_Os02g42900	C	A								<i>Xoc</i>	3																					
	9	S2_26126554	LOC_Os02g43314	C	A								<i>Xoc</i>	4																					
	12	S2_27203917	LOC_Os02g44900	A	G								both	2																					

Table S2.11. Significantly associated SNP for resistance to multiple *X. oryzae* strains on chromosome 4, detected by GWAS in the indica MAGIC S8 subset. The locus ID for each SNP was predicted from the MSU7 rice reference annotation. Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes. Founders are indicated with letters as follows: A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; F: Sambha Mahsuri + Sub1; G: PSBRc158; H: IR45427-2B-2-2B-1-1. A colored box on the donor column indicates that founder carries the R allele. A colored box on the *X. oryzae* strains columns indicates that the SNP was found to be significantly associated with resistance to that particular strain (P -value < 0.001).

LD block	SNP	Locus	SNP allele		Donor of R allele							Pathovar	N° strains	Xoc									Xoo										
			R	S	A	D	H	B	F	C	G			BA15	BL5256	MA10	MA146	MA161	MA167	MA177	MA1123	MA1139	BA13	CFBP1951	MA170	MA172	MA193	MA1101	MA1130	MA1133	MA1134	MA1136	MA1145
qXO-4-1	1	S4_29548991	intergenic	A	G							both	2																				
	2	S4_29783427	LOC_Os04g49930	G	A							both	2																				
		S4_29797214	LOC_Os04g49950	G	A							both	2																				
		S4_29803185	LOC_Os04g49960	A	G							both	2																				
		S4_29809870	LOC_Os04g49970	T	A							both	2																				
		S4_29868104	intergenic	C	T							both	2																				
		S4_29922917	intergenic	T	C							both	2																				
		S4_29966056	LOC_Os04g50204	C	G							both	2																				
		S4_29968457	intergenic	T	C							both	2																				
		S4_29968490	intergenic	G	C							both	2																				
	5	S4_31420093	LOC_Os04g52770	T	A							both	2																				
		S4_31498999	LOC_Os04g52890	C	G							Xoc	2																				
	6	S4_31531412	LOC_Os04g52940	T	A							both	5																				
		S4_31553238	LOC_Os04g52970	T	C							Xoc	2																				
		S4_31553264	LOC_Os04g52970	T	C							Xoc	2																				
		S4_31559540	LOC_Os04g52980	A	C							Xoc	2																				
		S4_31559557	LOC_Os04g52980	G	T							Xoc	2																				
		S4_31559582	LOC_Os04g52980	T	C							Xoc	2																				
	7	S4_31669472	LOC_Os04g53195	A	G							both	2																				
		S4_31670015	LOC_Os04g53190	T	G							both	2																				
		S4_31716597	LOC_Os04g53240	A	G							both	14																				
		S4_31728040	LOC_Os04g53260	G	C							both	14																				
		S4_31751408	LOC_Os04g53300	C	T							both	14																				
		S4_31778051	LOC_Os04g53360	T	C							both	13																				
		S4_31787320	LOC_Os04g53370	C	G							both	5																				
		S4_31800256	LOC_Os04g53380	A	G							both	2																				
		S4_31801219	LOC_Os04g53380	A	C							both	13																				
		S4_31803015	LOC_Os04g53390	G	A							both	7																				
		S4_31803018	LOC_Os04g53390	T	C							both	14																				
		S4_31803029	LOC_Os04g53390	A	G							both	14																				
	8	S4_31812050	LOC_Os04g53410	T	G							Xoc	2																				
		S4_31819592	LOC_Os04g53440	T	G							both	15																				
		S4_31956274	LOC_Os04g53600	T	C							both	12																				
		S4_31962475	LOC_Os04g53612	A	G							both	15																				
	9	S4_31981005	LOC_Os04g53660	A	G							both	15																				
		S4_32181189	LOC_Os04g53998	G	T							both	3																				
		S4_32591580	LOC_Os04g54810	C	A							both	3																				
		S4_32593833	LOC_Os04g54810	A	T							both	3																				
		S4_32595542	LOC_Os04g54810	T	C							both	3																				

Table S2.12. Significantly associated SNP for resistance to multiple *X. oryzae* strains on chromosome 11, detected by GWAS in the indica MAGIC S8 subset. The locus ID for each SNP was predicted from the MSU7 rice reference annotation. Intergenic regions were defined as regions without predicted genes or located more than 1 Kb upstream of genes. Founders are indicated with letters as follows: A: IR4630-22-2-5-1-3; B: Fedearroz 50; C: IR77298-14-1-2-10; D: Shan-Huang Zhan-2; E: PSBRc82; G: PSBRc158; H: IR45427-2B-2-2B-1-1. A colored box on the donor column indicates that founder carries the R allele. A colored box on the *X. oryzae* strains columns indicates that the SNP was found to be significantly associated with resistance to that particular strain (P -value < 0.001).

LD block	SNP	Locus	SNP allele		Donor of R allele						Pathovar	N° strains	Xoc										Xoo												
			R	S	A	B	C	D	G	H			E	BA15	BLS256	MA10	MA146	MA161	MA167	MA177	MA123	MA139	BA13	CFBP1951	MA170	MA172	MA193	MA1101	MA1130	MA1133	MA1134	MA1136	MA1145		
1	S11_25082818	intergenic	T	C								Xoo	2																						
4	S11_26950888	LOC_Os11g44570	A	G								both	4																						
	S11_27033636	LOC_Os11g44700	A	G								both	3																						
	S11_27033687	LOC_Os11g44700	A	G								both	3																						
	S11_27181429	LOC_Os11g44910	C	G								both	5																						
	S11_27181436	LOC_Os11g44910	A	G								both	5																						
	S11_27192125	LOC_Os11g44920	G	A								Xoo	4																						
	S11_27197214	intergenic	T	C								both	5																						
	S11_27197220	intergenic	T	C								both	5																						
	S11_27205864	LOC_Os11g44950	T	G								both	4																						
	S11_27393912	intergenic	T	C								both	4																						
	S11_27442782	intergenic	A	G								both	5																						
	S11_27451641	LOC_Os11g45380	C	G								both	5																						
	S11_27464784	intergenic	T	C								both	4																						
	S11_27468322	LOC_Os11g45390	A	G								both	4																						
	S11_27483001	intergenic	A	G								both	5																						
	S11_27496126	LOC_Os11g45410	G	A								Xoo	2																						
	S11_27496991	LOC_Os11g45410	G	A								both	5																						
	S11_27603799	LOC_Os11g45620	A	C								both	4																						
	S11_27672705	LOC_Os11g45740	C	T								both	5																						
	S11_27672709	LOC_Os11g45740	A	G								both	5																						
	S11_27672719	LOC_Os11g45740	T	C								both	5																						
	7	S11_28483934	LOC_Os11g47350	A	C								Xoo	5																					
		S11_28483987	LOC_Os11g47350	C	T								Xoo	5																					
		S11_28652242	intergenic	T	C								both	7																					
		S11_28652283	intergenic	A	C								both	7																					
		S11_28697227	intergenic	A	G								both	6																					
		S11_28697250	intergenic	G	C								both	6																					
		S11_28775260	LOC_Os11g47650	T	C								both	7																					
S11_28794135		LOC_Os11g47730	G	T								Xoo	2																						
S11_28815283		LOC_Os11g47780	C	T								Xoo	3																						
S11_28815394		LOC_Os11g47780	G	A								both	3																						
8	S11_28852557	LOC_Os11g47830	T	G								Xoo	3																						
	S11_28865030	LOC_Os11g47860	C	G								both	5																						
	S11_28870403	LOC_Os11g47870	T	C								Xoo	2																						
	S11_28870482	LOC_Os11g47870	A	G								Xoo	3																						
	S11_28870897	LOC_Os11g47870	A	C								Xoo	2																						
	S11_28870941	LOC_Os11g47870	G	T								both	5																						
	S11_28895438	LOC_Os11g47910	C	A								Xoo	2																						
	S11_28920280	LOC_Os11g47944	T	A								both	5																						
	S11_28920303	LOC_Os11g47944	C	A								Xoo	2																						
	S11_28920325	LOC_Os11g47944	C	G								Xoo	2																						
	S11_28977691	intergenic	T	C								Xoo	2																						

B.2. APPENDIX A SUPPLEMENTARY MATERIAL

Supplementary Figures

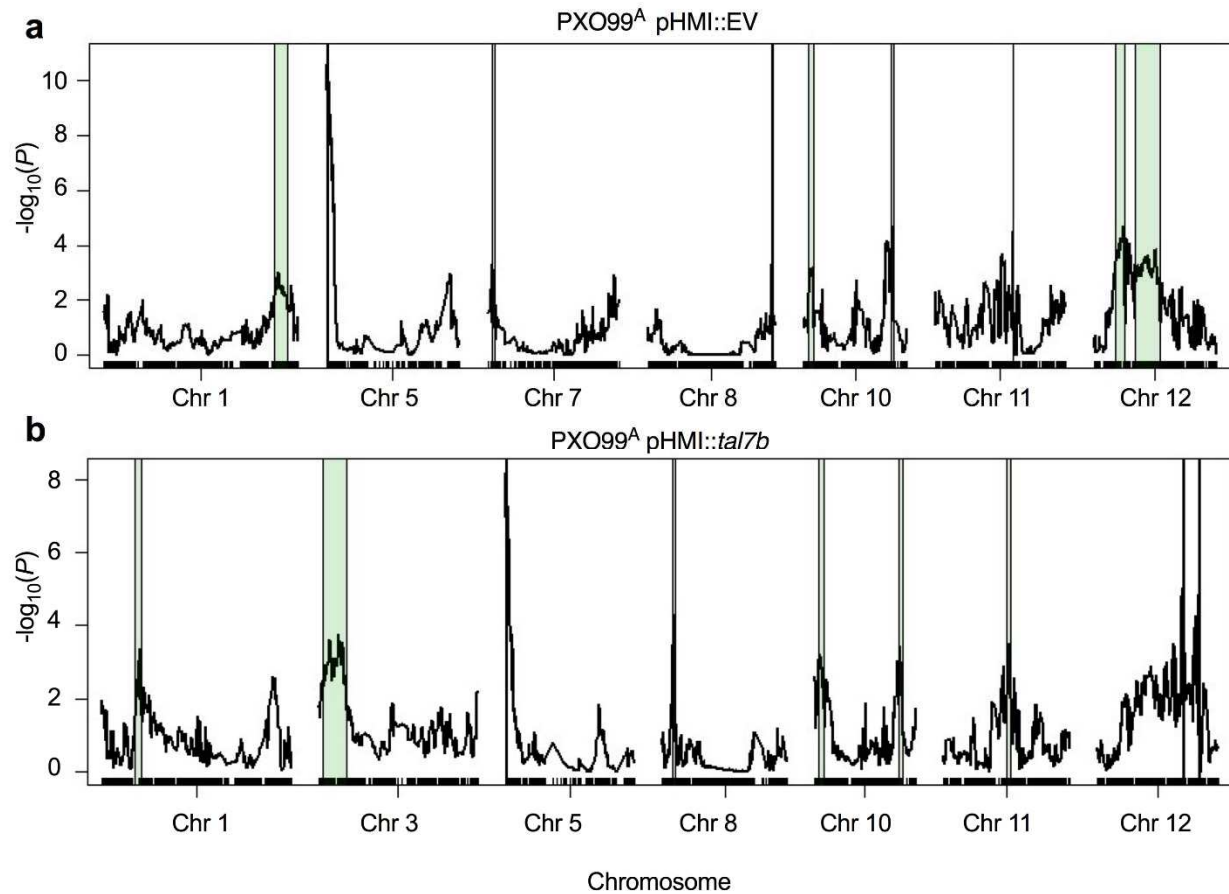


Figure S.A.1. QTL detection for resistance to *Xoo* PXO99^A pHM1::EV and PXO99^A pHM1::tal7b in indica MAGIC population. (a) *Xoo* PXO99^A pHM1::EV. (b) *Xoo* PXO99^A pHM1::tal7b. Simple interval mapping showing chromosomes with significant QTL (p-value < 0.001, using 14,561 SNP markers). Green regions indicate 1-LOD support intervals.

Supplementary Tables

Table S.A.1. Bacterial strains and plasmids used in this study.

Strain	Relevant Characteristic	Reference
<i>X. oryzae</i> pv. <i>oryzae</i>		
PXO86	Philippine Race 2, <i>tal7b</i> donor	Barton-Willis et al., (1989); Bai et al., (2000).
PXO99 ^A	Philippine Race 6	Hopkins et al., (1992)
PXO99 ^A pHMI::EV	PXO99 ^A carrying empty vector pHM1	This study
PXO99 ^A pHMI:: <i>tal7b</i>	PXO99 ^A carrying <i>tal7b</i> in pHM1 vector	This study
Plasmids		
pBluescript II KS+	Cloning vector; Amp ^r	Stratagene Inc. La Jolla, CA
pXO6-33	pHMI cosmid clone carrying the <i>tal7b</i> (previously name <i>avrXa5</i>) and <i>avrXa10</i> from PXO86	Hopkins et al., (1992)
pBS4.5b	pBluescript carrying the <i>tal7b</i> <i>Bam</i> HI gene fragment; Amp ^r	This study
pCS466	Gateway entry vector pCR8-GW (Invitrogen) containing <i>tal1c</i> gene of <i>Xoc</i> BLS256 without central repeat region <i>Sph</i> I fragment; Sp ^r	Verdier et al., (2012)
pCS466:: <i>tal7b</i>	pCS466 with repeat-containing the <i>Sph</i> I <i>tal7b</i> fragment replaced y that of <i>tal7b</i> from pBS4.5b	This study
pKEB31	pDD62 derivative containing Gateway destination vector cassette (Invitrogen) between <i>Xba</i> I and <i>Bam</i> HI sites; Tc ^r	Cermak et al., (2011)
pKEB31::EV	pKEB31 containing the <i>tal1c</i> gene of <i>Xoc</i> BLS256 without the central repeat region containing <i>Sph</i> I fragment, Tc ^r	Verdier et al., 2012
pKEB31:: <i>tal7b</i>	pKEB- <i>tal1c</i> with central repeat region containing <i>Sph</i> I fragment replaced by that of <i>tal7b</i> gene of <i>Xoo</i> PXO86; Tc ^r	This study
pHMI	Broad host-range cosmid derivative of pRI40, Sp ^r , Sm ^r	Hopkins et al., (1992)
pHMI::EV	pHMI containing the <i>tal1c</i> gene of <i>Xoc</i> BLS256 without the central repeat region containing <i>Sph</i> I fragment; Sp ^r , Sm ^r	This study
pHMI:: <i>tal7b</i>	pHM1 with central repeat region containing <i>Sph</i> I fragment replaced by that of <i>tal7b</i> gene of <i>Xoo</i> PXO86; Sp ^r , Sm ^r	This study

Table S.A.2. Indica MAGIC population response, measured as average lesion length (LL) in centimeters (cm) to PXO99^A pHM1::EV and pHMI::*tal7b*.

Strain	Average LL [†] (cm)	Min. and Max. [†] LL(cm)	Res. AILs [‡] (LL < 5.0 cm)	Mod. Res. AILs [¶] (LL < 10.0 cm)	Sus. AILs [§] (LL > 20.0 cm)
PXO99 ^A pHM1::EV	13.8	4.4 - 22.9	1	34	4
PXO99 ^A pHM1:: <i>tal7b</i>	17.1	3.2 – 26	1	10	81

[†] Min. and Max. represent the minimum and maximum lesion length measured in AILs of the MAGIC population to PXO99^A pHM1::EV and PXO99^A pHMI::*tal7b*

[‡] Res. AILs, represent the number of AILs displaying a resistant phenotype.

[¶] Mod. Res. AILs, represents the number of AILs displaying moderately resistant phenotype.

[§]Sus. AILs, represent the number of AILs displaying a susceptibility phenotype.

Table S.A.3. Mixed model ANOVA for the MAGIC population response to PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*. *P*-values of significant differences in variance show that the MAGIC population (including parents and AILs) are significantly different in resistance response. Additionally, the two strains, PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b* are significantly different in virulence on the MAGIC lines.

Type 3 Analysis of Variance								
Source	DF [†]	SS [‡]	MS [¶]	Expected MS	Error Term	Error DF	F value	Pr> F
MAGIC AILs	338	18693	55.31	Var(Residual) + Q(Line, Line*Strain)	MS(Residual)	1251	4.20	<.0001
Strain	1	5277.37	5277.37	Var(Residual) + Q(Strain, Line*Strain)	MS(Residual)	1251	400.40	<.0001
AILs * Strain	336	3995.45	11.89	Var(Residual) + Q(Line*Strain)	MS(Residual)	1251	0.90	0.8760
Rep	2	8566.14	4283.07	Var(Residual) + 206.62 Var(Block(Rep)) + 619.86 Var(Rep)	1.48 MS(Block(Rep)) - 0.48 MS(Residual)	5.73	15.94	0.0046
Block (Rep)	6	1117.18	186.12	Var(Residual) + 139.89 Var(Block(Rep))	MS(Residual)	1251	14.13	<.0001
Residual	1251	16488	13.18	Var(Residual)				

[†] DF, represented degrees of freedom

[‡] SS, represented the total sum of squares

[¶] MS, represent the mean squares between groups

Table S.A.4. Response of MAGIC parents to PXO99^A pHM1::EV and PXO99^A pHM1::*tal7b*. Reported LL indicate average lesion lengths in cm.

	Screen with MAGIC population [¶] PXO99 ^A pHM1::		
	EV LL (cm)	<i>tal7b</i> LL (cm)	<i>P</i> -value
Fedearroz 50	12.0	18.4	0.002
IR45427-2B-2-2B-1-1	22.8	19.4	0.098
IR4630-22-2-5-1-3	11.3	19.2	0.000*
IR77298-14-1-2-10	11.8	16.2	0.013
PSBRc82	10.8	13.2	0.195
PSBRc158 [†]	ND [†]	11.5	ND
Sanhuangzhan-2	11.3	13.8	0.022
Samba Mahsuri- <i>sub1</i>	9.8	13.5	0.291

* *P*-value < 0.0001.

[†] PSBRc158 was not included in the PXO99^A inoculation screen due to poor germination.

[¶] Screen with MAGIC population refers to the full screen which included, founding parents, 330 AIL of the indica MAGIC population and Nipponbare.

Table S.A.5. Significant SNPs in indica MAGIC population associated with disease resistance to *Xoo* PXO99^A pHM1::EV. The most significant SNP in each region are designated in bold and SNP markers that overlapped with interval mapping QTL are shaded in gray.

Marker ^a	P-value ^b	q-value ^c	R ² ^d	Effect Estimate ^e	Allele ^f	Allele Ratio ^g
S5_37878	6.40 x 10 ⁻⁵	3.59 x 10 ⁻²	5.84	-1.7506	A/G	211/70
S5_69302	5.20 x 10 ⁻⁵	3.29 x 10 ⁻²	5.55	-1.7540	C/T	228/70
S5_103237	2.42 x 10 ⁻⁷	3.92 x 10 ⁻⁴	9.41	-2.3715	C/T	59/238
S5_179519	5.79 x 10 ⁻⁵	3.51 x 10 ⁻²	5.57	1.9971	A/C	46/255
S5_189600	8.17 x 10 ⁻⁴	2.87 x 10 ⁻¹	4.01	-1.4934	G/T	213/65
S5_196176	6.36 x 10 ⁻⁵	3.59 x 10 ⁻²	5.53	1.9625	A/G	47/255
S5_201318	7.55 x 10 ⁻⁴	2.75 x 10 ⁻¹	4.45	1.7427	A/C	43/217
S5_219803	1.04 x 10 ⁻⁴	5.24 x 10 ⁻²	5.21	1.9146	G/T	47/253
S5_227187	8.76 x 10⁻¹⁰	7.78 x 10⁻⁶	13.12	-3.6367	A/C	33/270
S5_269480	2.01 x 10 ⁻⁴	9.46 x 10 ⁻²	5.32	-1.9453	A/G	222/41
S5_285834	2.14 x 10 ⁻⁹	7.78 x 10 ⁻⁶	12.47	-3.6822	A/G	30/277
S5_312457	1.40 x 10 ⁻⁴	6.81 x 10 ⁻²	5.01	-1.8589	A/C	252/48
S5_340482	6.82 x 10 ⁻⁵	3.68 x 10 ⁻²	5.76	-1.6047	C/T	80/194
S5_347328	6.82 x 10 ⁻⁵	6.82 x 10 ⁻⁵	8.28	2.2571	A/G	239/60
S5_353165	1.83 x 10 ⁻⁹	7.78 x 10 ⁻⁶	12.48	3.4620	C/T	269/35
S5_365871	9.48 x 10 ⁻⁷	1.30 x 10 ⁻³	9.28	-2.3527	A/G	52/218
S5_440644	2.78 x 10 ⁻⁸	6.74 x 10 ⁻⁵	10.88	-3.3204	A/G	33/260
S5_453169	1.83 x 10 ⁻⁹	7.78 x 10 ⁻⁶	12.41	-3.6474	A/G	32/276
S5_574926	1.23 x 10 ⁻⁸	3.59 x 10 ⁻⁵	11.36	3.3011	C/T	264/35
S5_704336	2.11 x 10 ⁻⁵	1.71 x 10 ⁻²	6.33	1.9380	A/G	230/67
S5_759048	1.45 x 10 ⁻⁵	1.29 x 10 ⁻²	6.44	-1.9789	C/T	65/227
S5_761061	3.61 x 10 ⁻⁵	2.63 x 10 ⁻²	5.90	1.6488	C/T	191/102
S5_761063	4.03 x 10 ⁻⁵	2.67 x 10 ⁻²	5.82	-1.6351	C/T	103/191
S5_761076	4.03 x 10 ⁻⁵	2.67 x 10 ⁻²	5.82	1.6351	C/T	191/103
S5_849335	5.42 x 10 ⁻⁶	5.26 x 10 ⁻³	7.27	2.9506	C/T	280/25
S5_850180	1.52 x 10 ⁻⁷	3.16 x 10 ⁻⁴	9.47	-3.1434	C/G	32/272
S5_904372	2.43 x 10 ⁻⁵	1.86 x 10 ⁻²	6.26	2.0142	G/T	242/50
S5_934093	1.74 x 10 ⁻⁷	3.16 x 10 ⁻⁴	11.55	-3.4352	A/T	26/228
S5_1200961	2.42 x 10 ⁻⁷	3.92 x 10 ⁻⁴	7.44	-2.7203	A/G	34/274
S5_1200964	2.49 x 10 ⁻⁶	2.59 x 10 ⁻³	7.44	-2.7203	C/G	34/274
S5_1200971	2.49 x 10 ⁻⁶	2.59 x 10 ⁻³	7.44	2.7203	G/T	274/34
S5_1224178	2.49 x 10 ⁻⁶	2.59 x 10 ⁻³	6.42	-2.4618	A/G	33/275
S5_1509216	4.53 x 10 ⁻⁴	2.00 x 10 ⁻¹	4.21	1.3925	G/T	125/168
S11_15413301	8.32 x 10 ⁻⁴	2.87 x 10 ⁻¹	4.26	1.6276	G/T	205/60
S11_15423317	5.56 x 10 ⁻⁴	2.25 x 10 ⁻¹	4.23	1.5742	A/G	222/68
S11_25591134	5.47x 10 ⁻⁴	2.25 x 10 ⁻¹	4.03	-2.5468	G/T	281/19
S11_28483987	1.02 x 10⁻⁴	5.24x 10⁻²	5.61	-3.0436	C/T	267/16
S11_28652283	8.48 x 10 ⁻⁴	2.87 x 10 ⁻¹	3.82	-1.9981	A/C	269/37
S11_28852557	7.28 x 10 ⁻⁴	2.72 x 10 ⁻¹	3.72	2.4837	G/T	18/295
S11_28870400	6.98 x 10 ⁻⁴	2.68 x 10 ⁻¹	4.26	-2.5781	C/T	239/17
S11_28870403	4.68 x 10 ⁻⁴	2.00 x 10 ⁻¹	4.69	1.9954	C/T	40/213
S11_28920303	3.16 x 10 ⁻⁴	1.44 x 10 ⁻¹	4.70	2.8323	A/C	16/216
S11_28977691	6.28 x 10 ⁻⁴	2.47 x 10 ⁻¹	4.05	1.8822	C/T	42/258

^a Physical coordinate of marker, number following S designates chromosome, number following underscore designates the physical location on the chromosome in bp.

^b Threshold for significance $P \leq 0.001$

^c Measure of significance in terms of the false discovery rate.

^d R^2 estimates the percent of variance in PXO99^A pHM1::EV disease due to the given marker.

^e Effect estimate compares phenotypes, average lesion lengths (cm), with contrasting SNP allele. Negative effects correspond to a decrease in lesion length and a positive effect corresponds to an increase in lesion length.

^f Allele represents the SNP allele associated with the measured effect estimate in the numerator (Effect allele) whereas the Null allele is in the denominator.

^g Allele ratio represents the ratio of AILs with the Effect/Null allele as defined in Allele column.

Table S.A.6. Significant SNPs in indica MAGIC population associated with disease resistance to *Xoo* PXO99^A pHM1::*tal7b*. The most significant SNP in each region are designated in bold and SNP markers that overlapped with interval mapping QTL are shaded in gray.

Marker ^a	P-value ^b	q-value ^c	R ² ^d	Effect Estimate ^e	Allele ^f	Allele Ratio ^g
S5_103237	5.86 x 10 ⁻⁵	4.74 x 10 ⁻³	5.76	-2.2181	C/T	59/236
S5_227187	3.89 x 10⁻⁹	3.60 x 10⁻⁵	12.26	-4.3477	A/C	33/268
S5_285834	4.37 x 10 ⁻⁸	1.06 x 10 ⁻⁴	10.51	-4.1760	A/G	30/275
S5_347328	9.06 x 10 ⁻⁵	6.28 x 10 ⁻⁴	5.34	2.1757	A/G	237/60
S5_353165	7.42 x 10 ⁻⁹	3.60 x 10 ⁻⁵	11.65	4.1393	C/T	267/35
S5_365871	4.31 x 10 ⁻⁴	2.73 x 10 ⁻¹	4.69	-2.0290	A/G	52/217
S5_440644	3.22 x 10 ⁻⁸	9.39 x 10 ⁻⁵	11.29	-4.1221	A/G	33/258
S5_453169	5.17 x 10 ⁻⁹	3.60 x 10 ⁻⁵	11.91	-4.4172	A/G	32/274
S5_574926	2.46 x 10 ⁻⁸	8.97 x 10 ⁻⁵	11.18	4.0330	C/T	262/35
S5_849335	4.55 x 10 ⁻⁶	7.36 x 10 ⁻³	7.63	3.6595	C/T	278/25
S5_850180	5.32 x 10 ⁻⁷	1.11 x 10 ⁻³	8.73	-3.7390	C/G	32/270
S5_904372	7.88 x 10 ⁻⁵	5.74 x 10 ⁻²	5.53	2.2971	G/T	240/50
S5_934093	1.24 x 10 ⁻⁶	2.26 x 10 ⁻³	9.51	-3.9703	A/T	26/226
S5_1195956	9.68 x 10 ⁻⁴	4.86 x 10 ⁻¹	3.64	-1.7161	A/G	68/236
S5_1200961	1.72 x 10 ⁻⁵	2.08 x 10 ⁻²	6.23	-3.0855	A/G	34/272
S5_1200964	1.72 x 10 ⁻⁵	2.08 x 10 ⁻²	6.23	-3.0855	C/G	34/272
S5_1200971	1.72 x 10 ⁻⁵	2.08 x 10 ⁻²	6.23	3.0855	G/T	272/34
S5_1224178	6.65 x 10 ⁻⁵	5.09 x 10 ⁻²	5.51	-2.8137	A/G	33/273
S5_1258051	8.65 x 10 ⁻⁴	4.67 x 10 ⁻¹	3.72	-1.7399	G/T	67/235
S5_1320280	5.64 x 10 ⁻⁴	3.42 x 10 ⁻¹	4.03	-1.8139	A/G	65/236
S8_2774179	1.44 x 10 ⁻⁴	9.53 x 10 ⁻²	4.87	-3.5436	A/G	16/290
S8_2778495	5.22 x 10⁻⁵	4.46 x 10⁻²	5.53	-3.7745	C/T	16/288
S8_2778496	5.22 x 10⁻⁵	4.46 x 10⁻²	5.53	3.7745	C/T	288/16
S8_2778497	5.22 x 10⁻⁵	4.46 x 10⁻²	5.53	-3.7745	G/T	16/288
S11_28697250	7.58 x 10 ⁻⁴	4.41 x 10 ⁻¹	3.82	2.5488	C/G	36/268
S12_23060491	8.94 x 10 ⁻⁴	4.67 x 10 ⁻¹	4.02	1.8428	A/G	96/182
S12_23092043	4.04 x 10⁻⁵	4.21 x 10⁻²	6.12	-2.2773	C/T	196/93
S12_23120151	2.57 x 10 ⁻⁵	2.88 x 10 ⁻²	6.43	2.3934	A/G	91/197
S12_23825914	8.98 x 10 ⁻⁴	4.67 x 10 ⁻¹	4.17	1.8379	C/T	207/83

^aPhysical coordinate of marker, number following S designates chromosome, number following underscore designates the physical location on the chromosome in bp.

^bThreshold for significance $P \leq 0.001$

^cMeasure of significance in terms of the false discovery rate.

^dR² estimates the percent of variance in PXO99^A pHM1::*Tal7b* disease due to the given marker.

^eEffect estimate compares phenotypes, average lesion lengths (cm), with contrasting SNP allele. Negative effects correspond to a decrease in lesion length and a positive effect corresponds to an increase in lesion length.

^fAllele represents the SNP allele associated with the measured effect estimate in the numerator (Effect allele) whereas the Null allele is in the denominator.

^gAllele ratio represents the ratio of AILs with the Effect/Null allele as defined in Allele column.

Table S.A.7. QTL detection for resistance to *Xoo* PXO99^A pHM1::EV in indica MAGIC population (P -value < 0.001). Wald statistic for test that no parents have effects on trait (Wald, 7 df). Parental source of resistance determined by founder effects estimates relative to IR45427-2B-2-2b-1-1. QTL corroborated with significantly associated SNP markers from GWAS are highlighted in grey.

QTL	Chr	QTL position			Supporting interval		Interval size		Wald [¶]	P -value	Phenotypic variance (%)	Founder with largest R effect
		(cM) [†]	Left Mrk [‡]	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				
qPXO99 ^A -1	1	155.69	S1_38636497	S1_38949958	S1_37802120	S1_40985568	12.73	3,183	24.38	9.8E-04	5.24	IR77 and SHZ-2
qPXO99 ^A -5	5	1.29	S5_353165	S5_361080	S5_347328	S5_542193	0.78	195	65.24	1.3E-11	15.65	PSBRc 82
qPXO99 ^A -7	7	4.34	S7_1134913	S7_1186420	S7_1117844	S7_1712749	2.38	595	26.02	5.0E-04	5.71	IR46
qPXO99 ^A -8	8	110.2	S8_27583372	S8_27602730	S8_27521063	S8_27733890	0.85	213	26.19	4.7E-04	5.76	Fed 50
qPXO99 ^A -10-1	10	8.33	S10_2158327	S10_2185499	S10_1083022	S10_2299979	4.87	1,217	25.47	6.3E-04	5.55	Fed 50
qPXO99 ^A -10-2	10	79.09	S10_19847581	S10_19891163	S10_19580696	S10_19916740	1.34	336	33.56	2.1E-05	7.8	Fed 50
qPXO99 ^A -11	11	69.26	S11_17316468	S11_17323824	S11_17230702	S11_17352371	0.49	122	32.66	3.1E-05	7.55	SHZ-2
qPXO99 ^A -12-1	12	26.44	S12_6733540	S12_6755981	S12_4991054	S12_6913707	7.69	1,923	33.72	1.9E-05	7.84	Fed 50
qPXO99 ^A -12-2	12	54.55	S12_13696801	S12_13762396	S12_9182794	S12_14722562	22.16	5,540	29.03	1.4E-04	6.56	IR46 and SHZ-2

[†] cM, represents the genetic distance in centimorgans

[‡] Mrk, report the left and right physical position of the SNP markers that encompass a QTL, the number following S is the chromosome number followed by the bp coordinate of the SNP as inferred by the MSU7 Nipponbare reference genome.

[¶] Wald, Wald statistic for test that no parents have effects on trait (Wald, 7 df).

Table S.A.8. QTL detection for resistance to *Xoo* PXO99^A pHM1::*Ta/7b* in indica MAGIC population (*P*-value < 0.001). Parental source of resistance determined by founder effects estimates relative to IR45427-2B-2-2b-1-1. QTL corroborated with significantly associated SNP markers from GWAS are highlighted in grey.

QTL	Chr	QTL position			Supporting interval		Interval size		Wald [¶]	<i>P</i> -value	Phenotypic variance (%)	Founder with largest R effect
		(cM) [†]	Left Mrk [‡]	Right Mrk	Left Mrk	Right Mrk	(cM)	(kb)				
<i>qtal7b</i> -1	1	34.97	S1_8767682	S1_8770753	S1_7570978	S1_9001276	5.72	1,430	26.29	4.5E-04	5.84	SHZ-2
<i>qtal7b</i> -3	3	18.19	S3_4771783	S3_4775968	S3_1270943	S3_6494259	20.89	5,223	28.58	1.7E-04	6.49	Sambha
<i>qtal7b</i> -5	5	1.26	S5_347328	S5_353165	S5_37878	S5_574926	2.15	537	51.94	6.0E-09	12.63	PSBRc 82
<i>qtal7b</i> -8	8	10.91	S8_2778548	S8_2913918	S8_2208918	S8_2913918	2.82	705	31.48	5.1E-05	7.3	SHZ-2
<i>qtal7b</i> -10-1	10	5.32	S10_1381763	S10_1407056	S10_1083022	S10_2299979	4.87	1,217	25.52	6.1E-04	5.62	PSBRc 158
<i>qtal7b</i> -10-2	10	78.09	S10_19580696	S10_19598933	S10_19229371	S10_20082337	3.41	853	26.75	3.7E-04	5.97	Fed 50
<i>qtal7b</i> -11	11	59.91	S11_14754772	S11_14981109	S11_14608638	S11_15523604	3.66	915	27.26	3.0E-04	6.12	IR77
<i>qtal7b</i> -12-1	12	78.21	S12_19676337	S12_19687678	S12_19452481	S12_19836912	1.54	384	36.81	5.1E-06	8.75	Fed 50
<i>qtal7b</i> -12-2	12	92.13	S12_23137107	S12_23156740	S12_23016399	S12_23252872	0.95	236	34.39	1.5E-05	8.09	Fed 50

[†] cM, represents the genetic distance in centimorgans

[‡] Mrk, report the left and right physical position of the SNP markers that encompass a QTL, the number following S is the chromosome number followed by the bp coordinate of the SNP as inferred by the MSU7 Nipponbare reference genome.

[¶] Wald, reports the Wald statistical test value of each QTL detected based on the sample estimate.

[§] Phenotypic variance (%)

Table S.A.9. Phenotypic response of 15 MAGIC AILs with variant allele in resistance locus identified on chromosome 8 to *Xoo* PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b*. Shaded rows indicate no significant differences in measured lesion length in the presence of the virulence factor Tal7b.

AIL	N ^a	PXO99 ^A pHMI::EV		PXO99 ^A pHMI:: <i>tal7b</i>		P-value ^d
		Lesion Length (cm) ^b	Std Err ^c	Lesion Length (cm)	Std Err	
13	12	11.82	0.572	16.32	1.242	0.0082
24	12	15.65	0.693	15.55	0.925	0.9328 NS ^e
156	12	10.03	1.202	11.47	1.064	0.3928 NS
163	12	14.85	0.969	14.63	0.908	0.8737 NS
197	12	13.08	0.972	14.62	1.112	0.3237 NS
210	14	15.93	1.998	15.25	0.701	0.7243 NS
219	12	11.37	1.564	16.80	1.623	0.0366
222	12	13.13	1.047	14.33	1.106	0.4490 NS
225	8	9.70	0.882	11.60	1.537	0.3248 NS
229	12	12.70	1.121	17.23	1.351	0.0273
234	12	12.35	0.927	12.92	1.528	0.7577 NS
237	12	4.50	0.743	4.27	0.804	0.8355 NS
250	10	14.40	1.465	15.65	1.287	0.5672 NS
267	12	12.38	0.990	13.18	0.813	0.5463 NS
Nipponbare	12	13.00	0.647	17.25	0.972	0.0045

^a N represents the number of measurements made per AIL. Six plants (biological replicates) and two leaves per plants were measured.

^b Lesion length represents the mean of all measurements recorded.

^c Std Err indicates the Standard Error from the mean in cm.

^d P-value indicate the level of difference in lesion lengths between AILs inoculated with PXO99^A pHMI::EV and PXO99^A pHMI::*tal7b* as determined by one- way ANOVA.

^e **NS**, represents no-significance indicating the loss of enhanced susceptibility observed in the presence of *tal7b* observed in lines 13, 219, 229, and Nipponbare

ABBREVIATIONS

AIL	Advanced intercross line
BB	Bacterial blight
BLS	Bacterial leaf streak
bp	basepair
BSR	Broad-spectrum resistance
BTB	Bric-a-brac, tramtrack, broad complex domain
cM	Centimorgan
CRM	<i>cis</i> -regulatory module
DR-gene	Defense response gene
EBE	Effector-binding element
ETI	Effector-triggered immunity
ETS	Effector-triggered susceptibility
GWAS	Genome-wide association study
IM	Interval mapping
Kb	Kilo basepair
LL	Lesion length
LRR	Leucine-rich repeat
LS-Means	Least square means
MAGIC	Multi-parent advanced generation inter-cross population
MAMP	Microbial-associated molecular patterns
MATH	Meprin and TRAF homology domain
Mb	Mega basepair
MLM	Mixed linear model
NLR	Nucleotide-binding leucine-rich repeat protein

PAMP	Pathogen-associated molecular patterns
PRR	Pattern recognition receptor
PTI	PAMP-triggered immunity
QTL	Quantitative trait loci
<i>R</i> gene	Resistance gene
RVD	repeat variable di-residue
<i>S</i> gene	Susceptibility gene
SNP	Single nucleotide polymorphism
TAL effector	Transcription activator-like effector
TSS	Transcription start site
<i>Xoc</i>	<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>
<i>Xoo</i>	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>