

Plant Communications, Volume 2

Supplemental information

**The *Xa7* resistance gene guards the rice susceptibility gene *SWEET14*
against exploitation by the bacterial blight pathogen**

Dangping Luo, Jose C. Huguet-Tapia, R. Taylor Raborn, Frank F. White, Volker P. Brendel, and Bing Yang

The *Xa7* Resistance Gene Guards the Susceptibility Gene *SWEET14* of Rice Against Exploitation by Bacterial Blight Pathogen

Dangping Luo¹, Jose C. Huguet-Tapia², Taylor R. Raborn³, Frank F. White², Volker P. Brendel³, Bing Yang^{1,4,*}

¹ Division of Plant Sciences, Bond Life Sciences Center, University of Missouri, Columbia, MO 65211, USA

² Department of Plant Pathology, University of Florida, Gainesville, FL 32611, USA

³ Department of Biology, Department of Computer Science, Indiana University, Bloomington, IN 47405, USA

⁴ Donald Danforth Plant Science Center, St. Louis, MO 63132, USA

* Correspondence: Bing Yang (yangbi@missouri.edu)

Files:

Supplemental Table 1. Molecular markers used in this study

Supplemental Table 2. Oligonucleotides used in this study

Supplemental Information 1. The cDNA sequence of *Xa7*

Supplemental Information 2. gBlocks of *Xa7* homologous genes

Supplemental File 1. Program for genome assembly

Supplemental Figure 1. Large chromosomal fragment deletion of *Xa7* locus

Supplemental Figure 2. Screenshot of RAMPAGE analysis displayed with the Integrative Genomics Viewer (Thorvaldsdóttir, Robinson et al. 2013)

Supplemental Figure 3. *Xa7* and homologs in diverse grass species

Supplemental Table 1. Molecular markers used in this study.

Marker	Primer	Size in IRBB7 (bp)	Size in Nipponbare (bp)
RM7243	RM7243F	150	158
	RM7243R		
RM20571	RM20571F	123	117
	RM20571R		
RM5509	RM5509F	229	255
	RM5509R		
5610	5610F	261	231
	5610R		
M5	M5-F	343	1219
	M5-R		
M5-3k	M5-3kF	143	122
	M5-3kR		
M5-5k	M5-5kF	107	104
	M5-5kR		
M5-48k	M5-48kF	152	144
	M5-48kR		
M5-72k	M5-72kF	127	136
	M5-72kR		
RM20593	RM20593F	314	316
	RM20593R		
RM3723	RM3723F	130	138
	RM3723R		

Sequences of each markers in IRBB7 and Nipponbare

RM7243

IRBB7

AAGATGGCGTGCGTACGTACGTACGTGCGGCGCGGGCGTACAGGCGTACAGGGCGC
CGCGCGACGCATGGATGGATGGATCGATGGATCGATGGTCCCAGGGCGGCACAGGCA
GGGGCTCCCCGACCGGGCAACCCGTGAAGAACTTCGT

Nipponbare

AAGATGGCGTGCGTACGTACGTACGTGCGGCGCGGGCGTACAGGCGTACAGGGCGC
CGCGCGACGCATGGATGGATGGATGGATGGATCGATGGATCGATGGTCCCAGGGCGG
CACAGGCAGGGGCTCCCCGACCGGGCAACCCGTGAAGAACTTCGT

RM20571

IRBB7

GAGAGGTGGAGAGATGGATGTGGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGCG
CGCCGCCAGGGGGAGGAATTCTTGGGTAATCAATTAAGCTTTGGTTCTTGGTTTGG
TTCTTTGGTC

Nipponbare

CGATCTTACTGGCTCTGCAACTCTGTATTGCATGCTAAATCCGTTATGATTTACTACT
AATGATGGATGTACTGATACATAGTACTGATCGATGAGCTAGCTAGGGTTTTGGATG
GGTCGGAAGGTGAGAAAGAGGAGGAAAGAAGAGAGAATCTATTATATTATTAAG
GAATAGAAAAAGAAGCCTCCACGTTTCGCTCTCACGGCCTAGAAATTCTCACATTAAT
CGGAGAAAAGAAAAGCAGAGTCCATATAGAAATACAATTTAGAAATAGCTGAAAT
TCGGAATTATAAAATAAGGAATATTAGAAGAGGAGACTAGAGTCCATATGGAAATA
CAATTTAGAAATAGTTGAAATTCAGAATTAATAAATAAGAAATATTAGAAGAGGAG
ACTAGAGTCCATATAGAAATATAATTAGGAAATAACTGAAATTCGGAATTAATAAAT
AAGGAATATTAGAAGTAGAGTATAGAGTCCATATAAAAAATATAATTAGGAAATAAC
TGAAATTAGGAATTAATAATAAGGAATATTAGAGATAGAGTATAGAGTCCATATAA
AAATACAATTAGTAAATAACTGTAATTCGGAATTAATAAATAAGGAATATTAGAGGT
AGAGTATAGAGTCCATATAGAAATACAATTAGAAAATAACTGTAATTCGGAATTA
AAATAAGGAATATTAGAGGTAGAGTATAGAGTCCATATAAAAAATACAATTAGGAAA
TAACTGAAATTCGGAATTAATAAATAAGGAATATTAGAGGTAGAGTATAGAGTCCAT
ATAGAAATACAATTAGAAAATAATAAAAAATTCGGAATTAATAAATTTGATATTA
ATAATTAATAACTAACACGTATATATAATACAATATAAATATTACACATTAGTAGTT
TTACAAAATTTAAAATTATATTGTCATTTTAATAAATTTGAATAATACATTGAGAAA
ACATATATGCTATTACATGAGAGAAAATATAATGATGCTAGCCGCGCAATATGCAC
GGGCCACTATGCTAGTTGAAGATGATTAGAAGAAATCTAATCAATTCAGAGCATT
CTGTATTCATCTTTTCAGTGTATATTCGCTCTGGGTAGTGCTGATTGTGCCATTATA
GACGGGGTTCGTAATTCGTACGGACGAATCGACACAGACATGCATGATTGTCTTTAG
TACTTAGAATTAGTAGCAAAGTCGGTGGGACAAC

M5-3k

IRBB7

CATATGTAGCAAGTATGCATCCAGCGAAACCCCATGGATTAATTAATTTGGCGGTAG
ATCTCATCATAACAGAGAGTACGTACGTAGTAGTACTGTAGTACACTTGGATATATA
CAAATTAAGCCAACACATTAGTCTTCAGA

Nipponbare

CATATGTAGCAAGTATGCATCCAGCGAAACCCCTAGATCTCATCATAACAGAGAGT
ACGTACGTAGTAGTACTGTAGTACACTTGGATATATACAAATTAAGCCAACACATTA
GTCTTCAGA

M5-5k

IRBB7

TGTAGAGATTGTGACGAGGAGCAGTGCAAGTTTCAGGTAGTGATGCATCAGGCGTTT
GCCCTCTTTCCTTGCAATGCTACTCGCTGATGATCCATTCTGCAACATCA

Nipponbare

TGTAGAGATTGTGACGAGGAGCAATGCAAATTTTCAGGTAGTGATGCGTCAGGCGCT
TGCCCTCTTTCCTTGCAATGCTACTCGCTGATCCATTCTGCAACATCA

M5-48k

IRBB7

CTGTGTGAAAGTTCAGACGGATGGCGATTTTCGCAAAGATGTACTCCATTTGAGATCT
TTATGTGTATGTATGTATACTTGTCAAGTCTGATGGAGGTCCAAAGAAATGGCAGTC
TACTGATGCTGGAATGCAGTCTCATGTGCTCAAAGCAG

Nipponbare

CTGTGTGAAAGTTCAGACGGATGGCGATTTTGCAAAGATGTACTCCATTTGATATCT
TTGTGTGTATACTTGCCAGGTCTGATGGAGGTCCAAAGAAATGGCAGTCTACTGATG
CTGGAATACAGTCTCATGTGCTCAAAGCAG

M5-72k

IRBB7

TGGAAAGGAAGCTCCTCGACGGCGGCGTGGGCGGGCGCCGCGGGCGGCGGTACCATC
TACGGCTGCCCCGGTGATGGTTCGACGTCGATCTCAACAAGTTCGAGCCATGGGACCTT
CCTGGTAAGACCTA

Nipponbare

TGGAAAGGAAGCTCCTCGACGGCGGCGTGGGCGGGCGCCGCGGGCGGCGGGCGGC
GGTCACCATCTACGGCTGCCCCGGTGATGGTTCGACGTCGATCTCAACAAGTTCGAGCC
ATGGGACCTTCTGGTAAGACCTA

RM20593

IRBB7

AAGGTACACTTGCTCTGACGGTAGCAAAAGTTGATCATGCCCTACTTTAGCTGTAAC
ATGAGACATGTCAGCATATGCTTACATGCATGAATCAGCAGGGCTACAGTTTTATTA
TTTGCTTTGACAGCTTTCTCTCAACAATCATTCTCATTATATTTTTTATCCTAGGCTCC
TTAGGAACATAGTAATTTTACAGGATTTTTGCTGAAATCGATCAGTTCAGTTCCCGC
AAAATTCCACTGAAAATTAATCCTCTACTCCAAAGGCCTCTCTCTCTCTCTCTCTC
TCACGTAGGATTTGCCACTGAGGTCT

Nipponbare

AAGGTACACTTGCTCTGACGGTAGCAAAAGTTGATCATGCCCTACTTTAGCTGTAAC
ATGAGACATGTCAGCATATGCTTACATGCATGAATCAGCAGGGCTACAGTTTTATTA
TTTGCTTTGACAGCTTTCTCTCAACAATCATTCTCATTATATTTTTTATCCTAGGCTCC
TTAGGAACATAGTAATTTTACAGGATTTTTGCTGAAATCGATCAGTTCAGTTCCCGC
AAAATTCCACTGAAAATTAATCCTCTACTCCAAAGGCCTCTCTCTCTCTCTCTCTC
TCTCACGTAGGATTTGCCACTGAGGTCT

RM3723F

IRBB7

TAGACATGGGTCCCTCACAGATGGAACCCATTCTCATAGGCTCACATGTCAGCGGAC
ACATATTCCTCTAACTTAGAGGAGCCTCCCCCTAATGAAAGTGTAATATAGGATCAG
AAGCAAGACTTGTGGA

Nipponbare

TAGACATGGGTCCCTCACAGATGGAACCCATTCTCATAGGCTCACATGTCAGCGGAC
ACATATTCACATATTCCTCTAACTTAGAGGAGCCTCCCCCTAATGAAAGTGTAATAT
AGGATCAGAAGCAAGACTTGTGGA

Supplemental Table 2. Oligonucleotides used in this study

Oligos	Sequence (5' TO 3')	Usage	
RM7243F	ACGAAGTTCCTTCACGGGTTG	Mapping	
RM7243R	AAGATGGCGTGCGTACGTAC		
RM20571F	GAGAGGTGGAGAGATGGATGTGG		
RM20571R	GACCAAAGAACCAAACCAAGAACC		
RM5509F	GATGATCCATGCTTTGGCC		
RM5509R	TTCCAGCAGAAAGAAGACGC		
5610F	AAGCTCGTCACCTCACCCGTAC		
5610R	TGCACAGTAGCAGCATATCTGCAG		
M5-F	GTTGTCCCACCGACTTTGCTA		
M5-R	CGATCTTACTGGCTCTGCAACTCT		
M5-3kF	CATATGTAGCAAGTATGCATCC		
M5-3kR	TCTGAAGACTAATGTGTTGGCT		
M5-5kF	TGTAGAGATTGTGACGAG		
M5-5kR	TGATCCATTCTGCAAC		
M5-48kF	CTGTGTGAAAGTTCAGACGG		
M5-48kR	CTGCTTTGAGCACATGAGAC		
M5-72kF	TGGAAAGGAAGCTCCTCGAC		
M5-72kR	TAGGTCTTACCAGGAAGGTC		
RM20593F	AAGGTACACTTGCTCTGACGGTAGC		
RM20593R	AGACCTCAGTGGCAAATCCTACG		
RM3723F	TAGACATGGGTCCCTCACAGATG		
RM3723R	TCCACAAGTCTTGCTTCTGATCC		
3628F	TGTCCGGTGTCTCTAGCTTC		
3628R	ACCAAGCTATACCAAGTACT		
5760-14kF	CTCAACACTCCTCTTCACAG		
5760-14kR	AGTGAGAGAAGCGTAGAGAC		
RM53266F	AGCCTTCCTAACCAATCTGG		
RM53266R	CCATCATTTTCGGCTCTTCAC		
3770F	GTCACCAGTCACCACCGATC		
3770R	CGTGATAACCGCGAGACATA		
gRNA1-F	GCAGGTACGTATACCAAGTTGTCCG		For the 1 st guide RNA to delete the 53 kb of Xa7 locus
gRNA1-R	AAACCGGACAACCTGGTATACGTAC		
gRNA2-F	GCAGGTTTGTCCAATGAGTTGCTG		For the 2 nd guide RNA to delete the 53 kb of Xa7 locus
gRNA2-R	AAACCAGCAACTCATTTGGACAAAC		
gRNA3-F	TGTTGGATGATCAGCGGCCGCCA		For guide RNA at the 1 st site of Xa7
gRNA3-R	AAACTGGCGGCCGCTGATCATCC		
gRNA4-F	GTGTGAGGAAGACGCCGGAGTTGA		For guide RNA at the 2 nd site of Xa7
gRNA4-R	AAACTCAACTCCGGCGTCTTCCTC		
Xa7aRT-F	CGTATGCCCCGTTGCAGTTGCAG	RT-PCR for Xa7 expression	
Xa7aRT-R	CGGAGTTGACGGTCAGCAGTCG		
Xa27L-F4, 112.5R	ATAGGCCGGTATCCCAGCTCT ACTGGAGCAGAGGAATGTGC	For genotyping Xa7 CRISPR plant	
EP53-F	TGTAGAAACCATGTCTCATGC	For genotyping large deletion	
BTB-R1	ACTACCACACCAGCCAGCAAG		
EP53R	CTTGGATGGAGCTCCAGATG	With EP53-F as internal primers for zygosity of large deletion plants	
Pro2.7k HindF	TATGACCATGATTACGCCAAGCTTC TCATCCAACCGTTCTG	Amplify 2.7 kb Xa7 promoter	
Xa7aATG-R	AGAAATTTACCCTCAGATCTACCAT GGATGATGGATCCCCCAG		
DeleBEF3	ATACGAACGAAGGCTTTGAAGC	Delete 20 bp for mutant EBE	

DeleBER3	TTCAAAGCCTTCGTTTCGTATGGGTT ATATATTGGTTTTAGCAG	
----------	--	--

Supplemental Information 1. The cDNA sequence of *Xa7*.

CCCCTTCCCAACCACAGCCAGCGGTTTCCAAACTCCACGCCTCGCTCAACCTGGGGGATCCATCATCCATGGCGGCC
GCTGATCATCCTGATCGTATGCCCGTTGCGAGTTGCGAGGCTTGCGCCACCATTACGCCTTCCcTGCAAACCTTCGCC
CGCCGCTCGACTGCTGACCGTCAACTCCGGCGTCTTCTCATCTCCACCGCCGGGGCCATCGTCCTCGTCCACACCG
CCGGTAACCCACCCGCCATCGACAACGATCCAGCCTACGCCTTGGTCGCATTTCGTGCTCTTCTCCTCGGAATCTGG
CTCATGTCTATTGCCCTCGTCGCCGACCAGTTCCcGCGCGCCGCTGGGGTGCCTGGCCATTGCCAGGGCGCTGCA
GGATTACCTCATCGGTGGCAATTAAGTAGAAGCTTCGACCATGGCTCTGCACATTCcTCTGCTCCAGTTGTTCCCGG
CTTCCCGTACGTGTGCCTGATGATTGTCTTTCTCTGTTTATTTGGCTAGTATTTTAGGCTTGGAAAGTTGAAAACTG
TAAATCTGCTTCTTTTTCCCTCTGTACTACTACTAGACTTTCTTTTTTAAaGCTGACGTCATACACACAcCCCAGAT
TCATAACGTGTCGTATAGTAAATGTATTTCGAGGCTTGTAAATAAAaAGGCACCCGTAGGTGTATGCTCTGTTTCAGTCT
GATGTTCTAAATAATCAAGATACTATTAGTCGT

Supplemental Information 2. gBlocks of *Xa7* homologous genes.

gBlock cloned into pBY02 at EcoRI-HindIII through Gibson cloning. Sequences shaded in yellow are overlapping regions to facilitate the insertion of gBlocks in pBY02 through Gibson cloning. The start and stop codons are in red. Sequences for EcoRI and HindIII are underlined. The Kozac sequence for optimal expression of gene under 35S promoter is in bold.

Do_Xa7 gBlock

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGGCGGACCGGCCGCGCAGCAATCCATCAGGGCCTGGCGCCGG
TGGGCTTTGTGGTCCGGCAACAGCGAGCGATCGCCCCCTCGTCGCGCCCGACTCCTGATGATCAATTCCGGCACCCCTC
CTGATCTCGGCCGCCTGGTCCGTCATCATCATCCACAGCACTTCATCAGGCACTACAGCCGGTGGTGGTCCGGCTTT
CGCCCTCGTCACATTCCTCCTCTTCTTCTCGGCGTGTGCTGGTGATGGTGGCGCTTGTGCTTACAGGTTCCGGC
GAGCGGCAGCGGTGCGCGTGGCCATTGCGAGGGCGCTCCGCCGCTACTTGCTCGGTCTTGGGTGGTAAGCTTCTAGA
CTAGTGAGCTCGAAT

Si_Xa7 gBlock

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGGCGGGCCGGCCAGCAGAACTCCATCTCCAGCGAGTGATCG
CAGGCCGCGGTGCGCGGCTCCTGGTCAACGCCGGCGCCCTGCTCATCTCGGCCGCGGGTCCGTATCATCCACGCC
GCTGCCACGCCCTCTGACGCTTCTCTGGCCCGGCGCGCCGCTCATCGGTTTTGCATCTTCGTCTCCTCGGCGTGT
GCTGGTGATGTGCGCGCTCGTCGCCGACCGGTTCCCAAGAGCGGCAAGGGCCGCGTGGCCATTGCGAGGGCACTCC
AACGCTACGTGTTCCGTCTTGTGGGTGGTAAGCTTCTAGACTAGTGAGCTCGAAT

Ph_Xa7 gBlock. (codon optimized for *N. benthamiana* due to high GC of the original sequence)

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGGCCGGTCTCCAACCAGCAGCCATCCACCTTCAACGTAGAC
AACAGGCTATTGCTGGTAGGCGAGTACGTCTCTTAGTAAACGCAGGAGCACTGTTGGTATCCGCAGGAGGCAGTGT
GTTATCATTACGCAGCTACTCCTTCCAGACGACGCCGAGGAGGGCCCGCCTGCTCTCTGGTGGCCTTTTCTGTCTT
TCTGCTGGGAGTCTCTTTAGTCACGCTGGCCTTAGCTGCTGATAGATTCCACGTCAGCAAGGGTTGGGGCCGCCG
TAGCAACAGCTACTAATAGGTAATTTGTTGGACTCGGCTGGTAAAGCTTCTAGACTAGTGAGCTCGAAT

gBlock cloned into pBY02 at EcoRI-HindIII through Gibson cloning.

Sb_Xa7 gBlock (codon optimized for *N. benthamiana* due to high GC of the original sequence)

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGTCTCGACCCGCCGAGATGCGTAACCCCGTCACGCAGACG
ATGGCGATTTGCAGTTAGCTTGGATTGGTAGAAGGCGAAGGGCCTTCAACAACAACCTCTGTTGGATTCCGGAGGC

AGGGCCTGCATGTTGTTAGGGGCTCTGGTCCTCACTTGGGATCAGCTCGCCCTCGCAAGTTCTTCCAGCCCCGAGCA
TGTCCTGCTGGCTGCATTTGTTCTTTGGTTACTGGGGGCCGCCCTCGTGATGCTTAGTCTGGTAAGCCGAAGTTTC
CAAGACTGGCATCCGCCGGTGCAGCCCTGGTAATGGCACTTAGGAATTATTTGTTAGGGGGTGGTGGGCTCTAAGCT
TCTAGACTAGTGAGCTCGAAT

Op_Xa7 gBlock

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGGTGAACCGGACAGCCGCTCATCCGCAGATGCCTGTTTCAGG
CGCTGCGCCGCAATCGCATCGCGCAGGTAAACAGGGTGCCTCGCCGCTCGCCGTGCTCGAGCCCGACTGCTGATCGTC
AACTCCGGCGTTTTCTCATCTCCACCTCCGGAGCCATCGTCGTCTCCACACCGCTGGAAACCCCTTCGCCCTCGT
CGCATTCTGTCTCTTCTACTTGGCATCTGGCTCGTGCTTCTTGCCTCGTCGCCGACAAGTTCCCGCGAGCCGCCA
GGTTCGCCGTGCCATTGCCAGTGCCTGCAGGATCACCTCATAGGCGGCAACTAGTAAGCTTCTAGACTAGTGAGC
TCGAAT

O1_Xa7 gBlock

GAGAACACGGGGGACTCTAGGAATTCGATCTACCATGGCGAATCGGACAGCTGCTCATCCGCGGATGCCCGTACAGG
GGCTGCGCCGCAATCAAATCGCGCGGGGGCCCGCTCGCCGTTCTCGACTGCTGATCGTCAACACCGGCGTTTTTC
CTCATCTCCACCTCCGGGGCCATCGTCGTCTCCACACCGCTGGAAACCCCTCCTCCGCCATCGACGACGGTCCGTC
CTCCGCCCTCGTCGCATTCTGTCTCTTCTACTTGGCATCTGGCTCGTGCTTCTTGCCTCGTCGCCGACAAGTTCC
CGCGAGCCGCCAGGGTGCCTCGCCATTGCTAGTGCCTGCAGGATCACCTCATAGGCGGCAACTAGTAAGCTTCT
AGACTAGTGAGCTCGAAT

>O1_XA7 KN541332.1_FGP003 (*Oryza longistaminata*)

MANRRTAAHPRMPVQGLRRNQIARGPAARRSRLIVNTGVFLISTSGAIVVVHTAGNPSSAIDDG
PSSALVAFVLFLLGIWLVLALVADKFPRAARVAVAIASALQDHLIGGN

>Op_XA7 OPUNC06G22220 (*Oryza punctata*)

MVNRRTAAHPQMPVQALRRNRQAQVNRVPAARRARALLIVNSGVFLISTSGAIVVVHTAGNPF
LVAFLVLFLLGIWLVLALVADKFPRAARVAVAIASALQDHLIGGN

>Do_XA7 BAE44_0010678 (*Dichantheium oligosanthes*) (NCBI accession: OEL28303.1)

MADRPAAIHQGLAPVGFVVRQQRRAIAPRRARLLMINSGLLISAAWSVIIHSTSSGTTAGGGR
AFALVTFLFLLGVSLVMVALVAYRFRRAAVGVAIARALRRYLLGLGW

>Sl_XA7 LOC105914264 (*Setaria italica*) (NCBI accession: XP_012700797.1)

MAGRPAELHLQRVIAGRRARLLVNAGALLISAAGSVIIHAAATPSDASSGPAPPLIAFCIFVLG
VSLVMSALVADRFPRARAGVAIARALQRYVFLVGLGW

>Ph_XA7 LOC112891075 (*Panicum hallii*) (NCBI accession: XP_025813762.1)

MAGLQPAAIHLQRRQQAIAARRVLLVNAGALLVSAGGSVVIHAAATPSDDAAGGPACSLVAFS
VFLLGVSLVTLALAADRFPRARVGAATATNRYLFLGLGW

>Sb_XA7 SORBI_3K004400 (*Sorghum bicolor*) (NCBI accession: OQU75609.1)

MSRPAEMRNPRHADDGDLQLAWIGRRRRGLQQQLLLDSGGRACMLLGGALVLTWDQLALASSSSP
EHVLLAAFLVLLGAALVMLSLVSRFPRLASAGAALVMALRNYLLGGGGL

Supplemental File 1. Program for genome assembly.

```
####The script uses illumina reads downloaded form the 3K rice genomes project
#Raw sequence data is also available from the http://gigadb.org/dataset/200001 - SRA at
PRJEB6180
#deposited the reads in a new folder rice3k
## use the Xa7 region as reference and create an index using bowtie2
bowtie2-build complete_Xa7.fasta cXa7

##create an accession list from the reads_dictionary that contains the sample accession and the run
id
## sample_accession (1st collumn) run_accession (2dn collum) in reads_dictionary
for x in `cut -f 1 reads_dictionary`
do
grep $x reads_dictionary | sed 's/$//g' | cut -f 2 > copy_list
#####
    for i in `cat copy_list`
    do
    cp "/rice3k/"$i"_1.fastq.gz" ./
    cp "/rice3k/"$i"_2.fastq.gz" ./
    gunzip *.fastq.gz
    done
####
##generate temporary files to map
cat *_1.fastq > $x"_1.fq"
cat *_2.fastq > $x"_2.fq"
rm *_1.fastq
rm *_2.fastq
rm *.fastq.gz
####

bowtie2 -x cXa7 -1 $x"_1.fq" -2 $x"_2.fq" -S $x"_results.sam" -p 8
rm *.fq

samtools view -bS -o $x"_results.bam" $x"_results.sam"
rm $x"_results.sam"

samtools view -b -F 4 $x"_results.bam" > $x"_mapped.bam"
rm *_results.bam

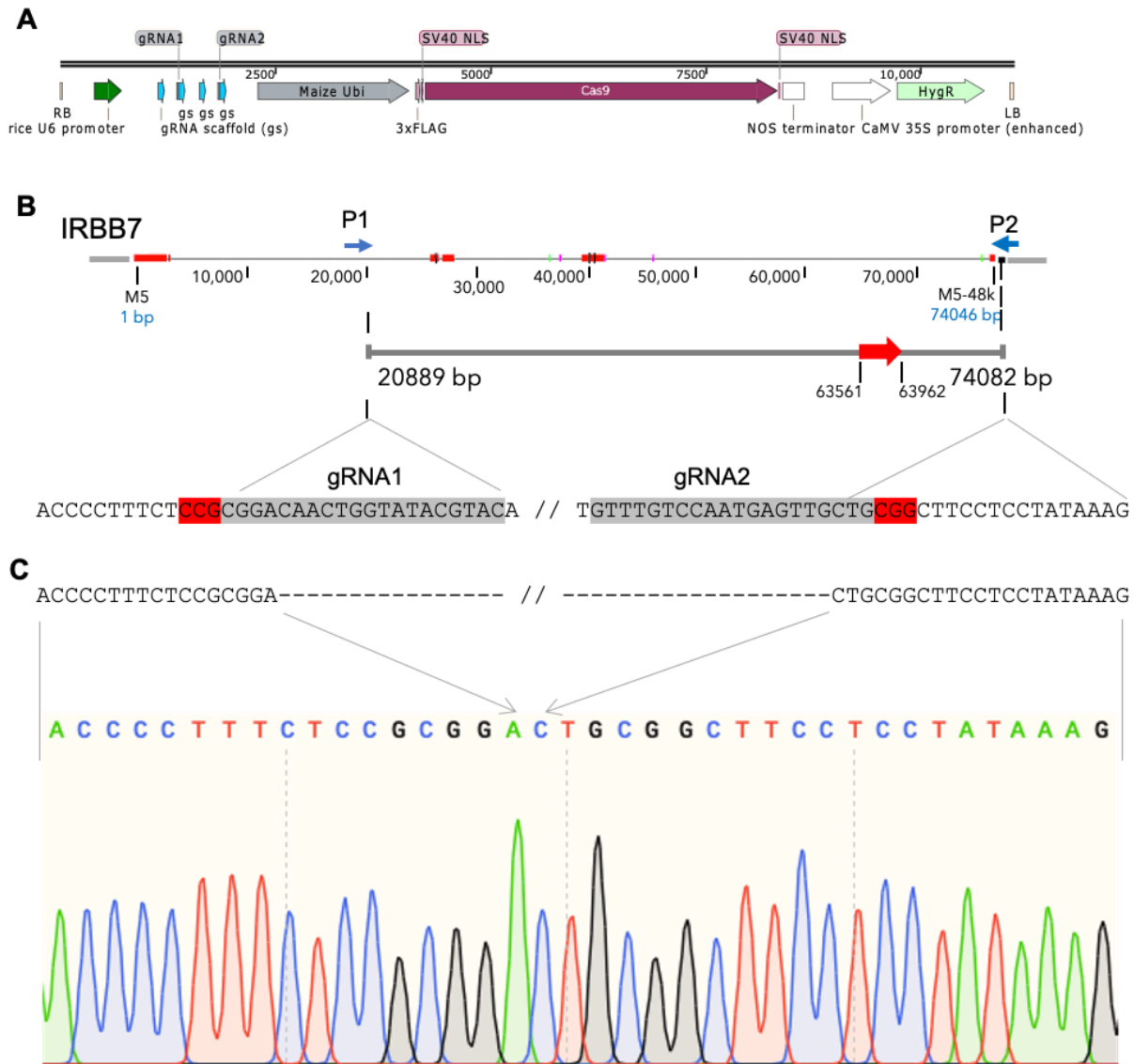
samtools sort $x"_mapped.bam" -o $x"_results_mapped.sorted.bam"

rm $x"_mapped.bam"

samtools index $x"_results_mapped.sorted.bam"
#####
done
```

```
###Generate a consensus Xa7 for each mapped rice3k  
# sam_list is the list of bam files generate above
```

```
for x in `cat sam_list`  
do  
samtools mpileup -uf complete_Xa7.fasta "$x"_results_mapped.sorted.bam" | bcftools call -c |  
vcfutils.pl vcf2fq > "$x"_cns.fq"  
done
```

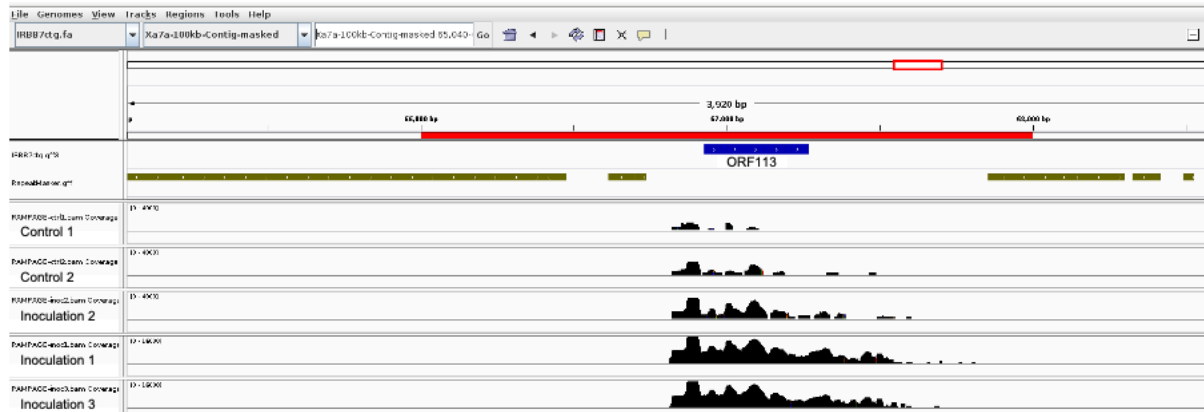


Supplemental Figure 1. Large chromosomal fragment deletion of *Xa7* locus.

(A) Schematic map of the CRISPR/Cas9 construct used for genome editing of *Xa7* locus. Guide RNA guides are under rice U6 promoters and Cas9 under maize ubiquitin 1 gene promoter. Hygromycin resistance gene is under the CaMV 35S promoter.

(B) *Xa7* locus delimited by two markers with guide RNA target sites. P1 and P2 are two deletion-specific primers to screen and identify the CRISPR-induced large deletion lines. Guide RNA target sites are in shaded with adjacent Cas9 PAM (protospacer adjacent motif) shaded in red.


(C) Sequencing chromatogram of PCR-amplicon from the T0 nb7-1 line. PCR-amplicon with two primers (P1 and P2) and genomic DNA of nb7-1 was subjected to Sanger sequencing.



Supplemental Figure 2. Screenshot of RAMPAGE analysis displayed with the Integrative Genomics Viewer (Thorvaldsdóttir, Robinson et al. 2013).

RAMPAGE reads from two RNA samples derived from IRBB7 leaves inoculated with MX53 (Control 1 and 2) and three RNA samples (Inoculation 1, 2, and 3) derived from IRBB7 leaves inoculated with PXO86 were used for analysis. The tracks show read coverage per position. Note that Control 1 and 2 and Inoculation 2 coverage is shown on a scale 0-4000, compared to 0-16000 for Inoculation 1 and 3, in order to accommodate different library sizes (read pairs aligned are 7,021,714; 8,098,348; and 6,507,082 for Control 1 and 2 and Inoculation 2, respectively; compared to 32,296,182 and 37,344,426 for Inoculation 1 and 3, respectively); Alignment and analysis were done with GoRAMPAGE (<https://github.com/BrendelGroup/GoRAMPAGE>). Counts are displayed on a log scale. For example, site 66,859 has coverage 9 and 31 for Control, compared to 9144, 217, and 6100 for Inoculated.

Thorvaldsdóttir, H., J. T. Robinson and J. P. Mesirov (2013). "Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration." *Brief Bioinform* **14**(2): 178-192.

A


```

MA--XAXXXXXXXXXXPAXXXXLXXXXXXXXXRRXXAXXXXXRARLLXVNSGXXLISXXGA/VXXHXAXXXX-XXX
Sb_XA7 MS-RPAEMRNPRHADDGDLQLAWIGRRRR-----GLQQQLLLDSGGRACMLL GALVLTWDQLALA-SSS 62
Ph_XA7 MA-----GLQPAAIH-----LQRRQQA IAGRRVRLL-VNAGALLVSAGGSVVIHAAATPSD-DAA 53
Si_XA7 MA-----G-RPAELH-----LQR---VIAGRRARLL-VNAGALLISAAGSVIIHAAATPSD--AS 48
Do_XA7 MA-----D-RPAAIHQGLAPVGFVVRQQRAIAPRRARLLMINSGLTLLISAASVSVIIHSTSSGT-TAG 61
Op_XA7 MVNRTAAHP-QMPVQ--ALRRNRIAQVNRVPAARRARARLLIVNSGVFLISTSGAIVVHTAGNPF---- 67
Ol_XA7 MANRTAAHP-RMPVQ--GLRRNQIA---RGPAAARRS--LLIVNTGVFLISTSGAIVVHTAGNPPSAID 62
XA7 MA--AADHPDRMPVAVAGLRHHYAF-----PANLRPAARLLTVNSGVFLISTAGAIVLVHTAGNPP-AID 62

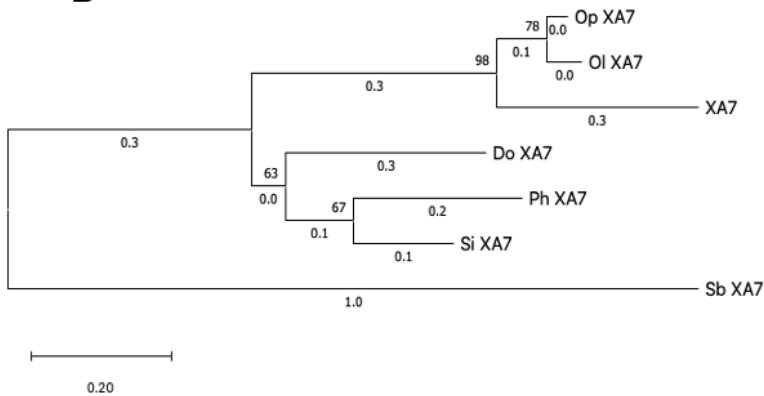
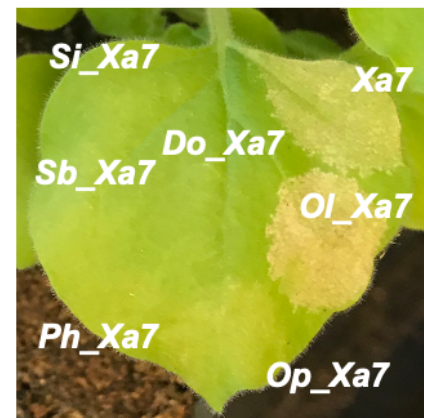
```



```

XGPAALVAFVLFLLGXXLVX LALVADRFPRARVGVAVIAXALQXYLXGX-GX-
Sb_XA7 SPEHVLAAAFVLWLLGAALVMLSLVSRFPRLASAGAALVMALRNYLLGG-GGL 115
Ph_XA7 GGPACSLVAFSVFLLGVS LVT LALAADRFPRAARVGA AVATATNRYLFG L-GW- 105
Si_XA7 SGPARPLIAFCIFVLGVS LVM SALVADRFPRAARAGVAIARALQRYVFG L-VG- 101
Do_XA7 GGRAFALVTFLLFLLGVS LVM VALVAYRFRRAAAVGVAVIARALRRYLLGL-GW- 113
Op_XA7 -----ALVAFVLFLLGIWLVLLALVADKFPRAARVAVAIASALQDHLIG--GN- 109
Ol_XA7 DGPSSALVAFVLFLLGIWLVLLALVADKFPRAARVAVAIASALQDHLIG--GN- 113
XA7 NDPAYALVAFVLFLLGIW LMSIALVADQFPRAAGVAVAIARALQDYLIG--GN- 113

```

B**C**

Supplemental Figure 3. *Xa7* and homologs in diverse grass species.

(A) Amino acid alignment of seven *Xa7* homologs generated by ClustalX. Sequences are from *Do_Xa7*, *Dichanthelium oligosanthes*; *Si_Xa7*, *Setaria italica*; *Ph_Xa7*, *Panicum hallii*; *Sb_Xa7*, *Sorghum bicolor*; *Op_Xa7*, *Oryza punctata*; *Ol_Xa7*, *Oryza longistaminata*.

(B) Phylogenetic tree of seven *Xa7* homologs. The unrooted phylogenetic tree of 7 proteins was generated by using the Maximum Likelihood method and JTT matrix-based model. The tree with the highest log likelihood (-1290.17) is shown. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). The analyses were conducted in MEGA X (<http://www.megasoftware.net>).

(C) Cell death phenotypes caused by overexpression of *Xa7* and its homologs in *N. benthamiana* through agroinfiltration. Leaf image was taken three days post infiltration.