

**Table S1. Identifying sub-cellular location**

Location weights	LocDB	PotLocDB	Neural Nets	Pentamers	Integral
Vacuolar	10.0	0.0	0.00	1.51	9.89
Plasma membrane	0.0	0.0	2.63	0.15	0.01
Mitochondrial	0.0	0.0	0.00	0.85	0.00

Note: Integral Prediction of protein location: Membrane bound Vacuolar with score 9.9. Neural Nets -Plasma membrane with score 2.6. Pentamers- Mitochondrial with score 0.85.

**Table S2. Primers used in this study**

Primer name	Sequence 5'-3'	Remark
MoAE4-L-S	GGACTAGTCCGCATTTTCAGTTCGTC	Amplify <i>MoAE4</i> left
MoAE4-L-A	GGGGTACC ACCCCTTGCCACTCTTC	flank sequence
MoAE4-R-S	GCTCTAGACCACACCATCTCCCTGCT	Amplify <i>MoAE4</i> right
MoAE4-R-A	CCCAAGCTTCCATCCTCCCGTCAACAC	flank sequence
MoAE4-LHYG-S	ACAACCTACCCTGAACCT	Verify <i>MoAE4</i>
MoAE4-LHYG-A	TCCATACAAGCCAACCAC	knockout mutant sequences
MoAE4-G-S	TCGGGATGGGAACGGT	Amplify <i>MoAE4</i>
MoAE4-G-A	TGGGTCGGGCGGAGGT	sequence
MoAE4-C-S	GAAGATCTATGACGGCCC ACACATCATC	Amplify <i>MoAE4</i>
MoAE4-C-A	GGACTAGTCTGTTCACCCGAGCCGACCC	complementation sequence
qRT-MoAE4-S	TGGCAGGTCGAAAACTGGT	qRT-PCR primer of
qRT-MoAE4-A	TTCCACGCATCCTTCCAGTC	<i>MoAE4</i>
qRT-MoCA-S	AGATGAACGTCGAGGCC	qRT-PCR primer of
qRT-MoCA-A	CACCACGGAAGACAAGC	<i>MoCA</i>
HYG-S	GATGTAGGAGGGCGTGGATATGTCCT	Amplify HYG
HYG-A	AACCCGCGGTCGGCATCTACTCTATTC	sequence
Actin-S	CGTTGTTTCCTATTTACGAGGG	qRT-PCR primer of
Actin-A	TTGATGTCACGGACGATTTC	<i>Actin</i>
Sc-MoAE4-S	CCCAAGCTTATGACGGCCC ACACATCATC	Amplify <i>MoAE4</i>
Sc-MoAE4-A	GGAATTCCTGTTCACCCGAGCCGACCC	complementation
Sc-MoACT-S	CGGGATCCCATGGAAGAGGAGGTCGCCG	Amplify <i>MoACT</i>
Sc-MoACT-A	GCTCTAGAGAAGCACTTGCGGTGGAC	complementation
Sc-MoACT-S	ATGTCGAATGAGAGCACACGAG	Amplify <i>ScBor1</i>
Sc-MoACT-A	TTAGTCTTCATGCTTATCACAGA	complementation

Figure S1. Sequence alignment and prediction of MoAE4 structure. A Sequence alignment. The transmembrane domain of MoAE4 was compared with *A. nidulans* SbtA gene and *S. cerevisiae* BOR1 gene. B Prediction of MoAE4 structure Protein. Possible membrane topologies of MoAE4 were predicted 10 transmembrane-spanning domains. The sequence of 87-263 was predicted as HCO<sub>3</sub><sup>-</sup> cotransport domain. EC, extracellular side; IC, intracellular side of plasma membrane. C Three-dimensional (3-D) structures of MoAE4. 3-D structures of MoAE4 were viewed from different directions.

Figure S2. The construction strategies for MoAE4 deletion and complementation strains. A Construction of pCAMBIA1303-MoAE4:: GFP. Details of the construction are described in Experimental procedures. B The *MoAE4* gene was replaced by the hygromycin resistant cassette (HYG). To construct the replacement vector, the flanking sequences were amplified with their corresponding primer pairs and fused with the *HYG* cassette. C The strategy of  $\Delta$ *MoAE4*/*MoAE4*. Details of the construction are described in Experimental procedures. D The relative expression of *MoAE4* in strains. The wild type, deletion mutant, and complementation strains were detected via qPCR using cDNA as a template. The relative mRNA levels were calculated using the 2<sup>- $\Delta\Delta$ Ct</sup> method. The *Actin* was used as an internal standard reference. The data represent the means  $\pm$  standard deviation (SD) of three experiments. The error bars represent the SD.

Figure S3. The green fluorescence signals detection of intracellular pH in conidia. The light (left), fluorescence confocal (middle), and merge (right) microscope observations of strains were in conidia. The green fluorescence signal of intracellular pH value of  $\Delta$ *MoAE4* strains was significantly enhanced. Bar = 10  $\mu$ m.

Figure S4. The loss of the *MoAE4* gene has a negative effect on sporulation, appressorial development. A Conidia formation. Conidia of the wild type,  $\Delta$ *MoAE4* and  $\Delta$ *MoAE4*/*MoAE4* strains from 3-day-old mycelium grown on oatmeal agar were transferred to cover slips, induced for 6, 12, 24, and 48 h, and observed and counted under a light microscope at room temperature. Bar=50  $\mu$ m. B Observation of conidial germination. Conidial germination was observed on a hydrophobic cover slips under the microscope at 1, 2, and 3 hours post inoculation. Bars = 20  $\mu$ m. C Observation of the formation of appressoria. Appressorial formation was observed on a hydrophobic cover slips under the microscope at 4 and 6 hours per inoculation. Bars = 20  $\mu$ m.

Figure S5. Transcription abundance of *MoCA* during disease development.

Figure S6. Standard curve line and the endogenous H<sub>2</sub>O<sub>2</sub> of strains hyphae. A Standard curve line of absorbance and hydrogen peroxide content. R<sup>2</sup>=0.9955. B DAB staining of hyphae of the wild type, mutant and complementation strains.

Fig S1.

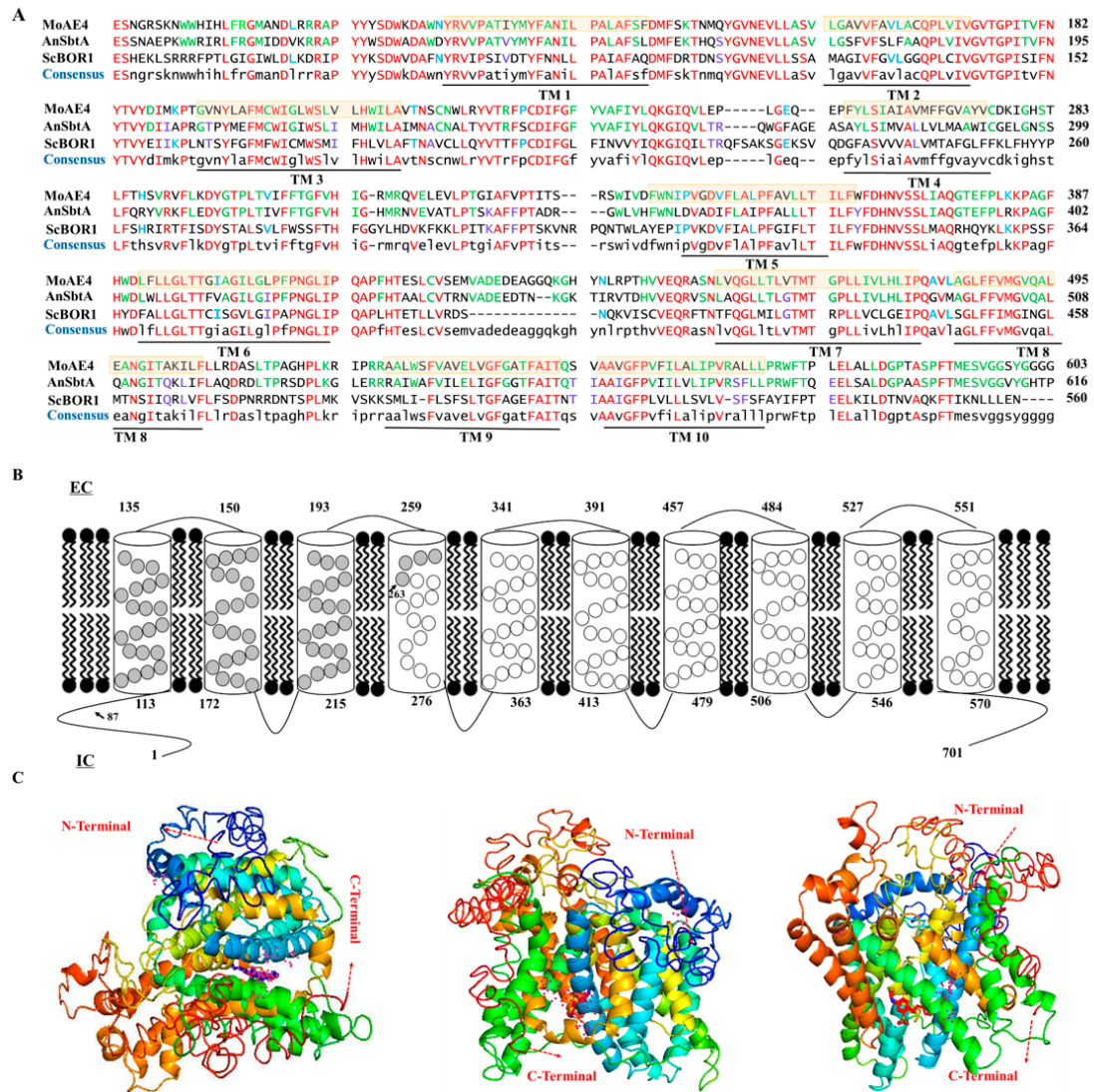


Fig S2.

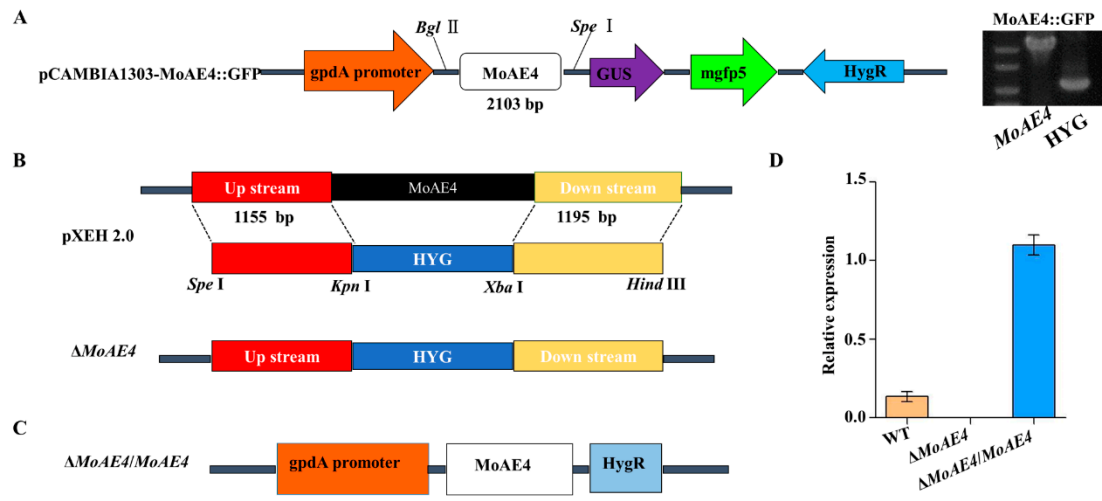


Fig S3.

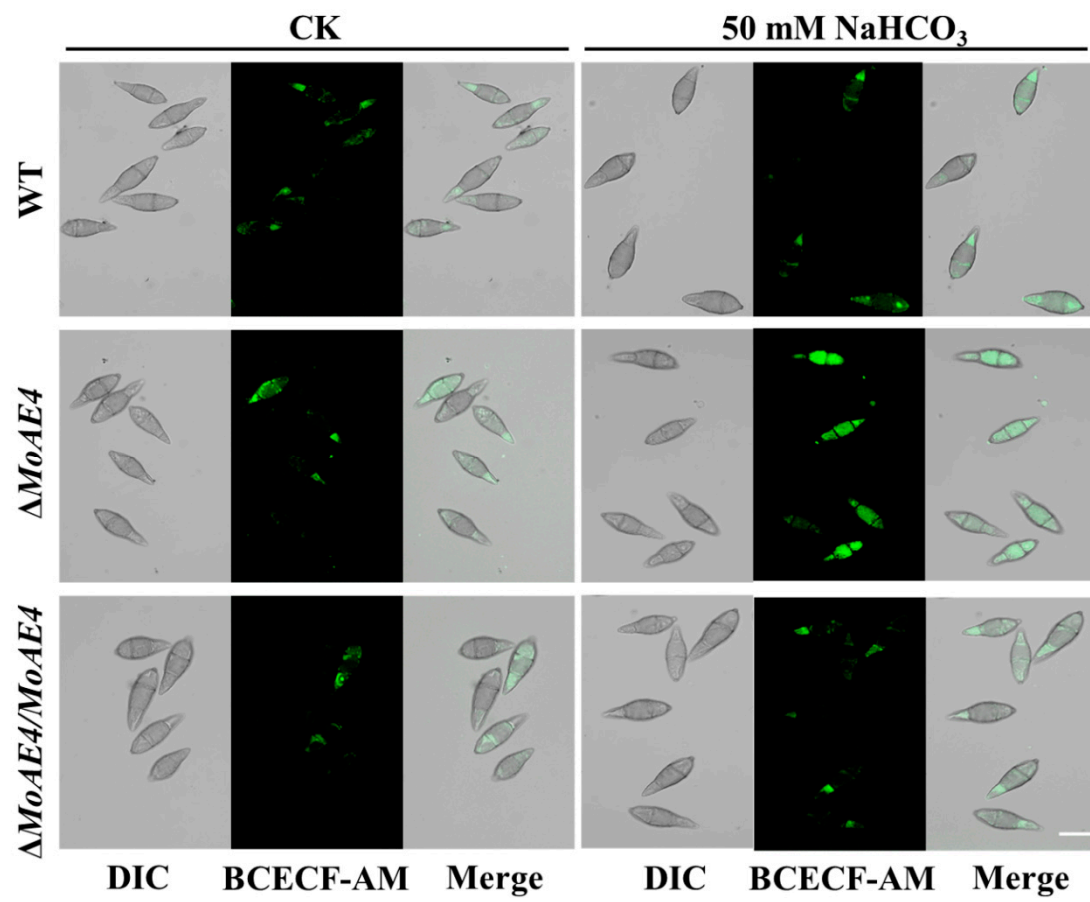


Fig S4.

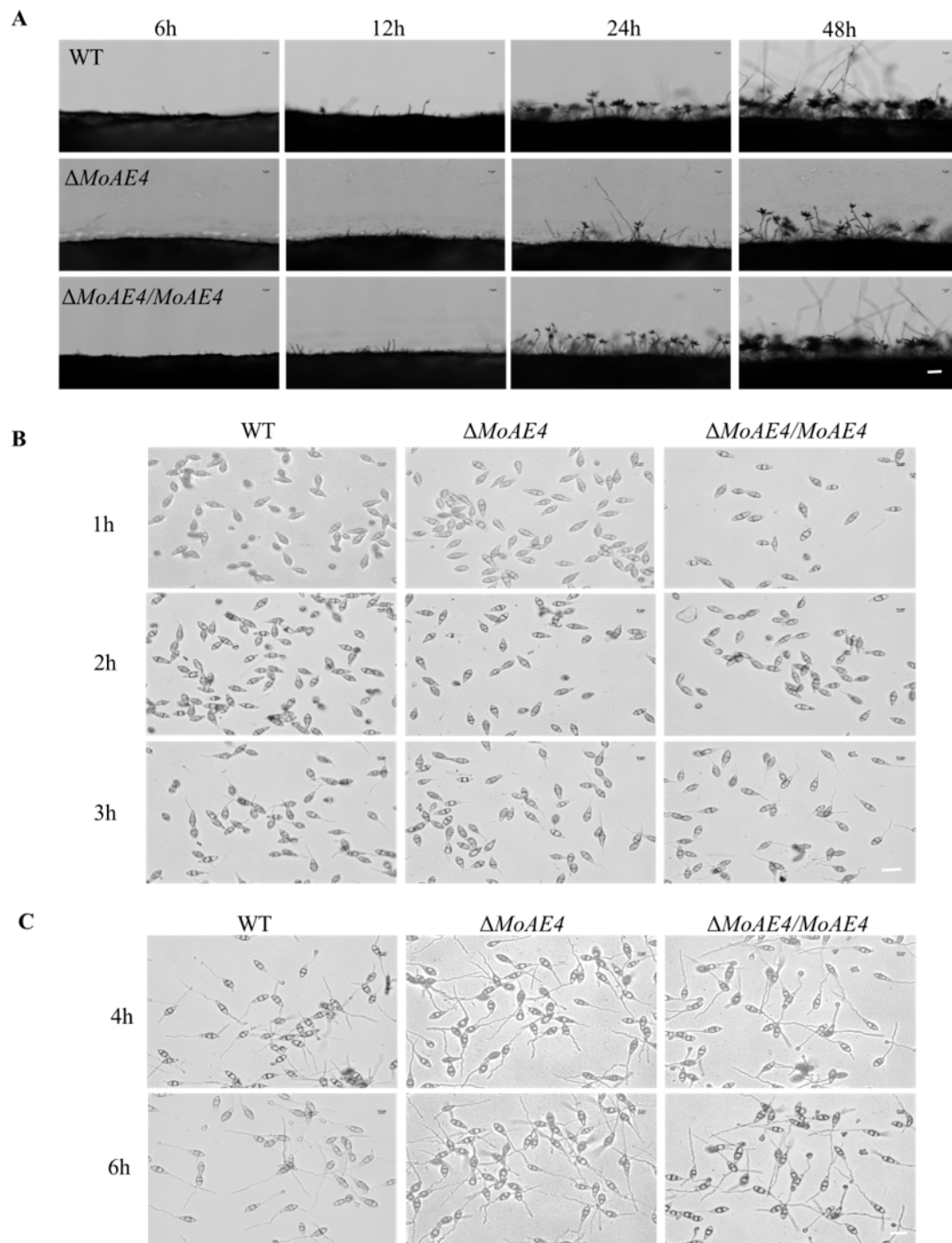


Fig S5.

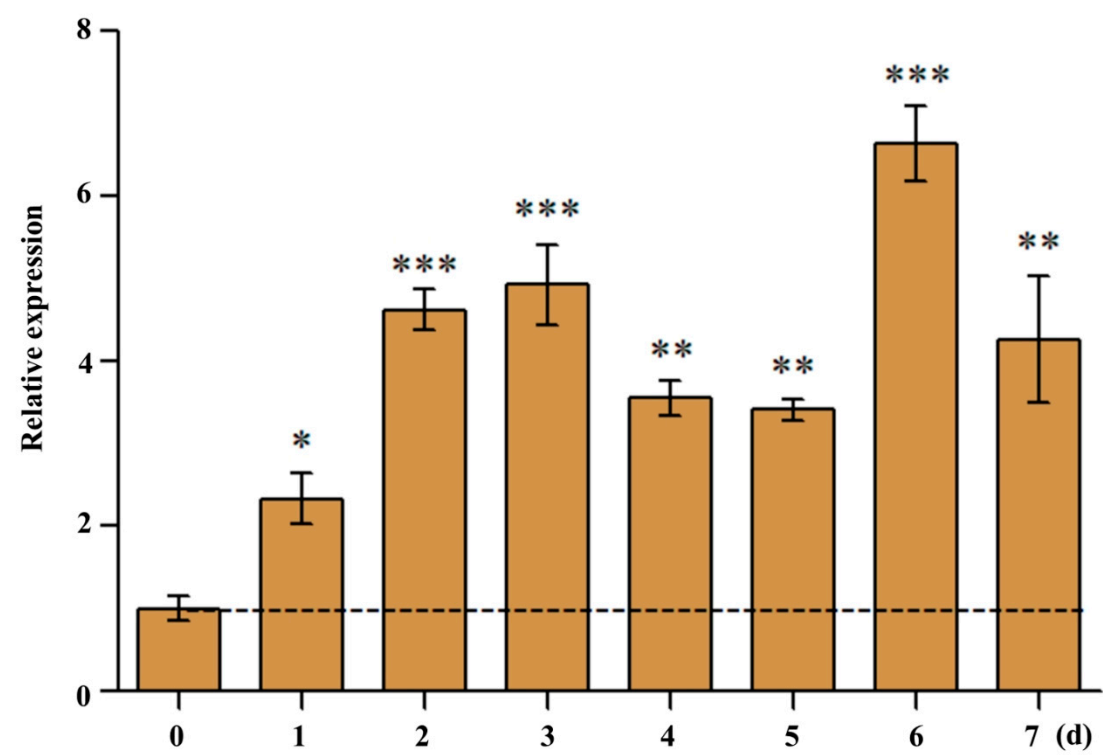


Fig S6.

