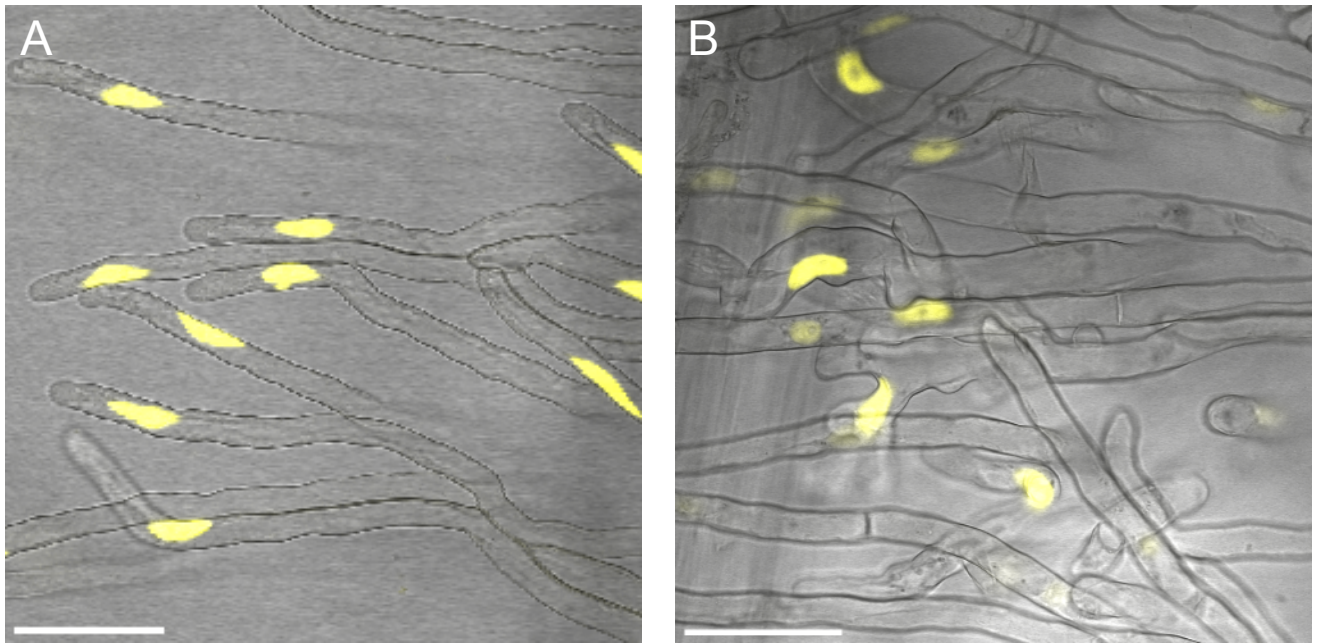
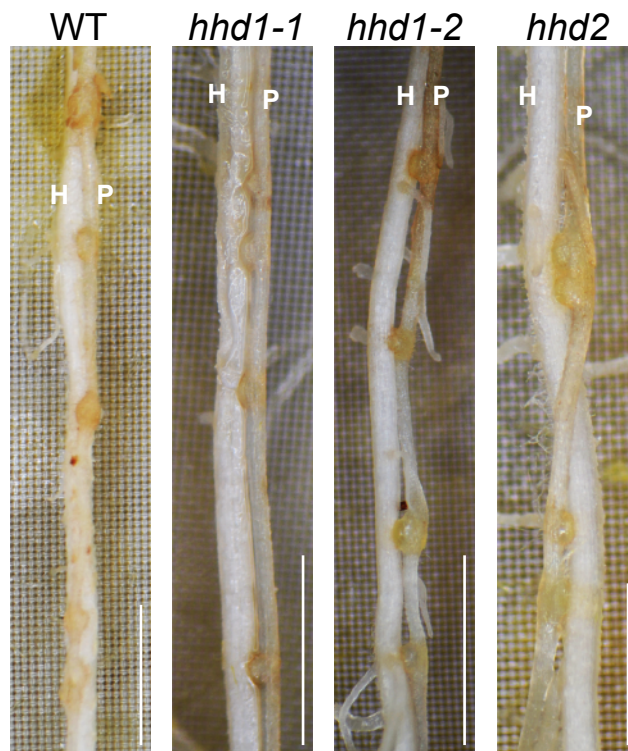


**Supplemental Figure S1.** Phylogenetic analysis and promoter comparison of *Expansin* genes in *Arabidopsis* and *P. japonicum*. A, *P. japonicum* (Pj) contigs were derived from the blast result using *AtEXP7* as a query against *P. japonicum* transcriptome data. The contigs containing ninety-conserved central core amino acids were selected for the alignment against *AtEXP7* as well as its close homologs. The neighbor-joining distance analysis was then performed using CLC Main Workbench software (Ver. 7) to construct a phylogenetic tree with 1000 bootstrap replicates. The *P. japonicum* contig closest to *AtEXP7* is highlighted in red and named *PjEXP7*. B, An alignment of promoter regions indicates that the RHE consensus sequence (underline) is conserved in *PjEXP7*. The highly conserved CACG motif is marked by asterisks.



**Supplemental Figure S2.** Magnified images of the root hairs and haustorial hairs expressing *PjEXP7* in *P. japonicum* roots. (A) Magnified image of root hairs. The image was derived a single plane of Fig 5B. (B) Magnified image of haustorial hairs at 57 h after *Arabidopsis* root infection. Bars, 50  $\mu$ m.



**Supplemental Figure S3.** Haustoria formed using the rhizotron system with a narrow slit. Images were taken after 10 days of rice host root infection. H and P indicate host and parasite roots, respectively. Bars, 2 mm.

Supplemental Table S1. Primer sequences.

1st Venus	Forward	5'-TTGAAGACAAAATGGTGAGCAAGGGCGAGGA-3'
	Reverse	5'-TTGAAGACAACCTTGTACAGCTCGTCCATGC-3'
2nd Venus	Forward	5'-TTGAAGACAACAAGATGGTGAGCAAGGGCGAGGA-3'
	Reverse	5'-TTGAAGACAAAATCTTGTACAGCTCGTCCATGCCG-3'
3rd Venus	Forward	5'-TTGAAGACAAGATGGTGAGCAAGGGCGAGGAG-3'
	Reverse	5'-TTGAAGACAACGATCTTGTACAGCTCGTCCATGC-3'
NLS	Forward	5'-TTGAAGACAAATCGCTGCAGCGGCCGAATT-3'
	Reverse	5'-TTGAAGACAAAAGCTTACTCTTCTTCTTGATCAG-3'
<i>PjEXP7</i> promoter	Forward	5'-TTGAAGACAAGGAGAGTAGTTTTGGTGGGTTGT-3'
	Reverse	5'-TTGAAGACAACATTGATTTTCTTGATAACCTTAATTTG-3'