	Gene	Forward Primer	Reverse Primer
1	Actin	CAGCCACACTGTCCCCATCTA	AGCAAGGTCGAGACGAAGGA
2	LOC_Os01g43540	CGCATCTGGTGACTCAAGGTT	AGCAATGCGCTCATCACACT
3	LOC_Os01g63420	GCCACTTGACAATGGTGTCTGT	TAGAGAGCAAACCTCCGAAGCT
4	LOC_Os01g69080	GGATGAGAGGGCACAATCGA	TACCCAGCTGAAAGGCAATGT
5	LOC_Os02g08440	GCCCAAGAGCCTACTTCAGATG	GCTTCTCTGAACCTTCTTCTTGACA
6	LOC_Os05g02070	AAGATGTTCCCTGATGTGGAGA	AGCTGGTGCCACACTTGCA
7	LOC_Os06g50300	AGCAAGCACAATGACGACAAA	GATAGCGAATGATCCATCAGCTTT
8	LOC_Os07g48020	GGCGCAGTGCCAGAATTT	AGGCGGAATCGATGTTGGT
9	LOC_Os08g17680	GGAAGTACACCCGCATTGCT	GGACGTTTGTCGCCAACAC
10	LOC_Os12g36850	GCTAGCTATAGCCATCACAGCAAGT	GGCCGGAGCCATCTCTATC
11	LOC_Os12g36880	GACATCGTGGATGGCTACTATGG	CAGGGTGAGCGACGAGGTA
12	LOC_Os08g10310	TGGGTTGAGTGGCCCATT	CCGCAGGAGTTTTAGGTTCTTAAG
13	LOC_Os02g02980	GCTTTGGCATTGGAACCTTTC	CACCAGCATCCAGGCAAACT
14	LOC_Os12g38210	TCTCATTTCCCAGTGGTGTGAA	CTGGGTTGAGCGCTTTGG

Table S1. List of primers used for qRT-PCR analysis

Fig. S1. Rice plants carrying XA21 protein tagged with N-terminal Myc (A) and C-terminal CFP (B) under the control of its native promoter show resistance to *Xoo* strain PXO99Az.

(A) Kitaake wild type (Kit), Transgenic lines carrying *Xa21* under the control of its native promoter (Nat XA21), and transgenic rice carrying *Myc-Xa21* under the control of its native promoter (Nat Myc-XA21), were inoculated at six weeks of age (9 to 10 leaves stage) and lesion lengths were measured 14 DAI. Each data point represents the average and standard deviation of at least four independent replicates.

(B) Kitaake wild type (Kit), Transgenic lines carrying *Xa21* under the control of its native promoter (Nat XA21), and transgenic rice carrying *Xa21-CFP* under the control of its native promoter (Nat XA21-CFP), were inoculated at six weeks of age and lesion lengths were measured 14 DAI. Each data point represents the average and standard deviation of at least independent replicates.

Fig. S2. Rice plants overexpressing *Myc-Xa21* (Ubi Myc-XA21) show enhanced resistance to *Xoo* strain PXO99Az.

(A) Lesion length development of *Xoo* PXO99Az-inoculated six-week-old plants, Kitaake control (Kit), Nat Myc-XA21, and Ubi Myc-XA21. Each data point represents the average and standard deviation of at least four samples.

(B) *Xoo* strain PXO99Az populations were monitored over 12 days in six-week-old plants, Kit, Nat Myc-XA21, and Ubi Myc-XA21 (7A-8-123) rice lines. For each time point, bacterial populations were determined in three separate leaves for each genotype. Capped vertical bars represent standard deviation values (cfu/leaf) obtained from the three samples.

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Fig. S3. Rice plants overexpressing *Xa21-CFP* (Ubi XA21-CFP) show enhanced resistance to *Xoo* strain PXO99Az.

Kitaake wild type (Kit), transgenic rice carrying *Xa21-CFP* under the control of its native promoter (Nat XA21-CFP), and transgenic lines carrying *Xa21-CFP* under the control of the *Ubi* promoter (Ubi XA21-CFP) were inoculated at six weeks of age and lesion lengths were measured 12 DAI. Each data point represents the average and standard deviation of at least four independent replicates. Gray bars in Ubi Myc-XA21 represent segregants carrying the transgene. Black bars represent segregants not carrying the transgene.

Fig. S4. Rice plants overexpressing *Xa21* does not display enhanced resistance to *Xoo* PXO99∆*raxST*.

Six-week-old Kitaake control, Nat Myc-XA21 (T_3 , 20-12) and Ubi Myc-XA21 (T_3) were inoculated with *Xoo* PXO99 Δ *raxST* and then lesion lengths were measured 12DAI. Each data point represents the average and standard deviation of at least five samples harvested from each plant.

Fig. S5. Rice plants overexpressing *Xa21* does not show enhanced resistance to a fungal pathogen *Magnaporthe oryzae*.

(A) Five-week-old Kitaake control, Nat Myc-XA21 and Ubi Myc-XA21 (T_2) were inoculated with *M*. *oryzae* and then lesion lengths were measured 10 DAI. Two representative leaves from each line were displayed.

(B) Lesion lengths of each line, Kitaake control, Nat Myc-XA21 and Ubi Myc-XA21 (T₂). Each data point represents the average and standard deviation of at least 42 lesion lengths.

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