

Supporting information

Table S1 All primers used in this study.

Primer Name	Sequence (5'-3')
RcXYN1-F	5'-CCACCTTCACTATGCTCG-3'
RcXYN1-R	5'-TACGTGGTACACAATTCTC-3'
RcXYN2-F	5'-ACTCGATTCTGCTACCAT-3'
RcXYN2-R	5'-AGGGAGCAACACTCTGTA-3'
RcXYN3-F	5'-GGGGATGCCAGTTAGACG-3'
RcXYN3-R	5'-TGTGCTGCGACGGTATT-3'
RcXYN4-F	5'-GCTCTTCTAATGGTCTCGCC-3'
RcXYN4-R	5'-GCTGGTATCCCAAACCGTAAT-3'
RcXYN5-F	5'-ACATTGGCTGACTTGGAC-3'
RcXYN5-R	5'-TCCGAAAGCACAATCTACAAA -3'
RcXYN6-F	5'-ATAGAATGGTAGGGACAAGAC-3'
RcXYN6-R	5'-AACAGGCAAAGCATTACAG -3'
RcXYN7-F	5'-AACTCCGATCTAACTAGGACA-3'
RcXYN7-R	5'-ATTTACTAGAAATTGAAAGAA -3'
RcXYN8-F	5'-CAACGGAGGACTAAATGC-3'
RcXYN8-R	5'-AAAGCATCATAGAGCCAATTIC -3'
RcXYN9-F	5'-GCCCAATGGTTTGTTC-3'
RcXYN9-R	5'-AGTAAATTCTTCATCCGG-3'
pCOLD-TF-RcXYN1-F	5'-ggtaccctcgagggatccATGCTCGCGCTCTGCTC-3'
pCOLD-TF-RcXYN1-R	5'-aagctgaattcggtatccTCATGCCCAAAGCCTTTC-3'
pCOLD-TF-RcXYN2-F	5'-ggtaccctcgagggatccATCGCTTTACTGTTGCCAC-3'
pCOLD-TF-RcXYN2-R	5'-aagctgaattcggtatccTCAATTCAAAGCCGAGATGA-3'
TaActin-F	5'-CACTGGAATGGTCAAGGCTG-3'
TaActin-R	5'-CTCCATGTATCCCAGTTG-3'
RcActin-F	5'-GCATCCACGAGACCACCTAC-3'
RcActin-R	5'-GCGTCCCGCTGCTCAAGAT-3'
QRcXYN1-F	5'-CCACCGAGTCTTACAACATCCA-3'
QRcXYN1-R	5'-CCACGCATTTCTTCCCATTT-3'
QRcXYN2-F	5'-GGAGGCTTGATACCTTGGTC-3'
QRcXYN2-R	5'-TGGCATTCCGTCCGCAGAGC-3'
QRcXYN3-F	5'-TCTCAGACCGCCGCTGGCACTC-3'
QRcXYN3-R	5'-CCTGGGCTTGAAGTTGAGTCATA-3'
QRcXYN4-F	5'-CCACCGCTATCTCAGTCCCTC-3'
QRcXYN4-R	5'-TGGCAGTTGGGTCTACAGCAC-3'
QRcXYN5-F	5'-GGTGGTATCGGCTACAGTGGT-3'
QRcXYN5-R	5'-GACCGTCAAGTCCGCTACCTC-3'
QRcXYN6-F	5'-GTCGTAGTTCTCATGCCACAAGC-3'
QRcXYN6-R	5'-CCGCCTCCAGGATTAGGGTTA-3'
QRcXYN7-F	5'-CGTCGCCATCCTCAAGTCTGA-3'
QRcXYN7-R	5'-CTGACTGTGCCAGATGAAGGTG-3'
QRcXYN8-F	5'-CCTCAGTATGGCACAATGTTCTT-3'
QRcXYN8-R	5'-TGCATCTCCCCACTCAGGTGA-3'
QRcXYN9-F	5'-GCTGCTCTGGCGTTCTGCT-3'
QRcXYN9-R	5'-TCGGACGGTTCCAGTGAGG-3'

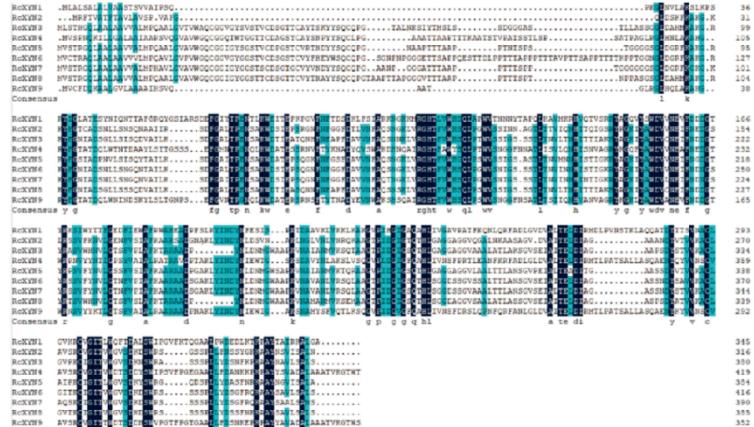
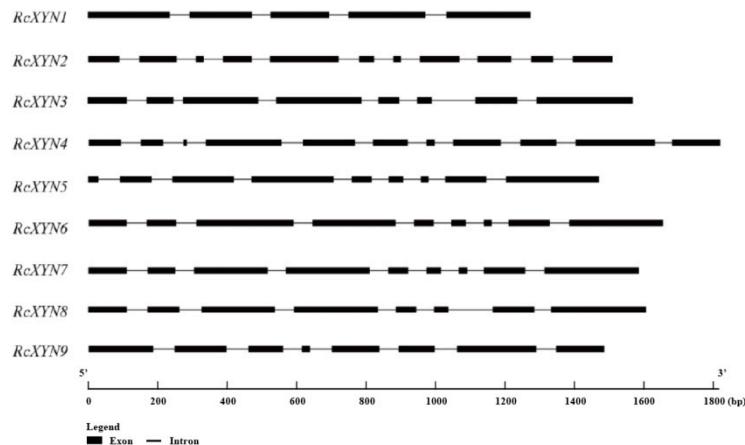
A**B**

Figure S1 Sequence alignment among *RcXYN*proteins in *Rhizoctonia cerealis* andstructures of their coding genes. (A) Sequence alignment among nine *Rhizoctonia cerealis* xylanases proteins.(B) Exons and introns are indicated by black boxes and lines, respectively. The 5'-3' scale indicates the DNA sequence size. The names of the *RcXYN* genes and intron-exon structures are indicated at the left and right sides, respectively.

File S1 Amino acid sequences of the 53 GH10 family xylanases from *Rhizoctonia cerealis* and other fungi (*Rhizoctonia solani*, *Magnaporthe oryzae*, *Fusarium oxysporum*, *Aspergillus niger*, *Aureobasidium pullulans*, *Penicillium purpurogenum*, *Penicillium oxalicum*, *Talaromyces aerugineus*, *Aspergillus kawachii*, *Aspergillus fumigatus*, *Aspergillus sojae*, *Aspergillus terreus*, *Aspergillus aculeatus*, *Penicillium crysogenum*, *Penicillium citrinum*, *Penicillium simplicissimum*, *Penicillium canescens*, *Coprinopsis cinerea*).