Indian J. Genet., 78(2): 196-201 (2018)
DOI: 10.5958/0975-6906.2018.00025.1

Identification of quantitative trait loci (QTL) associated with sheath blight tolerance in rice

Ashok Koshariya, Indra Kumar, Ashish Pradhan, Umesh Shinde[1], S. B. Verulkar[1], Toshy Agrawal[1] and Anil Kotasthane

Department of Plant Pathology, [1]Department of Plant Molecular Biology and Biotechnology CoA, Indira Gandhi Krishi Vishwavidyalaya, Raipur

(Received: May 2017; Revised: February 2018; Accepted: March 2018)

Abstract

Sheath blight, caused by the pathogen *Rhizoctonia solani* Kühn, is one of the most serious diseases of rice and leads to severe yield losses worldwide. A recombinant inbred line (RIL) population consisting of 122 lines was constructed from a cross between Danteshwari a high yielding popular rice cultivar but moderately susceptible to water stress, susceptible to sheath blight and Dagad Deshi a tall deep rooted poor yielder and tolerant to water stress and sheath blight. Five traits, namely infected tillers per hill, lesion size (total coalescing lesions) and individual lesion (one spot) and lesion's length and width) were used to evaluate sheath blight resistance. Using the RIL population and 162 molecular markers, 11 quantitative trait loci (QTLs) were identified for the five traits. Identification of map position was accomplished by identifying BAC or PAC clones that simultaneously contained a hit from the microsatellite / HvSSR marker further helped us to generate a high resolution molecular marker map of the identified QTL region. Identified QTLs were located on seven chromosomes. A major QTL for infected tillers per hill on chromosome 1 was identified with phenotypic variance of 18.02%. Six QTL's with positive additive effect and one with negative additive effects was identified indicating alleles at these loci are being contributed by either of the parents respectively.

Key words: QTL, rice, sheath blight, markers

Introduction

Sheath blight (ShB) disease of rice (*Oryza sativa* L.), caused by *Rhizoctonia solani* Ku¨hn, is particularly important in intensive rice production systems worldwide (Ou 1985; Teng et al. 1990; Savary et al. 2000, 2006). Rice crops with high attainable yields (Savary and Mew 1996) are especially affected. Yield loss estimates of 5-10% for tropical lowland rice in Asia has been reported (Savary et al. 2000). Breeding for sheath blight resistance has been difficult, owing to the lack of identified resistant donors in cultivated varieties (Bonman et al. 1992) and semi-saprophytic character and wide host range of the pathogen affecting 32 plant families and 188 genera (Gangopadhyay and Chakrabarti 1982). Few varieties with varying levels of rice sheath blight resistance were identified after large-scale screening of cultivated germplasm and related wild species (Eizenga et al. 2002; Prasad and Eizenga 2008). Resistance to rice ShB is a complex, quantitative trait controlled by polygenes (Sha and Zhu 1990; Li et al. 1995; Pinson et al. 2005). So far, nearly 70 QTLs for sheath blight resistance have been identified in rice, distributed on all 12 chromosomes (Li et al. 1995; Zou et al. 2000; Che et al. 2003; Han et al. 2002; Kunihiro et al. 2002; Pinson et al. 2005; Tan et al. 2005; Xiang et al. 2007; Xie et al. 2008; Liu et al. 2009; Sharma et al. 2009; Channamallikarjuna et al. 2010). However, a number of researchers (Xie et al. 1992; Pan et al. 1999) proposed that ShB resistance in some rice varieties is controlled by a only a few major genes. The quantitative resistance in some of the most resistant varieties, such as Tetep and Tadukan, can offer excellent protection against the pathogen under field conditions (Groth and Nowick 1992). The development of molecular markers has led to rapid progress in understanding the mechanisms underlying resistance to sheath blight using the quantitative trait locus (QTL) mapping method. Identification of genomic loci governing complex traits has been facilitated by the development of quantitative trait locus (QTL) mapping approaches using segregating bi-parental

*Corresponding author's e-mail: kotasthaneaj@yahoo.com
Published by the Indian Society of Genetics & Plant Breeding, A-Block, F2, First Floor, NASC Complex, IARI P.O., Pusa Campus, New Delhi 110 012; Online management by indianjournals.com; www.isgpb.org

populations. Limited population size with low density marker coverage usually proves sufficient to identify QTLs for different traits. These roughly estimated QTL intervals extend over several cM, a genetic distance that translates into genomic regions with large number of candidate genes. This limited resolution results mainly from the small number of recombination events that are accumulated over the few generations needed to develop a bi-parental mapping population (Balasubramanian et al. 2009). In this study an attempt was made to map QTLs for sheath blight tolerance using 122 RILs in rice.

Materials and methods

Mapping population and phenotyping

The population used in this study consisted of 122 F_{13} recombinant inbred lines (RILs) derived by single seed descent method from a cross between Danteshwari (D_1) (high yielding popular rice cultivar but moderately susceptible to water stress, susceptible to sheath blight) and Dagad Deshi (D_2) (a tall deep rooted poor yielder and tolerant to water stress and sheath blight). The D_1 X D_2 derived population was phenotyped at Indira Gandhi Krishi Vishwavidyalaya , Raipur during 2014 wet monsoon. Raipur is located at 21^o 16' N and 81^o 36' E at an altitude of 289.6 m above sea level. Each line having 3 rows of 1.5 m length were screened. Standard agronomic practices were followed to raise the crop in nursery and field conditions.

Inoculum production and inoculation procedure

Multinucleate compatible isolate of *R. solani* isolate rice, belonging to the AG-1 IA anastomosis was grown on potato dextrose agar at 28±1^{o}C for 6 days for mass multiplication. Rice bran supplemented with dextrose (@ 17g/kg), was moistened, thoroughly mixed and filled to 3/4th the volume of glass bottles. These were then sterilized at 121.6^{o}C for 45 minutes. Small bits of PDA blocks containing actively growing mycelium of *R solani* was inoculated in bottles containing pre-sterilized cooled rice bran and incubated at 25^o±1^{o}C. Growth of *R solani* appeared over night and the fungus completely colonized the rice bran within one week at 25^o±1^{o}C. No sclerotial were produced in the colonized rice bran. *R solani* colonized rice bran was harvested and pooled in a tray. Clumps in rice bran were formed due to colonization of *R solani* and were further pulverized by passing them through a wire mesh. This resulted in the breaking of the mycelium into small fragments. Every particle of the pulverized rice bran was of uniform size and contained colonized mycelial bits of *R. solani* and therefore served as inoculum. The method of inoculum deposition in our present investigation mimics high contact frequency between tissues essentially required for sheath blight epidemics. Inoculation was done at maximum tillering stage. Pulverized rice bran containing colonized mycelial bits of *R. solani* were deposited uniformly in the whorls of plant hills. The inoculum also got deposited near the base of the plant. The incubation period (IP) was estimated as the period from inoculation to appearance of approximately 50% water soaked lesions (Yeh and Bonman 1986). Observations were recorded for number of infected tillers per hill, and by measuring the total (coalescing lesions) and individual (one spot) lesion length and width. Two disease criteria were assessed for each inoculated plant i.e. number of infected tillers per hill represents the horizontal spread of the disease between the tillers and measurement of lesions size represents the vertical and horizontal spreading degree of the disease on individual tiller and severity.

Construction of linkage map and QTL analysis

Genotypic data generated from SSR HvSSR markers were used for linkage map construction using computer software MAPMAKER/EXP, version 3.0. Kosambi function was used to calculate the genetic distances between the markers (Kosambi, 1943). QTL mapping (Composite Interval Mapping) was carried out (Zeng et al. 1994) with a threshold value of 2.5 to 3.0 LOD, was used for declaring the presence of a suggestive QTL. Contribution rate (R^2) was estimated as the percentage of the total phenotypic variation explained by each locus. Graphical presentation of the linkage map was carried out by using MapChart2.2 (http://www.biometris.wur.nl).

The genotypic data and field based phenotypic data of sheath blight lesion size (number of infected tillers per hill, total (coalescing lesions) and individual lesion (one spot) lesion length and width) was analyzed using QTL cartographer 2.5.

Results and discussion

QTL analysis

The parents along with RILs exhibited marked variation for the reaction to sheath blight. The two parents (Danteshwari and Dagaddeshi) showed differences for number of infected tillers per hill but not for lesion size (total (coalescing lesions) and individual lesion (one spot) lesion length and width) (Table 1, Fig. 1). The

Table 1. Reaction of parents, Danteshwari and Dagaddeshi for number of infected tillers per hill and lesion size in total (coalescing lesions) lesion width and length, individual lesion length and width

Parents	Total no. of tillers infected/hill	All coalescing lesions		Individual lesion	
		Length	Width	Length	Width
Danteshwai	41.73913	4.5625	0.625	2.0375	0.6
Dagaddeshi	26.37363	5.125	0.6875	2.275	0.625
Min.	13.38583	1.7	0.3875	1.3375	0.425
Max.	95.65217	9.5875	1.057143	4.425	0.886

Min. = Minimum; Max. = Maximum

Table 2. Identified QTL on D X D derived RIL population

S. No.	CH #	No. of QTLs
1	1	2
2	3	1
3	4	1
4	5	1
5	6	1
6	7	1
7	12	4
	Total	11

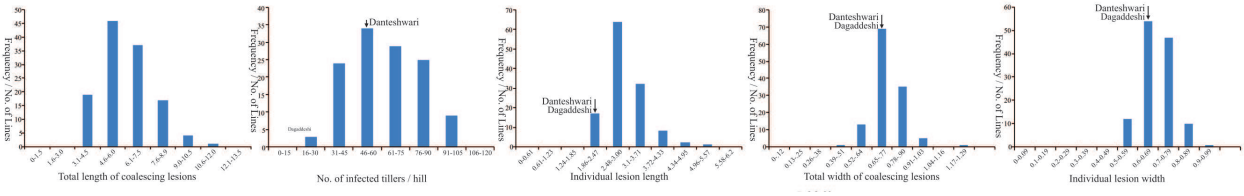

Fig. 1. Frequency distributions of 122 genotype (RIL) for sheath blight lesion size

RILs exhibited transgressive segregation in both directions, which indicated that neither parent contained all the alleles for resistance or susceptibility. Reaction of RILs, for sheath blight, could not be classified into discrete classes of resistance and susceptibility as they showed continuous variation and skewed distribution that suggested the inheritance is quantitative. Transgressive segregations among the RILs were observed for the number of infected tillers per hill, total (coalescing lesions) and individual lesion (one spot) lesion length and width.

The genotypic data and field based phenotypic data of sheath blight lesion size (number of infected tillers per hill, total lesion width, total lesion length, individual lesion length and individual lesion width) was analyzed using QTL cartographer 2.5. Eleven QTL's were identified on chromosomes 1, 3, 4, 5, 6, 7 and 12 for sheath blight reactions (number of infected tillers per hill but not for lesion size {total (coalescing lesions) and individual lesion (one spot) lesion length and width} under artificial inoculated conditions (Table 2). QTL mapping was carried out following composite interval mapping (Zeng et al. 1994) with a threshold value of 2.5 and 3.0 LOD, was used for declaring the presence of a suggestive QTL. Contribution rate (R_2) was estimated as the percentage of the total phenotypic variation explained by each locus. The LOD score and phenotypic variance for QTL (LOD 3 and above) ranged from 3.00 to 5.13 and 4.18 to 18.02, respectively (Table 3). QTL's with positive additive effect influencing: number of tillers infected per hill on Ch# 1, two each for lesion width (Total) on Ch#3 and 12, lesion length (individual) on Ch#1 and 12, and one lesion width (individual) on Ch# 5 were identified. A QTL with negative additive effects influencing individual lesion width on Ch# 5, was identified indicating. This suggests that alleles at these loci are contributed by either of the parents respectively (Table 3).

The LOD score and phenotypic variance for QTL (LOD 2.5 and above but below 3) ranged from 2.51 to 2.83 and 1.16 to 10.95 respectively (Table 3). Two QTLs influencing total (coalescing lesions) width on Ch# 4, 12 were with positive additive effect were identified. Two QTLs with negative additive effects influencing total (coalescing lesions) width on Ch# 6, 7 was identified indicating that alleles at these loci are being contributed by either of the parents respectively (Table 3). The location of QTLs reported for sheath blight varies in different populations and at different environments. Many important traits are quantitatively expressed and influenced by the environment and tend to show varied degree of genotype x environment (GxE) interaction (Zhuang et

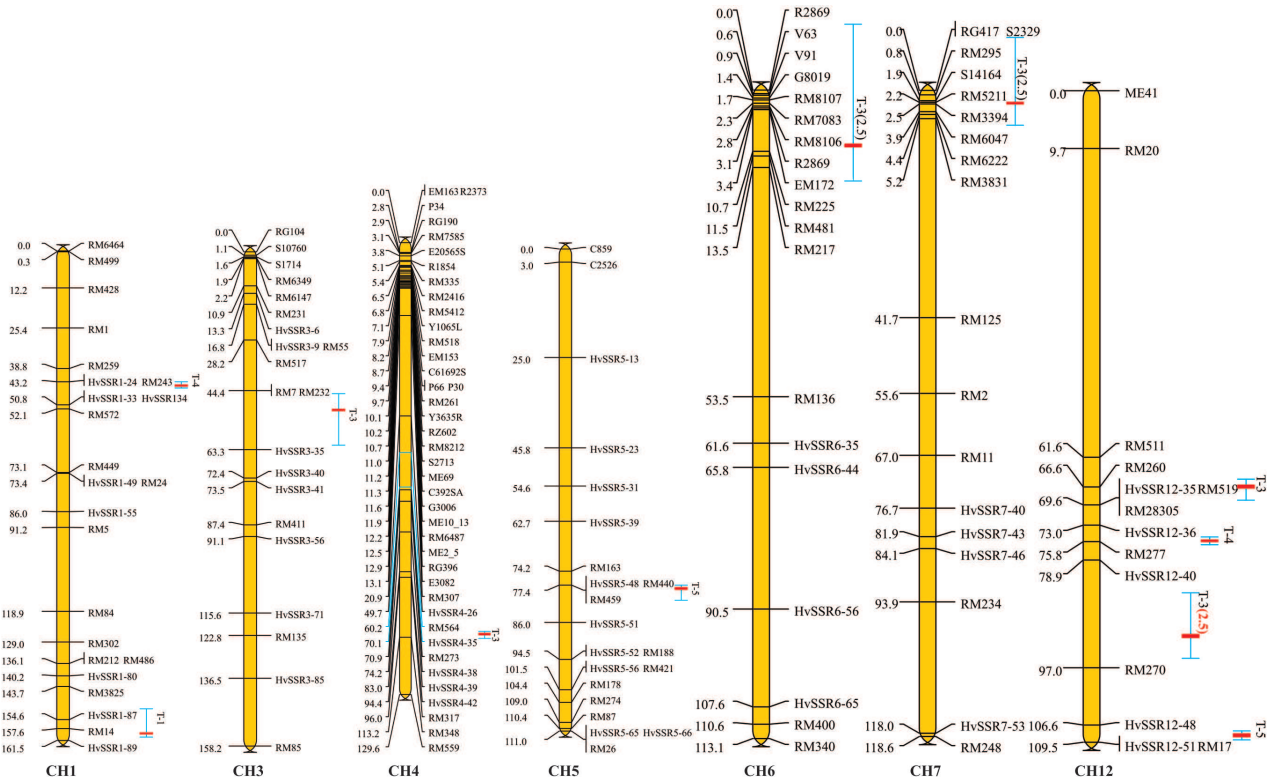

Fig. 2. Mapped QTLs on different chromosomes for sheath blight tolerance using 122 RILs in rice

al. 1997). Over the past two decades several ShB resistance quantitative trait loci (QTL) have been mapped, but consistency across results from different studies has not always been observed (Pinson et al. 2005).

Table 3. Identified QTL influencing sheath blight lesion size on D_1 x D_2 derived genotyped RIL population under artificial inoculated conditions

S.No.	Trait	Ch.	Marker	Position	LOD	a0	R^2
	QTL's with threshold value 3 and above						
	QTL's with Positive additive effect						
1	Number of tillers infected per hill	1	HvSSR1-87	155.11	4.23	9.44	18.02
2	Lesion Width (Total)	3	RM232	50.91	5.13	0.02	4.18
3	Lesion Width (Total)	12	RM260	69.11	3.23	0.03	11.85
4	Lesion length (individual one spot)	1	RM243	43.21	3.42	0.18	10.31
5	Lesion length (individual one spot)	12	RM277	75.81	3.00	0.23	9.28
6	Lesion width (individual one spot)	5	RM459	77.91	3.31	0.04	11.21
	QTL's with negative additive effect						
7	Lesion width (individual one spot)	12	HvSSR12-48	108.61	3.08	-0.03	10.70
	QTL's with threshold value 2.5 and above but <3						
	QTL's with positive additive effect						
1	Lesion Width (Total coalescing lesions)	4	RM564	66.21	2.51	0.01	1.16
2	Lesion Width (Total coalescing lesions)	12	HvSSR12-40	91.91	2.83	0.02	3.14
	QTL's with negative additive effect						
1	Lesion Width (Total coalescing lesions)	6	EM1_72	10.41	2.52	-0.02	3.17
2	Lesion Width (Total coalescing lesions)	7	RM3394	3.01	2.73	-0.03	10.95

Ch.= Chromosome No; *= figures in parenthesis indicate trait number

QTL's with threshold value 3 and above

Rice doubled haploid lines and RILs have been extensively used for QTL mapping for sheath blight resistance (Kunihiro et al. 2002; Han et al. 2002). Two QTLs have been identified for sheath blight resistance on chromosomes 3 and 12 in rice line WSS2 which is derived from Tetep (Sato et al. 2004). The accurate measurement of ShB resistance under field conditions i.e., of disease intensity and observed susceptibility (Yuen and Forbes 2009) depends on a range of environmental factors (Ou 1985; Castilla et al. 1996; Eizenga, Lee, and Rutger 2002) and plant morphological traits, such as plant height (Li et al. 1995; Zou et al. 2000; Pinson et al. 2005), which interact, resulting in the observed variation in resistant (susceptible) phenotypes. During the present investigation quantitative trait loci on D X D derived genotyped RIL population under artificial inoculated condition was identified which influenced number of tillers infected per hill with LOD value 4.23 which explained 18.025 % phenotypic variation. Two QTL's for lesion width (total) with LOD value 5.13 (Maker RM232) and 3.23 (Maker RM260) explained 4.18 and 11.85 % phenotypic variation on chromosome 3 and 12, respectively (Table 3). Only two QTLs were identified for lesion length (individual) with LOD value 3.42 (Maker RM243), 3.00 (Maker RM277) and one QTL for lesion width (individual) with LOD value 3.31 (Maker RM459) explained 10.31, 9.28, and 11.21 % phenotypic variation on chromosomes 1, 12 and 5 respectively (Table 3). QTL on D X D derived genotyped RIL population under artificial inoculated condition was identified which influenced lesion width with LOD value 3.08 which explained 10.70 % phenotypic variation respectively was positioned on CH#12 (Table 3).

QTL's with threshold value 2.5 and above but <3

Four QTL's for Lesion Width (Total) (3) with LOD value 2.51 (Maker RM564), 2.83 (Maker HvSSR12-40), 2.52 (Maker EM1_72) and 2.73 (Maker RM3394) explained 1.16, 3.14, 3.14, and 10.95 % phenotypic variation on chromosomes 4, 12, 6 and 7 respectively (Table 3). Absolute resistance to *R. solani* is not available in any of the rice germplasm grown worldwide. However, it has been reported that resistance to *R. solani* is a typical quantitative trait controlled by polygenes in rice (Sha and Zhu 1990). There are some rice lines such as Tetep, Tadukan, Teqing, Jasmine 85, ZYQ8, Minghui 63, LSBR-5 and LSBR-33 in which a high degree of quantitative resistance is available against this pathogen under field conditions (Khush 1977; Xie et al. 1992; Groth and Nowick 1992; Li et al. 1995; Pan et al. 1999).

Tying genetic linkage map to physical map

Identification of map position was accomplished by identifying BAC or PAC clones that simultaneously contained a hit from the microsatellite / HvSSR marker. Forward primer sequences of genotyped polymorphic marker(s) (Supplementary Table S1) were used for blast analysis to detect the physical position of the molecular markers and the BAC / PAC clones to which they contained a hit. By way of these co-mapped markers, the map in this study is tied to the physical and sequence map developed by the International Rice Genome Sequencing Project (http://rgp.dna.affrc.go.jp/ ;http://www.usricegenome.org/;http://genome.arizona.edu/fpc/rice/;http://www.gramene. org/) and the principal mapping populations used by the rice scientific community.

Authors' contribution

Conceptualization of research (SBV, ASK); Designing of the experiments (SBV, ASK, TA); Contribution of experimental materials (SBV, ASK); Execution of field/ lab experiments and data collection (AK, AP, VS, IK); Analysis of data and interpretation (ASK, TA); Preparation of manuscript (ASK, SBV).

Declaration

The authors declare no conflict of interest.

References

Balasubramanian S., Schwartz C., Singh A., Warthmann N., Kim M. C., Maloof J. N. et al. 2009. QTL mapping in new *Arabidopsis thaliana* advanced intercross-recombinant inbred lines. PLoS One, **4**: e4318.

Bonman J. M., Khush G. S., and Nelson R. J. 1992. Breeding rice for resistance to pests. Ann. Rev. Phytopathol., **30**: 507-528. http://dx.doi.org/10.1146/annurev.py.30.090192.002451.

Castilla N. P., Leaño R. M., Elazhour F. A., Teng P. S. and Savary S. 1996. Effects of plant contact, inoculation pattern, leaf wetness regime, and nitrogen supply on inoculum efficiency in rice sheath blight. J. Phytopathol., **144**: 187-192. http://dx.doi.org/10.1111/j.1439-0434.1996.tb01512.x.

Channamallikarjuna V., Sonah H., Prasad M., Rao G. J. N., Chand S., Upreti H. C. et al. 2010. Identification of major quantitative trait loci qSBR11-1 for sheath blight resistance in rice. Mol. Breed., **25**: 155-166.

Che K., Zhan Q., Xing Q., Wang Z., Jin D., He D., et al. 2003. Tagging and mapping of rice sheath blight

resistant gene. Theor. Appl. Genet., **106**: 293-297.

Eizenga G. C., Lee F. N., and Rutger J. N. 2002. Screening Oryza species plants for rice sheath blight resistance. Plant Dis., **86**: 808-812. http://dx.doi.org/10.1094/PDIS.2002.86.7.808.

Gangopadhyay S. and Chakrabarti N. K. 1982. Sheath blight of rice. Review of Plant pathol., **61**: 451-460.

Groth D. E. and Nowick E. M. 1992. Selection for resistance to rice sheath blight through number of infection cushions and lesion type. Plant Dis., **76**: 721-723.

Han Y. P., Xing Y. Z., Chen Z. X., Gu S. L., Pan X. B., Chen X. L., et al. 2002. Mapping QTLs for horizontal resistance to sheath blight in an elite rice restorer line, Minghui 63. Yi chuan xue bao. Acta Genetica Sinica, **29**: 622-626.

Khush G. S. 1977. Disease and insect resistance in rice. Adv. Agron. Acad. Press, **29**: 265-341.

Kunihiro Y., Qian Q., Sato H., Teng S., Zeng D.-L., Fujimoto K. et al. 2002. QTL analysis of sheath blight resistance in rice (*Oryza sativa* L.). Yi chuan xue bao. Acta Genetica Sinica, **29**: 50-55.

Li Z., Pinson S. R. M., Marchetti M. A., Stansel J. W. and Park W. D. 1995. Characterization of quantitative trait loci (QTLs) in cultivated rice contributing to field resistance to sheath blight (*Rhizoctonia solani*). Theor. Appl. Genet., **91**: 382-388. http://dx.doi.org/10.1007/BF00220903.

Liu G., Jia Y., Prado G. A., Yeater K. M., Mcclung A., Correll J. C. et al. 2009. Mapping auantitative trait loci responsible for resistance to sheath blight in rice. Phytopathol., **99**: 1078-1084. http://dx.doi.org/10.1094/PHYTO-99-9-1078.

Ou S. H. 1985. Rice diseases Commonwealth Mycological Institute, Kew, Surrey.

Pan X. B., Rush M. C., Sha X. Y., Xie Q. J., Linscombe S. D., Stetina S. R. et al. 1999. Major gene, nonallelic sheath blight resistance from the rice cultivars jasmine 85 and teqing. Crop Sci., **39**(2): 338-346.

Pinson S. R. M., Capdevielle F. M. and Oard J. H. 2005. Confirming QTLs and finding additional loci conditioning sheath blight resistance in rice using recombinant inbred lines. Crop Sci., **45**: 503-510.

Prasad B. and Eizenga G. C. 2008. Sheath blight disease screening methods to identify resistant Oryza spp. accessions. Plant Dis., **92**: 1503-1509.

Sato H., Ideta O., Ando I., Kunihiro Y. and Hirabayashi H. 2004. Mapping QTLs for sheath blight resistance in the rice line WSS2. Breed. Sci., **54**(3): 265-271.

Savary S. and Mew T. W. 1996. Analyzing crop losses due to *Rhizoctonia solani*: rice sheath blight, a case study. *In*: *Rhizoctonia* Species: Taxonomy, molecular biology, ecology, pathology and disease control (Eds: Carling D. E., Sneh B., Jabaji-Hare S., Neate S. and Dijst G.). Springer Science and Business Media. p. 237-245.

Savary S., Teng P. S., Willocquet L. and Nutter Jr F. W. 2006. Quantification and modeling of crop losses: A review of purposes. Annu. Rev. Phytopathol., **44**: 89-112.

Savary S., Willocquet L., Elazegui F. A., Castilla N. P. and Teng P. S. 2000. Rice pest constraints in tropical Asia: quantification of yield losses due to rice pests in a range of production situations. Plant Dis., **84**: 357-369.

Sha X. Y. and Zhu L. H. 1990. Resistance of some rice varieties to sheath blight (ShB). IRRIN. **15**: 7-8.

Sharma A., McClung A. M., Pinson S. R. M., Kepiro J. L., Shank A. R., Tabien R. E. et al. 2009. Genetic mapping of sheath blight resistance qtls within tropical rice cultivars. Crop Sci., **49**: 256-264.

Tan C.-X., Ji X.-M., Yang Y., Pan X.-Y., Zuo S.-M., Zhang Y.-F. et al. 2005. Identification and marker-assisted selection of two major quantitative genes controlling rice sheath blight resistance in backcross generations. Acta Genetica Sinica, **32**: 399-405.

Teng P. S., Torres C. Q., Nuque, F. L. and Calvero S. B. 1990. Current knowledge on crop losses in tropical rice. In: International workshop on crop loss assessment to improve pest management in rice and rice-based cropping systems in South and Southeast Asia 11-17 Oct. 1987, Manila (Filipinas) (No. 633.180631 I61c 1987). International Rice Research Institute, Manila (Filipinas).

Xiang X. C., Li J. H., Zhang K. Z., Zhao P. and Li P. 2007. Genetic analysis of a rice mutant with resistance to sheath blight and its preliminary gene mapping. J Southwest Sci Tech Univ (Nat Sci). **22**: 76-81.

Xie Q. J., Linscombe S. D., Rush M. C. and Jodari-Karimi F. 1992. Registration of LSBR-33 and LSBR-5 sheath blight-resistant germplasm lines of rice. Crop Sci., **32**: 507.

Xie X.-W., Xu M.-R., Zang J.-P., Sun Y., Zhu L.-H., Xu J.-L. et al. 2008. Genetic background and environmental effects on QTLs for sheath blight resistance revealed by reciprocal introgression lines in rice. Acta Agronomica Sinica, **34**: 1885-1893. http://www.sciencedirect.com/science/article/pii/S1875278009600134.

Yeh W. H. and Bonman J. M. 1986. Assessment of partial resistance to *Pyricularia oryzae* in six rice cultivars. Plant Pathol., **35**: 319-323.

Yuen J. E. and Forbes G. A. 2009. Estimating the level of susceptibility to *Phytophthora infestans* in potato genotypes. Phytopathol., **99**: 782-786.

Zhuang J.-Y., Lin H.-X., Lu J., Qian H.-R., Hittalmani S., Huang N. et al. 1997. Analysis of QTL× environment interaction for yield components and plant height in rice. Theor. Appl. Genet., **95**: 799-808.

Zou J. H., Pan X. B., Chen Z. X., Xu J. Y., Lu J. F., Zhai W. X. et al. 2000. Mapping quantitative trait loci controlling sheath blight resistance in two rice cultivars (*Oryza sativa* L.). Theor. Appl. Genet., **101**: 569-573. http://dx.doi.org/10.1007/s001220051517.

Supplementary Table 1. Tying genetic linkage map to the Physical map (BAC or PAC clones)

S. No	Molecular marker	Physical position	BAC / PAC clones
	CHR#1		
1	RM - 499	387,909 - 391,928	P0005A05
2	HvSSR 1-24	8,129,356 - 8,133,375	OSJNBa0004G10
3	HvSSR 1-33	9,488,773 - 9,492,792	P0424A08
4	HvSSR 1-34	9,604,666 - 9,608,685	P0424A08
5	HvSSR 1-49	17,513,679 - 17,517,698	P0455H03
6	RM - 428	2,605,640 - 2,609,659	P0434B04
7	HvSSR 1-55	20,650,159-20,654,178	OJ1014_G12
8	RM - 84	29,741,292 - 29,745,307	P0019E03
9	RM - 1	4,634,793 - 4,638,812	P0695A04
10	HvSSR 1-80	34,546,822 - 34,550,842	P0454H12
11	HvSSR 1-87	38,614,232 - 38,618,251	P0674H09
12	HvSSR 1-89	40,251,592 - 40,255,611	B1033B05
13	RM - 259	7,444,796-7,448,813	P0702F03
14	RM - 243	7,969,722-7,973,741	B1008C01
15	RM - 572	9,864,595-9,868,615	P0025D05
16	RM - 24	18,975,580-18,979,599	B1080D07
17	RM449	15,122,386-15,126,405	P0043B10
18	RM - 5	23,970,505-23,974,524	P0013G02
19	RM - 212	33,052,668-33,056,687	B1100D10
20	RM - 3825	36,469,204-36,473,223	P0005H10
21	RM - 302*	32,986,381-32,990,401	P0481E12
22	RM - 486	34,919,186-34,931,693	B1100D10
23	RM - 14	41,361,934-41,365,952	P0456E05
	CHR#2		
24	RM109	181,386-185,407	OJ1212_C06
25	RM485*	932,577-936,596	OJ1217_F02
26	HvSSR 2-1	122,507-126,527	B1370C05
27	HvSSR 2-12	4,412,091-4,416,110	P0544B02
28	HvSSR 2-23	7,365,257-7,369,276	OJ1711_D06
29	HvSSR 2-27	8,183,942-8,187,961	OJ1134_F06
30	HvSSR 2-78	29,501,446-29,505,465	OJ1038_A06
31	RM174	7,004,088-7,008,109	P0495C02
32	RM492	7,283,843-7,287,862	OSJNBb0035N08
33	RM475	20403168-20,407,187	P0605D08
34	RM341	19340133-19,344,148	OSJNBb0071O21
35	RM221	27,613,509-27,617,768	OSJNBb0005A04
	CHR#3		
36	HvSSR 3-6	2,811,900-2,815,919	OSJNBb0050N02
37	HvSSR 3-9	3,815,980-3,819,999	OSJNBa0091P11

38	HvSSR 3-35	13,886,658-13,890,677	OSJNBb0033D20
39	HvSSR 3-40	15,382,420-15,386,439	B1166C06
40	HvSSR 3-41	15,390,054-15,394,073	OSJNBb0058G04
41	RM231	2,452,260-2,456,279	OJ1172F09
42	HvSSR 3-56	23,123,602-23,127,621	OSJNBb0007E22
43	HvSSR 3-71	26,523,498-26,527,517	OSJNBb0113I20
44	HvSSR 3-85	30,391,687-30,395,706	OSJNBa0057G07
45	RM517	6,165,253-6,169,272	OSJNAa0090D11
46	RM7	9,827,641-9,831,659	OSJNBa0013D02
47	RM232	9,753,759-9,757,778	OSJNBa0013D02
48	RM - 411	21,428,825-21,432,844	OSJNBa0010D22
49	RM135	27,416,737-27,420,758	OSJNBa0010B01
50	RM55	29,050,174-29,054,381	OJ1607A12
51	RM - 85	36,346,226-36,350,245	OSJNBa0032G11
	CHR#4		
52	RM307	13,149,235-13,153,256	OSJNBa0035B13
53	HvSSR 4-26	19,524,604-19,528,623	OSJNBb0039F02
54	HvSSR 4-35	23,095,462-23,099,481	OSJNBa0072F16
55	HvSSR 4-38	24,273,448-24,277,467	OSJNBa0081L15
56	HvSSR 4-39	27,040,523-27,044,542	OSJNBa0011L07
57	HvSSR 4-42	28,764,018-28,768,037	OSJNBa0088I22
58	RM564	20,984,190-20,988,209	OSJNBa0085H03
59	RM273	24046455-24,050,471	OSJNBa0089K21
60	RM348	32,833,623-32,837,642	OSJNBa0010D21
61	RM317	29,244,250-29,248,270	OSJNBa0064M23
62	RM559	35,334,860-35,338,879	OSJNBa0039K24
	CHR#5		
63	HvSSR 5-13	3,126,743-3,130,762	OSJNBa0072C16
64	HvSSR 5-23	7,015,095-7,019,114	OSJNBa0074P11
65	HvSSR 5-31	13,535,131-13,539,150	OJ1057_C01
66	HvSSR 5-39	16,902,129-16,906,148	OSJNBa0036C12
73	RM163	19,904,222-19,908,241	OSJNBb0092G21
67	HvSSR 5-48	21,256,238-21,260,258	P0040B10
74	RM440	22,663,747-22,667,766	P0668F02
75	RM459	24,096,546-24,100,565	OJ1123_C08
68	HvSSR 5-51	27,298,702-27,302,721	OJ1301_G07
69	HvSSR 5-52	27,373,889-27,377,908	OJ1281_H05
76	RM188	19,249,933-19,253,955	OJ1525_A02
70	HvSSR 5-56	19,973,190-19,977,209	OJ1119_H02
77	RM421	20,237,503-20,241,520	OJ1119_H02
78	RM178	22,731,956-22,735,977	B1155G07
80	RM274	24,037,135-24,041,154	OJ1362_G11
81	RM87	25,162,408-25,166,429	OJ1345_B12

71	HvSSR 5-65	27,402,666-27,406,683	P0554F08
72	HvSSR 5-66	26,908,927-26,912,946	P0554F08
79	RM26	27,102,235-27,106,254	OSJNBa0079H23
	CHR#6		
82	HvSSR 6-35	10,821,756-10,825,775	P0036B02
83	HvSSR 6-44	17,433,277-17,437,296	P0036C11
84	HvSSR 6-56	24,319,824-24,323,843	P0490F09
85	RM225	3,415,709-3,419,727	OSJNBa0033B09
86	HvSSR 6-65	27,827,252-27,831,271	P0485A07
87	RM217	4,233,183-4,237,200	P0554A06
88	RM136	8,750,539-8,754,562	OSJNBa0084K06
89	RM340	28,598,180-28,602,201	P0623A10
90	RM400	28,430,560-28,434,579	P0009H10
91	RM481	2874165-2,878,184	OSJNBa0085L11
	CHR#7		
92	HvSSR 7-40	21,869,995-21,874,014	P0534A03
93	HvSSR 7-43	23,788,635-23,792,654	OJ1060_D03
94	HvSSR 7-46	24,194,017-24,198,036	OJ1710_H11
95	RM125	5,478,476-5,482,497	OSJNBa0081K20
96	HvSSR 7-53	29,406,458-29,410,477	P0597G07
97	RM2	16,020,677-16,024,693	P0038F09
98	RM11	19,256,015-19,260,032	OSJNBb0062D12
99	RM234	25,471,682-25,475,700	B1056G08
100	RM248	29,339,016-29,343,035	P0597G07
	CHR#8		
101	RM337	151,299-155,318	
102	RM152	682,095-686,114	P0427G12
103	HvSSR 8-29	15,438,838-15,442,857	OSJNBa0062G05
104	RM310	5,114,842-5,118,863	B1099H05
105	RM44	11757419-11,761,434	P0467G09
106	RM483	11920423-11,924,437	OJ1705_A03
107	RM72	6761705-6,765,721	OSJNBa0002E10
108	RM515	20,284,519-20,288,538	P0456B03
109	RM256	24,271,349-24,275,368	P0686H11
110	RM230	25,835,022-25,839,039	OJ1003_A09
111	RM433	27,025,353-27,029,501	
112	RM281	27,896,219-27,900,238	P0562A06
	CHR#9		
113	HvSSR 9-5	2,289,530-2,293,547	P0448B11
114	RM444	5,924,433-5,928,452	P0701E06
115	HvSSR 9-7	4,352,692-4,356,711	P0523B07
116	HvSSR 9-19	10,512,921-10,516,940	P0448B03
117	HvSSR 9-25	14,564,956-14,568,975	OJ1294_G06

118	HvSSR 9-27	15,503,931-15,507,950	OJ1299_A11
119	HvSSR 9-37	16,814,708-16,818,727	P0047B10
120	HvSSR 9-57	22,817,613-22,821,632	B1331F11
121	RM296	10,783,217-10,787,234	P0512H04
122	RM434	15,661,583-15,665,602	OSJNBa0039E17
123	RM410	17,641,860-17,645,878	OJ1595_D08
124	RM108	19,302,831-19,306,852	OSJNBa0019D02
125	RM242	18,809,296-18,813,315	OSJNBb0052C07
126	RM288	18,561,724-18,565,742	P0463D04
127	RM553	19,323,086-19,327,105	OSJNBb0004A05
128	RM278	19,318,430-19,322,450	OSJNBb0004A05
129	RM201	20,172,770-20,176,791	P0217C03
130	RM245	22273295-22,277,563	P0478E02
	CHR#10		
131	HvSSR 10-1	50750-54,769	OJ1136E01
132	HvSSR 10-5	313,303-317,322	OSJNBa0096E22
133	HvSSR 10-17	7,564,813-7,568,832	OSJNBa0004P12
134	RM222	2618378-2,622,396	OSJNBa0034A02
135	HvSSR 10-34	16232734-16,236,753	OSJNBb0016G17
136	RM171	19118546-19,122,566	OSJNBa0051D19
137	RM228	22,312,690-22,316,707	OSJNBa0027P10
138	RM484	21,136,250-21,140,269	OSJNBb0015I11
	CHR#11		
139	HvSSR 11-1	59,214-63,233	OSJNBa0029D01
140	HvSSR 11-2	363,185-367,204	OSJNBa0010K05
141	HvSSR 11-3	575,267-579,286	OSJNBa0025K19
142	HvSSR 11-13	5921762-5,925,781	OSJNBa0034O04
143	RM202	9,005,215-9,009,236	OSJNBb0011I07
144	RM229	18872070-18,876,089	
145	RM21	19637144-19,641,316	OSJNBb0089M05
146	RM26334	7,575,108-7,579,133	OSJNBb0084F23
147	RM206	22,478,961-22,482,980	
148	RM254	24228433-24,232,648	OSJNBa0060K21
149	RM224	27671251-27,675,269	OSJNBa0041L19
	CHR#12		
150	RM - 20	969,495-973,514	OJ1126_F08
151	HvSSR 12-35	19,955,683-19,959,702	OJ1118_C12
152	HvSSR 12-36	21,172,336-21,176,355	OSJNBb0094E08
153	HvSSR 12-40	22,644,455-22,648,474	OSJNBa0027H05
154	HvSSR 12-48	26,261,615-26,265,637	OSJNBb0016A10
155	HvSSR 12-51	27,056,829-27,060,848	OJ1584_D02
156	RM277	22362797-22,366,812	OJ1123_B09
157	RM511	17,399,642-17,403,659	
158	RM - 260	19547223-19,551,237	OSJNBa0022M02
159	RM - 519	19,930,321-19,934,340	
160	RM28305	19,955,847-19,959,869	OJ1118_C12
161	RM - 270	25,000,547-25,004,561	OSJNBa0010M16
162	RM - 17	26,986,415-26,990,436	OSJNBa0063N15

Chr. = Chromosome number