

Supplementary Materials:

Table S1 Primers used in this study.

Primer	Sequence (5'-3')	Application
porin-AF	AGTGCGAGTGTCCGGTGAATG	amplify <i>Fgporin</i> 5' flank sequence
porin-AR	TTGACCTCCACTAGCTCCAGCCAAGCC GGACGGGAGAGAGAAACGG	
porin-BF	GAATAGAGTAGATGCCGACCGCGGGTT TCCC GTTGATGTGTTCCG	amplify <i>Fgporin</i> 3' flank sequence
porin-BR	CCTGGATGATTGGGTGCTT	amplify <i>Hph</i> N-terminal sequence
HYG-F	GGCTTGGCTGGAGCTAGTGGAGGTCAA	
HY-R	AACCCGCGGTCCGCATCTACTCTATTC	amplify <i>Hph</i> C-terminal sequence
YG-F	GATGTAGGAGGGCGTGGATATGTCCT	
HYG-R	GTATTGACCGATTCTTGC GGTC CGAA	for identification of <i>Fgporin</i> deletion transformants
porin-K1F	GAGGGTGTGAGGTTGTGCTC	
porin-K1R	GTTGGCGACCTCGTATTGG	for identification of <i>Fgporin</i> deletion transformants
porin-K2F	GCGAAGAATCTCGTGCTTTC	
porin-K2R	CGCCGCTCTTACTACGCT	for identification of <i>Fgporin</i> deletion transformants
porin-MF	AGATACCAAACACCGCAATCA	
porin-MR	CTTCACGGACATAAAGAGGCA	quantitative RT-PCR analysis
GAPDH-F	CTTACTGCCTCCACCAACTG	quantitative RT-PCR analysis
GAPDH-R	TGACGTTGGAAGGAGCGAAG	
Tri5-F	GAGTGTTTCATGCATGGCTACGTC	quantitative RT-PCR analysis
Tri5-R	CTGAGCCTCCTTCACATCGTCC	
Tri6-F	CTGAGGGCATTCTGAGTAGCGACA	quantitative RT-PCR analysis
Tri6-R	CGTTATGTTTATCGGCACTTTC	
Tri10-F	GCGACAGGAGCAAGAACATAA	quantitative RT-PCR analysis
Tri10-R	GGCGGCGTAAATCTGAGTG	
porin-CF	CACCATCACCATCACTCGAGCAGTTCTC TGATGGTGTCGG	<i>Fgporin</i> complementation
porin-CR	CGCCCTTGCTCACCTCGAGTGAAAGCA TGAAGGCAACCT	
Tri1-GFP-F	TCGTGGTTCTCATCACCATCACCATCAC TCGAGGAAAGAGGCTGGTAGCTGCG	For <i>FgTri1-GFP</i> fusion construct generation
Tri1-GFP-R	CCGGTGAACAGCTCCTCGCCCTTGCTCA CGTCATCCTGTACCAATTCCAATCGC	
Tri4-GFP-F	TCGTGGTTCTCATCACCATCACCATCAC TCGAGAGTAGCGACAGAAAAAGCGCTT	For <i>FgTri4-GFP</i> fusion construct generation

	G	
Tri4-GFP-R	CCGGTGAACAGCTCCTCGCCCTTGCTCA CCAAAGCCTTGAGAACCTTGACTCG	
GFP-Atg8-1F	CGACTCACTATAGGGCGAATTGGGTAC TCAAATTGGGAACAACCTGAGAACTCGG GTGA	amplify <i>GFP-FgAtg8</i> sequence
GFP-Atg8-1R	GGTGAACAGCTCCTCGCCCTTGCTCACC ATGTTGACGGTGATGGTTGTTG	
GFP-Atg8-2F	GGTGAACAGCTCCTCGCCCTTGCTCACC ATGTTGACGGTGATGGTTGTTG	amplify <i>GFP-FgAtg8</i> sequence
GFP-Atg8-2R	ACCATCACCGTCAACATGGTGAGCAAG GGCGAGGAGCTGTT	
GFP-Atg8-3F	CCTTGAATTTGCTGCGCTGTACAGCTC GTCCATGCCGAGAG	amplify <i>GFP-FgAtg8</i> sequence
GFP-Atg8-3R	CTCGGCATGGACGAGCTGTACAAGCGC AGCAAATTCAAGGACGA	
AD-porin-F	AGATTACGCTCATATGGCCATGGAGGC CAGTGAATTCATGTCTGTCCCCGCCTTC T	amplify pGADT7- <i>Fgporin</i> sequence
AD-porin-R	GATGGATCCCGTATCGATGCCCACCCG GGTGGAATTCTTAACCCTCGAAGGTGA AGC	
AD-Mdm35-F	TACGCTCATATGGCCATGGAGGCCAGT GAATTCATGTCAGCTTCACTATCACC	amplify pGADT7- <i>FgMdm35</i> sequence
AD-Mdm35-R	CGCTGCAGGTCGACGGATCCCCGGGAA TTCCTACTCACGGGCCTCTTGACCAG	
AD-Ups1-F	AGATTACGCTCATATGGCCATGGAGGC CAGTGAATTCATGGTTCTCACTCGCACG A	amplify pGADT7- <i>FgUps1</i> sequence
AD-Ups1-R	ATGGATCCCGTATCGATGCCCACCCGG GTGGAATTCTTAAGCAAGTTGACGCTG ACG	
AD-Ups2-F	TACGCTCATATGGCCATGGAGGCCAGT GAATTCATGAAGGTCTTTAGCAACAGC G	amplify pGADT7- <i>FgUps2</i> sequence
AD-Ups2-R	ATGGATCCCGTATCGATGCCCACCCGG GTGGAATTCTTATAGAACCTGGCGAGC CCT	
BD-porin-F	TCAGAGGAGGACCTGCATATGGCCATG GAGGCCGAATTCATGTCTGTCCCCGCCT TC	amplify pGBKT7- <i>Fgporin</i> sequence
BD-porin-R	CCGCTGCAGGTCGACGGATCCCCGGGA ATTCTTAACCCTCGAAGGTGAAGCTG	
porin-YFP ^N -F	TGGTTCTCATCACCATCACCATCACTCG	amplify <i>Fgporin-YFP^N</i>

	AGACTGGTACCGATGCATGTTT	sequence
porin-YFP ^N - R	GCCCTTGCTCACCATCGTGGCGATGGA	
	GCGACCCTCGAAGGTGAAGCTGG	
Ups1-YFP ^N - F	TGGTTCTCATCACCATCACCATCACTCG	amplify <i>FgUps1-YFP^N</i>
	AGAGTGTGTGCATTACACATC	sequence
Ups1-YFP ^N - R	GCCCTTGCTCACCATCGTGGCGATGGA	
	GCGAGCAAGTTGACGCTGACGTT	
Ups2-YFP ^N - F	TGGTTCTCATCACCATCACCATCACTCG	amplify <i>FgUps2-YFP^N</i>
	AGGTATCCGCAACCTCACAGGA	sequence
Ups2-YFP ^N - R	GCCCTTGCTCACCATCGTGGCGATGGA	
	GCGTAGAACCTGGCGAGCCCTCT	
porin-YFP ^C - F	TGGTTCTCATCACCATCACCATCACTCG	amplify <i>Fgporin-YFP^C</i>
	AGACTGGTACCGATGCATGTTT	sequence
porin-YFP ^C - R	CAGGTCGTTTCGGGATCTTGCAGGCCGG	
	GCGACCCTCGAAGGTGAAGCTGG	

Table S2 The amino acid similarity of Fgporin with other fungal porins.

	<i>Fusarium</i> <i>graminearum</i> porin	<i>Fusarium</i> <i>oxysporum</i> porin	<i>Neurospora</i> <i>crassa</i> porin	<i>Saccharomyces</i> <i>cerevisiae</i> porin1	<i>Saccharomyces</i> <i>cerevisiae</i> porin2
Number of Amino acids	283	283	283	283	281
Similarity		100%	82%	43%	33%

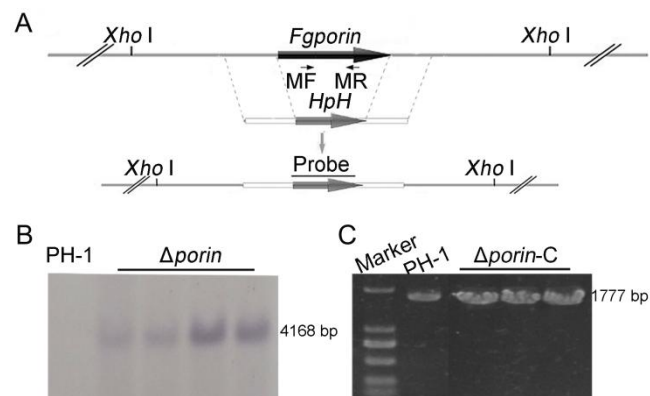


Figure S1 Generation and identification of *Fgporin* deletion mutants. (A) Deletion strategy used for *Fgporin*. The gene replacement cassette contained the whole *hygromycin-phosphotransferase* (*HpH*) gene. (B) Southern blot analysis of *Fgporin* deletion mutants. Genomic DNA was digested with *Xho* I. (C) PCR verification of *Fgporin* complementation strains.

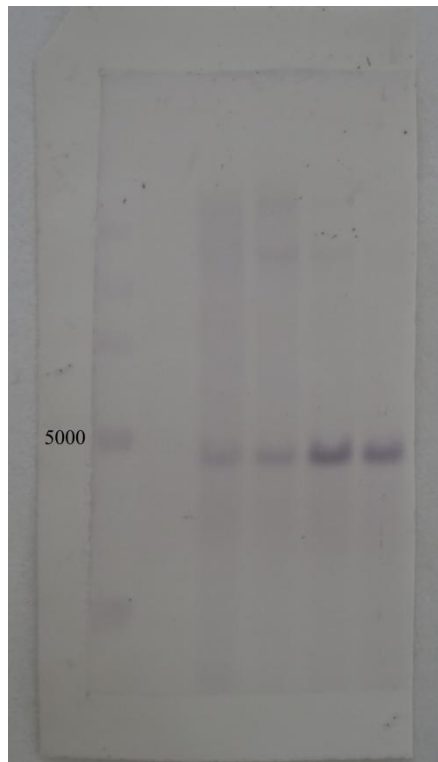


Figure S2 Southern blot analysis of *Fgporin* deletion mutants. Genomic DNA was digested with *Xho* I.

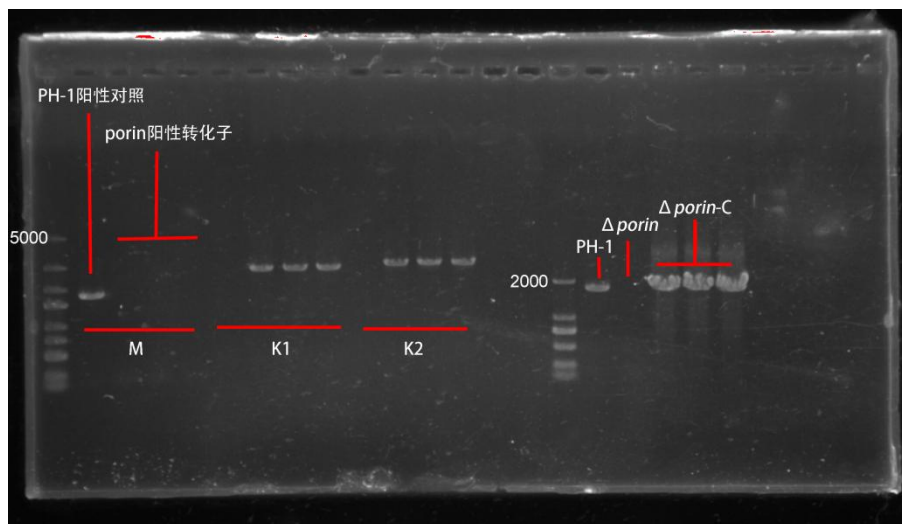


Figure S3 PCR verification of *Fgporin* deletion mutants and *Fgporin* complementation strains.

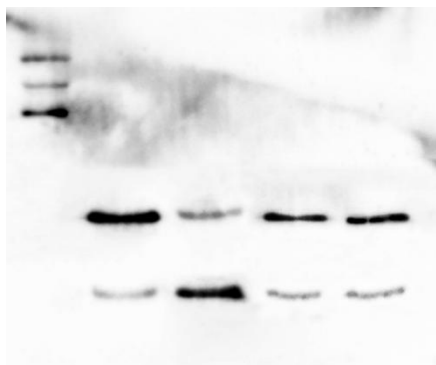


Figure S4 The original picture of Western Blot. The upper band was GFP-FgAtg8, and the lower band was GFP.

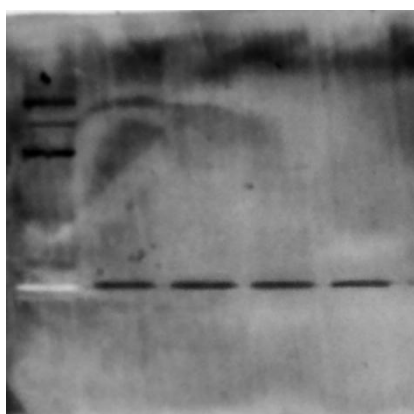


Figure S5 The original picture of Western Blot. The band was GAPDH.