

1 **A sugarcane smut fungus effector simulates the host endogenous elicitor peptide**
2 **to suppress plant immunity**

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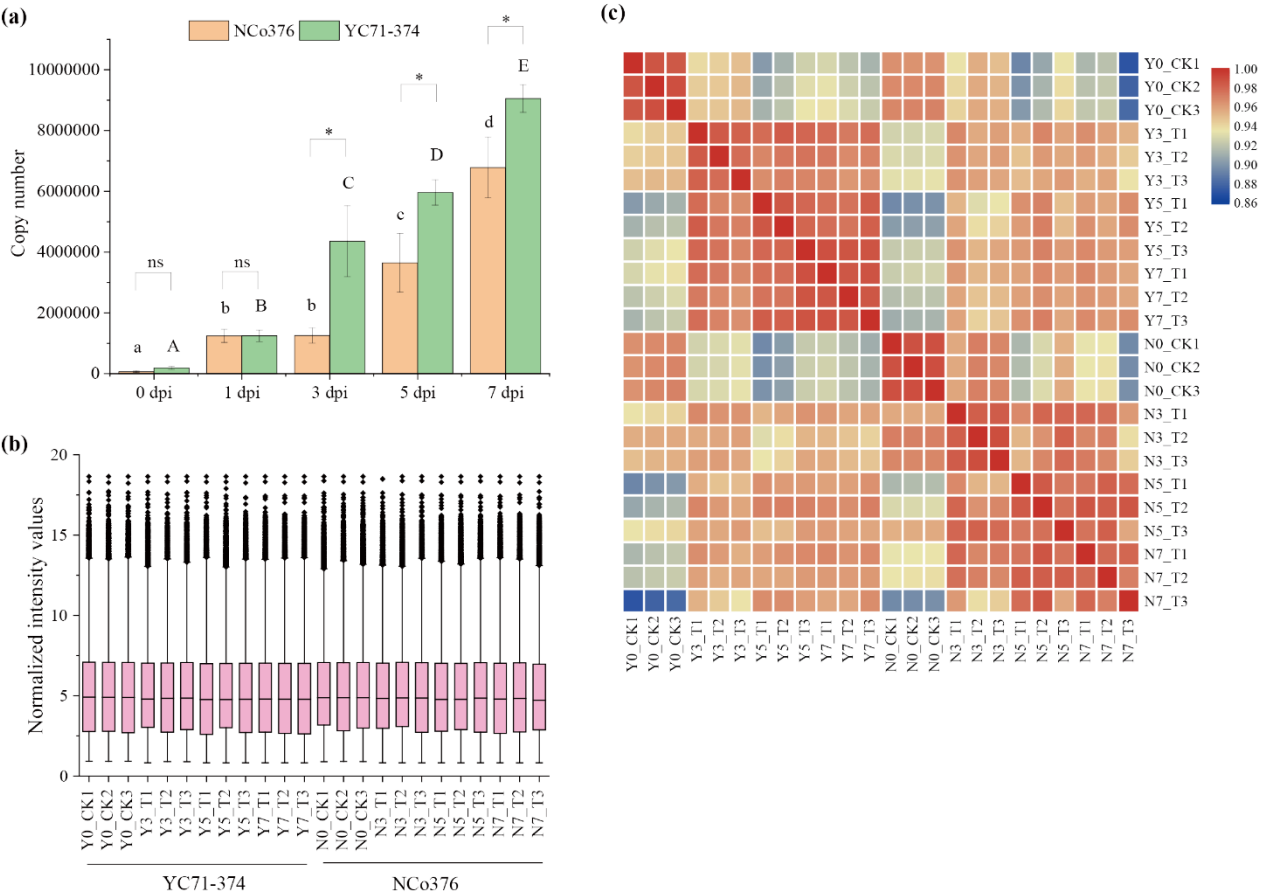
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18 **Supplementary Figures**



19 CK: Control replicate T: Treatment replicate

20 **Fig. S1 Fungal biomass accumulation and microarray hybridization in the sugarcane-*S.***

21 ***scitamineum* interaction**

22 (a) The accumulation of fungal biomass (copy number of fungal cells) in the resistance genotype NCo376 and the

23 susceptible genotype YC71-374 infected with *S. scitamineum* at 0, 1, 3, 5, and 7 dpi using TaqMan based qPCR.

24 The different letters in lowercase or uppercase indicate the significant difference of fungal biomass accumulation

25 at different time point in Nco376 or in YC71-374 respectively ($P < 0.05$). ns, no significant difference between

26 groups; *, the significant difference between groups ($P < 0.01$).

27 (b) The normalized intensity value of the expression of all targeted genes in 24 microarray samples as illustrated

28 by the boxplot. Horizontal line indicates different samples N/Y0, 3, 5, and 7, the 0 dpi, 3 dpi, 5 dpi, and 7 dpi from

29 NCo376 or YC71-374. CK/T1, 2, and 3, the biological replicate 1, 2, and 3 of the control or the treatment of *S.*

30 *scitamineum*. The normalized intensity value of gene expression was achieved from the normalization and

31 log-transformation of microarray hybridization signaling value. The whiskers represent the gene expression level

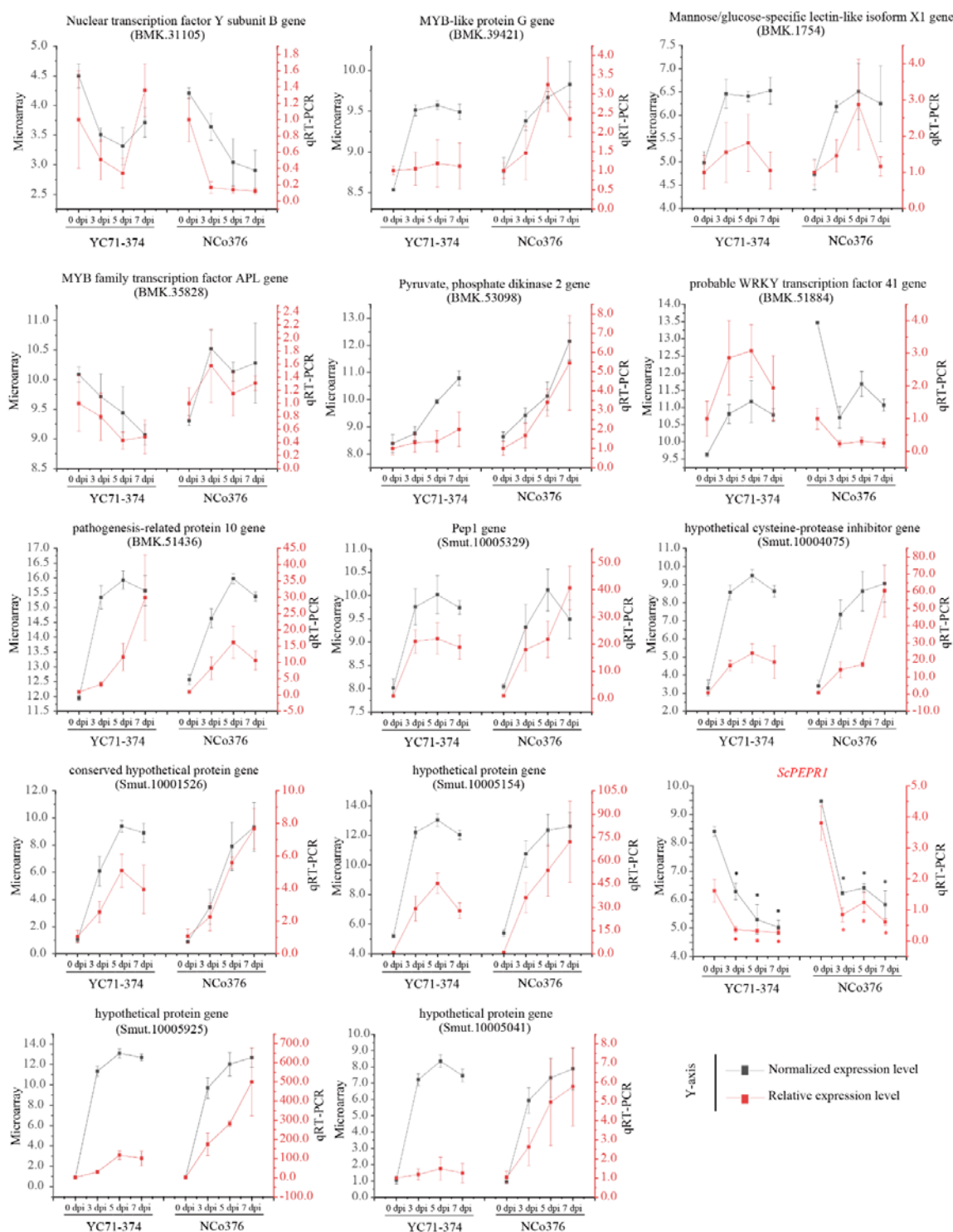
32 with values within 1.5 times the median. Black dots beyond the whiskers are the individual values out of 1.5 time

33 the interquartile range with outliers shown as fliers.

34 (c) Pearson's correlation analysis of the 24 microarray samples based on the normalized gene expression data. The

35 table cell is color-coded by correlation according to the color legend. CK/T1, 2, and 3, the biological replicate 1, 2,

36 and 3 of the control or the treatment of *S. scitamineum*.



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38 **Fig. S2 The expression of 14 selected DEGs revealed by microarray hybridization and**
 39 **qRT-PCR**

40 Based on the DEGs (differentially expressed genes) from the microarray hybridization, 8 DEGs from sugarcane
 41 and 6 DEGs from *S. scitamineum* were selected, and the gene expression was validated in the smut-susceptible
 42 genotype YC71-374 and smut-resistant genotype NCo376 using qRT-PCR. The accession number under the
 43 functional annotation of gene indicates a gene from sugarcane (BMK.xxx) or *S. scitamineum* (Smut.xxx). The
 44 error bars indicate standard deviation (n=3). * indicates a significant difference between the 0 dpi and 3, 5, or 7
 45 dpi ($P < 0.05$) determined by Student's t test.

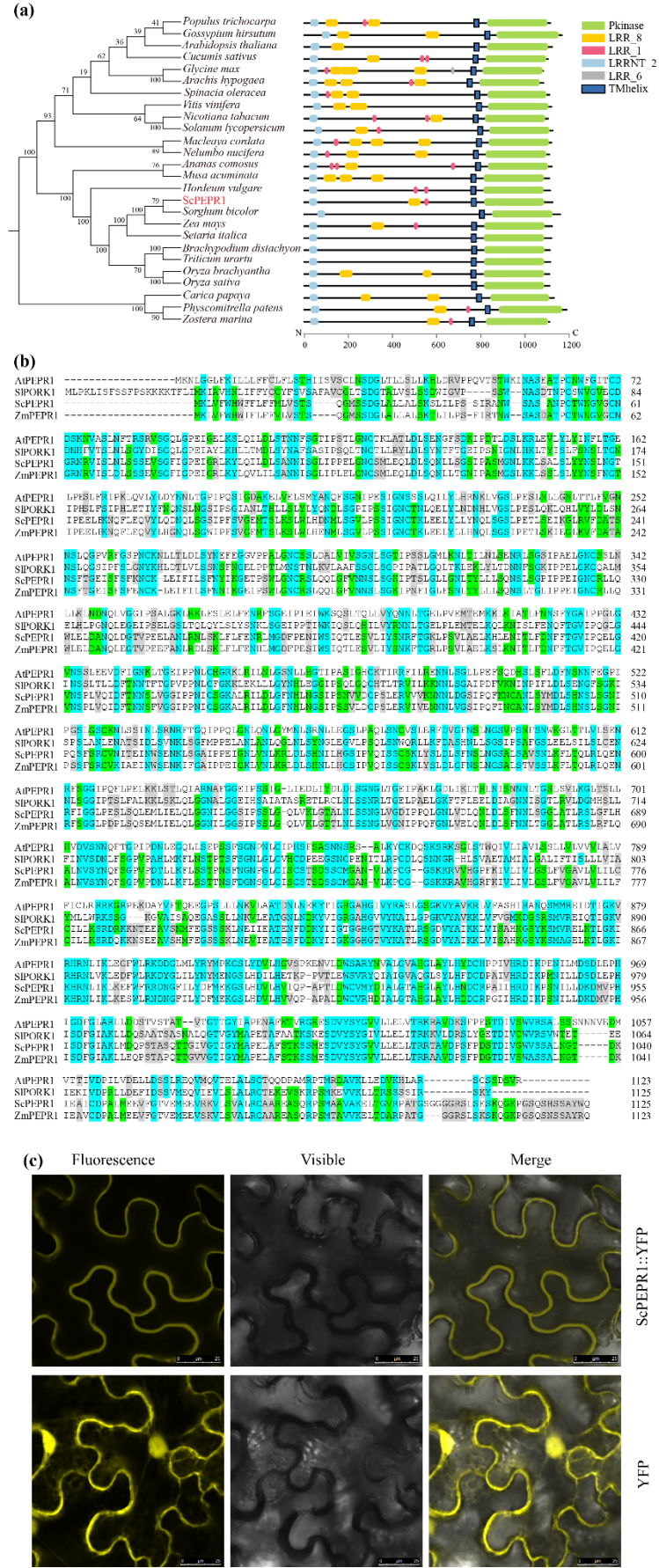


Fig. S3 The phylogenetic analysis of PEPR1 and the expression of ScPEPR1 in sugarcane

49 (a) Phylogenetic and conserved domain analysis of ScPEPR1. The ScPEPR1 orthologs were obtained from
50 *Sorghum bicolor*, *Zea mays*, *Setaria italic*, *Brachypodium distachyon*, *Oryza brachyantha*, *Oryza sativa* Japonica,
51 *Triticum urartu*, *Hordeum vulgare*, *Ananas comosus*, *Musa acuminata*, *Macleaya cordata*, *Vitis vinifera*, *Nelumbo*
52 *nucifera*, *Nicotiana tabacum*, *Spinacia oleracea*, *Populus trichocarpa*, *Solanum lycopersicum*, *Gossypium*
53 *hirsutum*, *Glycine max*, *Arabidopsis thaliana*, *Arachis hypogaea*, *Cucumis sativus*, *Physcomitrella patens*, *Carica*
54 *papaya*, and *Zostera marina*. The rectangle with different colors represents different conserved protein domain.
55 The accession number can be found in the table S3. Numbers at the branches indicate bootstrap values.

56 (b) The protein alignment of plant PEPR. ScPEPR1 and its orthologs from *Arabidopsis thaliana*, *Zea mays*, and
57 *Solanum lycopersicum* were aligned using DNAMAN and Genedoc, and the low homologous sites were removed.
58 The highly conserved residues were marked with color. The accession number of the sequences used in the
59 present study can be found in table S3.

60 (c) ScPEPR1 is located on the cytomembrane. YFP and ScPEPR1-YFP were expressed in *N. benthamiana* leaves.
61 The protein subcellular localization was observed using a confocal microscope 2 d after *Agrobacterium*
62 *tumefaciens* transformation. Bar scale = 5 μ m.

63 These experiments were repeated at least three times with consistent results.

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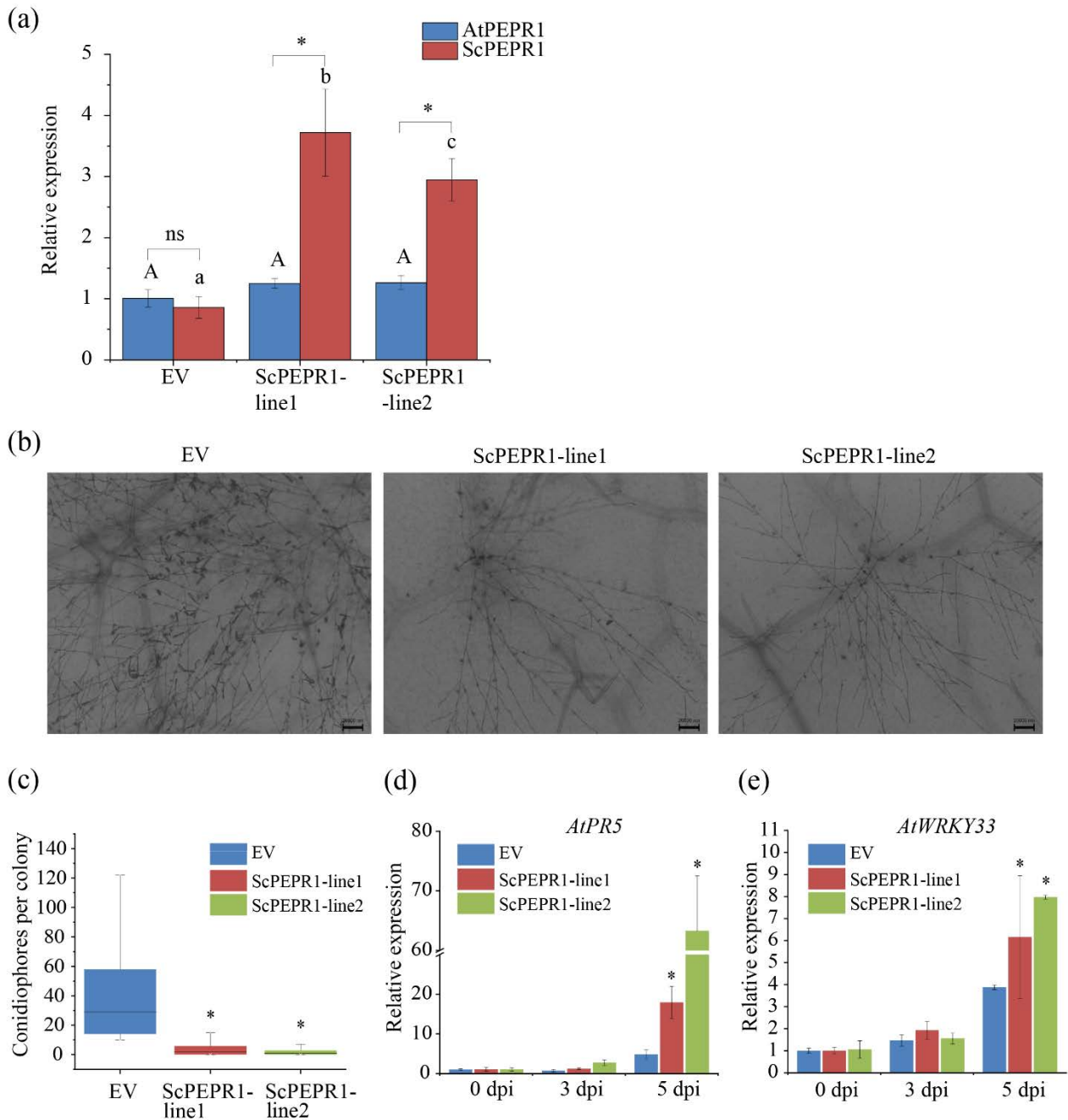


Fig. S4 Overexpression of *ScPEPR1* in *Arabidopsis* enhances plant resistance to powdery mildew

(a) The expression of *ScPEPR1* and *AtPEPR1* in *ScPEPR1* transgenic lines. The bars indicate relative fold change $\pm$ SD (n=3) among bio-replicates. The different letters in lowercase or uppercase indicate the significant difference of the gene expression in different lines ($P < 0.01$). ns, no significant difference between two genes in the same line; *, the significant difference between two genes in the same line ($P < 0.01$).

(b) Trypan blue staining of hyphae and conidiophores on leaves of empty-vector (EV) transgenic lines and *ScPEPR1* transgenic lines (*ScPEPR1*-line1 and line2) after infection with *G. cichoracearum* at 5 dpi. Scale bar = 20 μ m. These experiments were repeated three times with consistent results.

75 (c) Quantification of fungal growth on *ScPEPR1* transgenic *Arabidopsis* line1/2 and empty-vector (EV) transgenic
76 line at 5 dpi by counting the number of conidiophores per colony of the powdery mildew fungus *G.*
77 *cichoracearum*. Bars represent mean and SD (n >= 68).

78 (d-e) The expression of the defense-related marker gene *AtWRKY33* and the SA-dependent marker gene *AtPR5* on
79 *ScPEPR1* transgenic line1/2 and empty-vector (EV) transgenic line at indicated time after infection by *G.*
80 *cichoracearum*. The bars indicate relative fold change $\pm$ SD (n=3) compared to EV line at 0 dpi. In a-c, *
81 indicates a significant difference compared to the empty-vector (EV) transgenic line ($P < 0.05$) determined by
82 Student's *t* test.

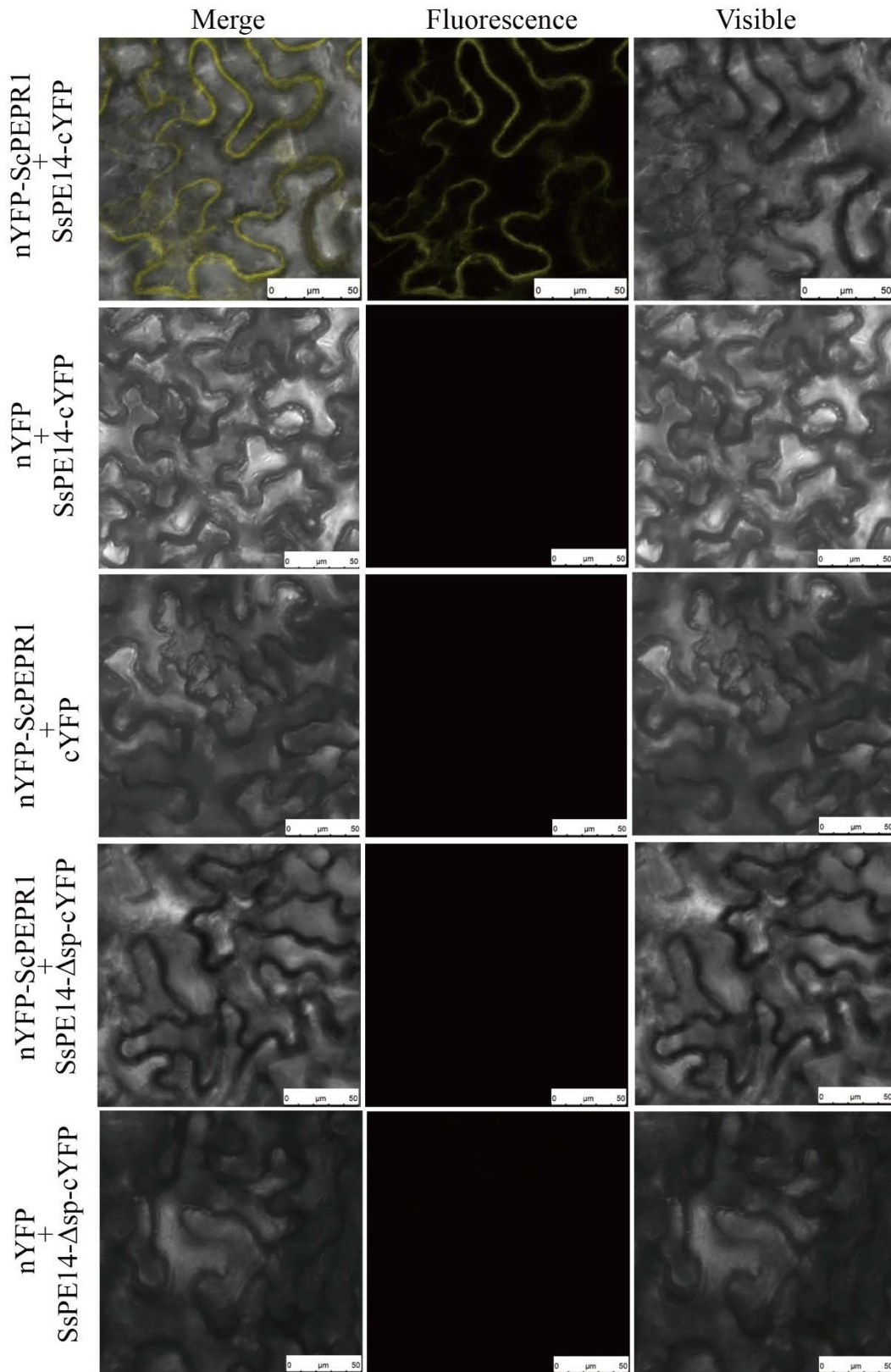


Fig. S5 SsPE14-Δsp lacking signal peptide does not interact with ScPEPR1 in BiFC assay

The binding assay between ScPEPR1 and SsPE14-Δsp in *Nicotiana benthamiana*, revealed by BiFC. The *N. benthamiana* leaves were co-infiltrated with 35S:nYFP-ScPEPR1 and 35S:SsPE14-cYFP, or 35S:SsPE14-Δsp-cYFP. Images were captured by a confocal microscope at 2 d after *Agrobacterium tumefaciens* transformation. SsPE14-Δsp, a signal peptides deletion mutant of SsPE14. Scale bars, 10 μm.

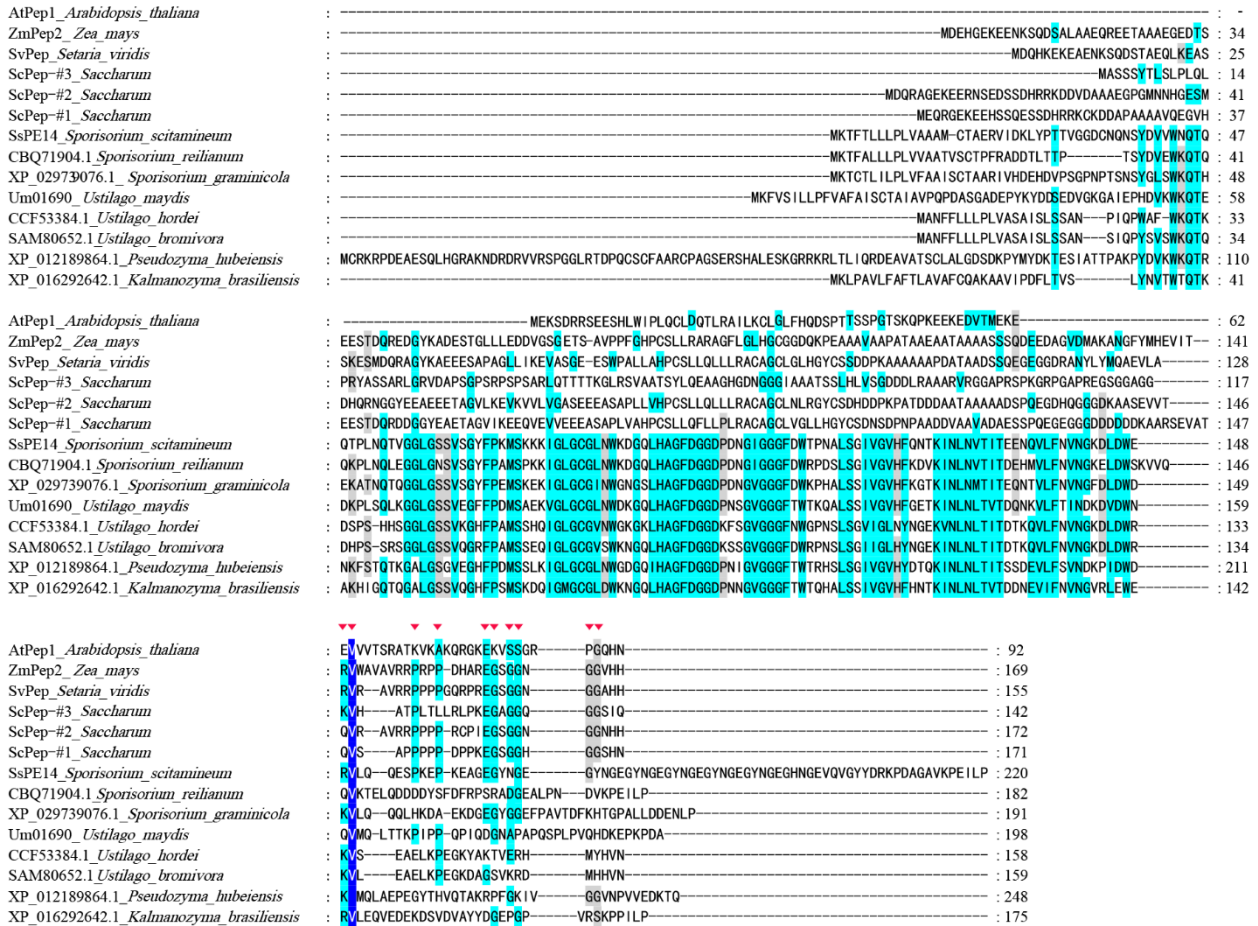


Fig. S6 The alignment of the amino acid sequences of plant elicitor peptides and the fungal homologs of SsPele1

The Pep1 protein sequences of Arabidopsis AtPep1, maize ZmPep2, green foxtail SvPep and sugarcane ScPep-#1/#2/#3 and the Pele1 protein sequences from *Sporisorium reilianum*, *Sporisorium graminicola*, *Ustilago maydis*, *Ustilago hordei*, *Ustilago bromivora*, *Pseudozyma hubeiensis*, and *Kalmanozyma brasiliensis* obtained from the NCBI database (Table S3) were aligned with DNAMAN and DNAMAN (Version 7.0.2.176) and Genedoc (<http://www.flu.org.cn/en/download-47.html>). The highly conserved sites are colored and marked with red triangle symbol on the top row. The accession number of the sequences used in the present study can be found in table S3.

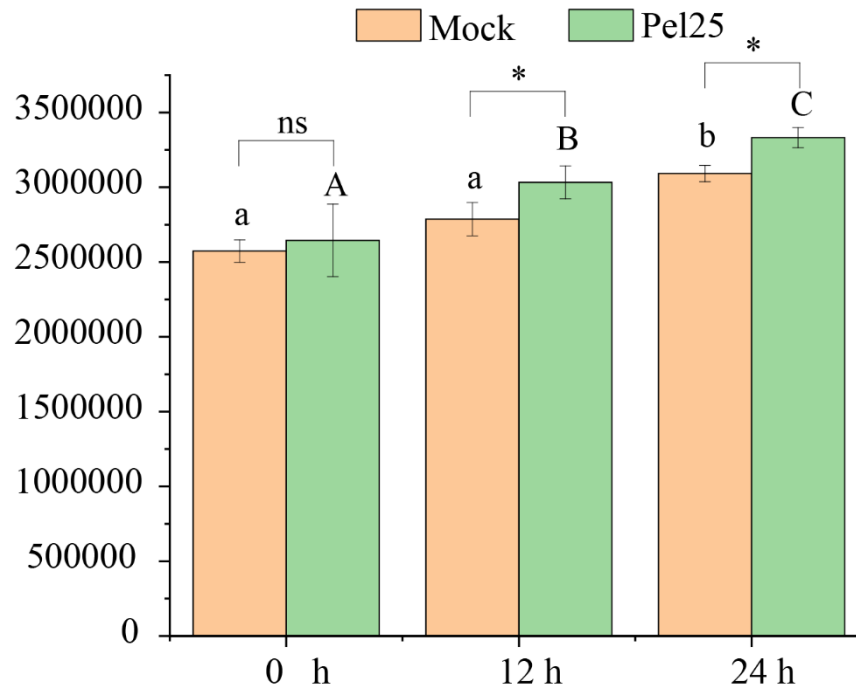


Fig. S7 SsPel25 promotes the propagation of smut fungus on the sugarcane sheath tissue

Sheath tissues were treated with 5 μ M SsPel25, and immersed into the diploid-type smut fungus ($OD_{600}=0.008$) solution and sampled at the indicated time points. A TaqMan-based qPCR detection of the increase of the fungal biomass were conducted according to Su et al. (2013). The different letters in lowercase or uppercase indicate the significant difference of fungal biomass accumulation at different time point in the mock samples or the SsPel25 treated samples, respectively ($P < 0.05$). ns, no significant difference between two groups; *, the significant difference between two groups ($P < 0.01$).

106 **Supplementary Tables**

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108 Table S1 The primers and constructs used in the present study

Genes	Sequences (Forward/Reverse primer)	Application
<i>bE</i>	TGAAAGTTCTCATGCAAGCC/TGAGAGGTCGATTGAGGTTG	Su <i>et al.</i> (2013), for Taqman based qPCR detection of smut fungus
<i>bE</i>	TGCTCGACGCCAATTCGGAG (probe)	Su <i>et al.</i> (2013), for Taqman based qPCR detection of smut fungus
<i>SsPele1*</i>	ATGAAGACCTTCACGCTCCTCCTG/TCAAGGCAGTATCTCAGGCTTGACG	For cloning
<i>SsPele1</i>	CATATGGCCATGGAGGCCGAATTCATGAAGACCTTCACGCTCCT/GCGGCCGCTGCAGGTCGACGGATCCAGGCA	pGBKT7, for Y-2-H
	GTATCTCAGGCTTGA	
<i>SsPele1-ΔC</i>	ATGGCCATGGAGGCCGAATTCATGAAGACCTTCACGCTCCT/GCGGCCGCTGCAGGTCGACGGATCCCTGGAGA	pGBKT7, for Y-2-H
	ACCCTCTCCCAGT	
<i>SsPele1</i>	CTCGAGGGGGGGCCCGGTACCATGAAGACCTTCACGCTCCTC/TTGAACGATCTGCAGCCCGGGTCAAGGCAGT	pCambia1301, for <i>Arabidopsis</i> transformation
	ATCTCAGGC	
<i>SsPele1</i>	CGACTCTAGGAGCTCGGTACCCGGGATGAAGACCTTCACGCTCCTC/GGAACATCGTATGGGTACATACTAGTAG	pCambia2300S-YC, for BiFC
	GCAGTATCTCAGGCTTGAC	
<i>SsPele1</i>	TCGGTACCTCGCGAATACATCTAGATGGATCCATGGAACGCGTGATTGATAAAC/TGCAGTCGACGGGCCCGGGA	pGEX-4T-1_ <i>SsPele1</i> , for ectopic expression in <i>Escherichia coli</i> **
	TCCGATGCGGCCGCATGGTTCGGTCTCTTA	
<i>SsPele1</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGAAGACCTTCACGCTCCTCC/GGGGACCACTTTGTACAAGA	pDONR207, for construction of pFAST-R06- <i>SsPele1::eGFP</i>
	AAGCTGGGTTCAGGCAGTATCTCAGGCTTGACG	
<i>SsPele1</i>	AAGGTCTCAAATGAAGACCTTCACGCTCCTCC/AAGGTCTCACGAATTCACATTGAACAGTACCT	pXCSG- <i>SsPE14::eYFP</i> , for CoIP
<i>SsPele1</i>	CGGAATTTTAATTAAGAATTCATGAAGACCTTCACGCTCCTC/CACTATAGGGAGAACCTCGAGGTCGCCGCCGA	pSUC2T7M13ori- <i>SsPE14</i>
	CAGTAGT	
<i>SsPele1-ΔC</i>	ATGAAGACAAAATGAAACCTTCACGCTCCTCC/CTGAAGACTTAAGCTCAAGGCAGTATCTCAGGCT	pXCSG- <i>SsPele1::eYFP</i> , for CoIP
<i>SsPele1-Δsp</i>	CGACTCTAGGAGCTCGGTACCCGGGATGCGAGTCATCGACAAGCTCTA/GGAACATCGTATGGGTACATACTAGT	pCambia2300S-YC, for BiFC
	AGGCAGTATCTCAGGCTTGAC	
<i>SsPE1</i>	ATGATCGAGCTCACTACCGCGTTTGTTCGC/TCACTTCAAAGCGGCCTGGTAAAGGATAGGCTC	For cloning
<i>SsPE1</i>	CATATGGCCATGGAGGCCGAATTCATGATCGAGCTCACTACC/GCGGCCGCTGCAGGTCGACGGATCCCTTCAA	pGBKT7, for Y-2-H
	GCGGCCTGGTAAA	
<i>SsPE4</i>	ATGCTGGTTCACCTCAGCTCC/TCAATGAGAGCGACCCTGTTTC	For cloning

Table S1 continued

Genes	Sequences (Forward/Reverse primer)	Notes
<i>SsPE4</i>	CATATGGCCATGGAGGCCGAATTCATGCTGGTTCCTCAGCTCC/GCGGCCGCTGCAGGTCGACGGATCCATGAG AGCGACCCCTGTTTCTCG	pGBKT7, for Y-2-H
<i>SsPE15</i>	ATGAAGTTCGCCTTTGGATCC/CTAACCCCTGAGTGTTGATGTCG	For cloning
<i>SsPE15</i>	CATATGGCCATGGAGGCCGAATTCATGAAGTTCGCCTTTGGATC/GCGGCCGCTGCAGGTCGACGGATCCACCCT GAGTGTTGATGTCG	pGBKT7, for Y-2-H
<i>ScPEPR1</i>	GCGAAACTAGAGCAGCCCC/AACAGCTCGGCAGAATCAGAA	For cloning
<i>ScPEPR1</i>	GCCATGGAGGCCAGTGAATTCATGAAGCTGGTTTTCTGGC/CAGCTCGAGCTCGATGGATCCCTGCCAGTACGCG CTGC	pGADT7, for Y-2-H
<i>ScPEPR1</i>	CGGGGGACGAGCTCGGTACCATGAAGCTGGTTTTCTGGC/TCCAAGGGCGAATTGGTCGACCTGCCAGTACGCG CTGC	pCambia1306-flag, for Arabidopsis transformation
<i>ScPEPR1</i>	ATCACAAAGTGCATCATCATCATCATATGAGTAGTGATGGTCTG/CTGTGCTTTTAAGCAGAGATTACCTATCT AGATTAAACGGACCATGCACAACGCG	pCzn1, for ectopic expression in <i>Escherichia coli</i> **
<i>ScPEPR1</i>	GATTTCTGAGGAGGATCTTCCCGGGATGAAGCTGGTTTTCTGGC/GCAGGGCATGCCTGCAGGTCGACCTACTGCCAGT ACGC	pCambia1300S-YN::ScPE PR1
<i>ScPEPR1</i>	CGAACGATACTCGAGGTCGACATGAAGCTGGTTTTCTGGC/GCTCACCATACTAGTGGATCCCTGCCAGTACGCG CTGC	pCambia2300_ScPEPR1:: YFP, for subcellular location assay
<i>ScPEPR1-N</i>	GCCATGGAGGCCAGTGAATTCATGAAGCTGGTTTTCTGGC/CAGCTCGAGCTCGATGGATCCTTTGAATGGGCCA TGCAC	pGADT7, for Y-2-H
<i>ScPEPR1-N</i>	ATCACAAAGTGCATCATCATCATCATATGAGTAGTGATGGTCTGGC/CTGTGCTTTTAAGCAGAGATTACCTAA ATTTCCGGCGGAATGGCGCCA	pCzn1, for ectopic expression in <i>Escherichia coli</i> *
<i>ScPEPR1-C</i>	GCCATGGAGGCCAGTGAATTCATGTTGAAATCTCGAGATCGGA/CAGCTCGAGCTCGATGGATCCCTGCCAGTAC GCGCTGC	pGADT7, for Y-2-H
<i>ZmPEPR1</i>	CGGGGGACGAGCTCGGTACCATGAAGCTGGTTTTCTGGCA/CAGCTCGAGCTCGATGGATCCCGGATTGCGATCC TGGTTTCC	pCambia1306-flag, for CoIP
<i>AtPEPR1</i>	CGGGGGACGAGCTCGGTACCATGAAGAATCTTGGGGGGTT/TCCAAGGGCGAATTGGTCGACCCGAAGTGAATC AGAGGAGC	pCambia1306-flag, for immunoprecipitation
<i>AtPEPR1</i>	ATTCTATTGAGATATGGAAGAG/CCTCTTCTAAGCTGCTGTTTAC	For qRT-PCR

109 * *SsPele1* and *SsPE14* were the same gene.

110 ** Codon optimization and synthetic gene coding sequence were used to enhance protein expression in *Escherichia coli* strain BL21.

111 Table S2 Screening genes as the detection targets of sugarcane-*S. scitamineum* customization
 112 microarray

Category	Key word
Receptor	Receptor
Kinase	Kinase
Phosphatase	Phosphatase
signal transduction	Calmodulin, guanine-nucleotide-exchange etc.
Plant hormone	Auxin, cytokinin, ethylene, gibberellin, jasmonate, salicylate etc.
Transcription factor	Transcription factor, DNA binding
Reactive oxygen	Respiratory burst oxidase, superoxide dismutase, catalase etc.
Programmed cell death	senescence-associated, apoptosis, Metacaspase etc.
Ubiquitination	Ubiquitin
Resistance	Elicitor, R gene, cell wall-associated etc.
Energy metabolism	Glucanase, ATP, cytochrome b5 reductase etc.

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Table S3 The accession number of genes and proteins used in the present study

Species	Gene/protein name	GenBank accession NO.
<i>Saccharum</i>	<i>ScPEPR1</i>	MN445188
<i>Arabidopsis thaliana</i>	<i>AtPEPR1</i>	NP_177451
<i>Sorghum bicolor</i>	ortholog of <i>AtPEPR1</i>	XP_002445581
<i>Zea mays</i>	<i>ZmPEPR1</i>	PWZ26320
<i>Setaria italic</i>	ortholog of <i>AtPEPR1</i>	XP_012702562
<i>Brachypodium istachyon</i>	ortholog of <i>AtPEPR1</i>	XP_010235180
<i>Oryza brachyantha</i>	ortholog of <i>AtPEPR1</i>	XP_006659458
<i>Oryza sativa Japonica</i>	ortholog of <i>AtPEPR1</i>	XP_015648066
<i>Triticum urartu</i>	ortholog of <i>AtPEPR1</i>	EMS62275
<i>Hordeum vulgare</i>	ortholog of <i>AtPEPR1</i>	BAK08322
<i>Ananas comosus</i>	ortholog of <i>AtPEPR1</i>	XP_020083255
<i>Musa acuminata</i>	ortholog of <i>AtPEPR1</i>	XP_009383175
<i>Macleaya cordata</i>	ortholog of <i>AtPEPR1</i>	OVA13263
<i>Vitis vinifera</i>	ortholog of <i>AtPEPR1</i>	XP_002273607
<i>Nelumbo nucifera</i>	ortholog of <i>AtPEPR1</i>	XP_010246888
<i>Nicotiana tabacum</i>	ortholog of <i>AtPEPR1</i>	XP_016436237
<i>Spinacia oleracea</i>	ortholog of <i>AtPEPR1</i>	XP_021845333
<i>Populus trichocarpa</i>	ortholog of <i>AtPEPR1</i>	XP_002311912
<i>Solanum lycopersicum</i>	ortholog of <i>AtPEPR1</i>	XP_004235511
<i>Gossypium hirsutum</i>	ortholog of <i>AtPEPR1</i>	XP_016711407
<i>Glycine max</i>	ortholog of <i>AtPEPR1</i>	XP_003555482
<i>Arachis hypogaea</i>	ortholog of <i>AtPEPR1</i>	XP_025611232
<i>Cucumis sativus</i>	ortholog of <i>AtPEPR1</i>	XP_011651735
<i>Physcomitrella patens</i>	ortholog of <i>AtPEPR1</i>	XP_024359221
<i>Carica papaya</i>	ortholog of <i>AtPEPR1</i>	XP_021896791
<i>Zostera marina</i>	ortholog of <i>AtPEPR1</i>	KMZ64621
<i>Saccharum</i>	plant elicitor peptide/ <i>ScPep</i> -#3	Cluster-44244.0
<i>Saccharum</i>	plant elicitor peptide/ <i>ScPep</i> -#2	Sspon.05G0022590-1B
<i>Saccharum</i>	plant elicitor peptide/ <i>ScPep</i> -#1	Sspon.05G0022600-1B
<i>Zea mays</i>	<i>ZmPep2</i>	ALF84910.1
<i>Setaria viridis</i>	<i>SvPep</i>	TKW06853
<i>Sporisorium scitamineum</i>	putative effector 1(<i>SsPE1</i>)	MK756111
<i>Sporisorium scitamineum</i>	putative effector 4 (<i>SsPE4</i>)	MK756112
<i>Sporisorium scitamineum</i>	putative effector 14 (<i>SsPE14</i>)	MK756113
<i>Sporisorium scitamineum</i>	putative effector 15 (<i>SsPE15</i>)	MK756114
<i>Sporisorium reilianum</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	CBQ71904.1
<i>Sporisorium graminicola</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	XP_029739076.1
<i>U. maydis</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	XP_011387667.1/um01690
<i>Ustilago hordei</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	CCF53384.1
<i>Ustilago bromivora</i> ;	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	SAM80652.1
<i>Pseudozyma hubeiensis</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	XP_012189864.1
<i>Kalmanozyma brasiliensis</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	XP_016292642.1
<i>Moesziomyces antarcticus</i>	ortholog of <i>SsPe1</i> / <i>SsPE14</i>	XP_014658179.1

126 Table S4 Twenty-nine candidate secreted effector protein genes coexpressed with sugarcane *plant*
127 *elicitor peptide receptor1 gene*

	Gene ID*	Genbank accession NO.	Functional Annotation
1	Smut.1000502	MK756113	plant elicitor peptide-like effector1
2	Smut.10000247	CBQ71258.1	hypothetical protein
3	Smut.10000198	CBQ71336.1	hypothetical protein
4	Smut.10004248	XP_757351.1	hypothetical protein UM01204.1
5	Smut.10002383	CBQ72682.1	hypothetical Ustilaginaceae-specific protein
6	Smut.10001535	CBQ70070.1	hypothetical Ustilaginaceae-specific protein
7	Smut.10002181	CBQ68784.1	probable alpha-galactosidase
8	Smut.10001520	CBQ70098.1	hypothetical protein
9	Smut.10000668	CBQ69161.1	related to fruiting body protein SC7 precursor
10	Smut.10002097	CBQ68888.1	hypothetical protein
11	Smut.10004684	CBQ70535.1	hypothetical protein
12	Smut.10005166	CBQ72054.1	related to α -L-arabinofuranosidase I precursor
13	Smut.10000851	CBQ68954.1	hypothetical protein
14	Smut.10004073	CBQ70787.1	hypothetical protein
15	Smut.10002573	CBQ72520.1	probable Endoglucanase 1 precursor (egl1)
16	Smut.10001004	CBQ69118.1	related to acetylxytan esterase
17	Smut.10005925	CBQ67365.1	hypothetical protein
18	Smut.10000512	CBQ69902.1	hypothetical protein
19	Smut.10002386	CBQ72684.1	hypothetical Ustilaginaceae-specific protein
20	Smut.10005024	CBQ71904.1	hypothetical protein
21	Smut.10002384	CBQ72682.1	hypothetical Ustilaginaceae-specific protein
22	Smut.10000388	CBQ69595.1	hypothetical protein
23	Smut.10004075	CBQ70785.1	hypothetical protein
24	Smut.10005136	CBQ72022.1	probable protein disulfide-isomerase precursor
25	Smut.10001934	CBQ73920.1	hypothetical protein
26	Smut.10006601	GAC98548.1	hypothetical protein PHSY_006142
27	Smut.10005041	CBQ71923.1	hypothetical protein
28	Smut.10003210	CBQ73627.1	related to Mig1 protein
29	Smut.10005154	CBQ72040.1	hypothetical protein

128 * Gene ID was achieved from the genomic sequencing data Que et al. (2014a).

Reference

- Su Y, Wang S, Guo J, Xue B, Xu L, Que Y. 2013.** A TaqMan real-time PCR assay for detection and quantification of *Sporisorium scitamineum* in sugarcane. *Scientific World Journal* **2013**(9): 942682.
- Que Y, Xu L, Wu Q, Liu Y, Ling H, Liu Y, Zhang Y, Guo J, Su Y, Chen J. 2014a.** Genome sequencing of *Sporisorium scitamineum* provides insights into the pathogenic mechanisms of sugarcane smut. *BMC Genomics* **15**(1): 996.