

Supplementary materials

Coding region	1 ATGCTCAACAAAGCTGTCCGGGAGCCGGAGAGCTATGAAAAGAGTACAGCCTCTTATCGTAGCTACCTTGCCCCACATTGCGTAACCTGATTTTCGCT	100
ORF	1 ATGCTCAACAAAGCTGTCCGGGAGCCGGAGAGCTATGAAAAGAA.....	45
Coding region	101 GGCCTATAGGGCTCTCTATAAATTCGACGGACGCTGGGCGCCGGTACATACGGAATTGTTTCGCGAGGCGGATTCTACCGACGGACAGAAAGGTTGCGGTCA	200
ORF	46GGCTCTCTATAAATTCGACGGACGCTGGGCGCCGGTACATACGGAATTGTTTCGCGAGGCGGATTCTACCGACGGACAGAAAGGTTGCGGTCA	136
Coding region	201 AGATAAATTCGAAAGAAAATGTTCTGGTAAACGAGGGCATGGTCCACGATGAGCTTGAAATGCTGCAATCACTCCAACATCCCCACATTGTTTCGTTCTG	300
ORF	137 AGATAAATTCGAAAGAAAATGTTCTGGTAAACGAGGGCATGGTCCACGATGAGCTTGAAATGCTGCAATCACTCCAACATCCCCACATTGTTTCGTTCTG	236
Coding region	301 CGACTGGTTGCAATCTAAGGTGAGCAGCTCTCTGTTTGGTCCGGTCGTTGCGAGAGCTCTAACCGTGGACCTAGGACAAATTCATATCGTTACACAGCTA	400
ORF	237 CGACTGGTTGCAATCTAAG.....GACAAATTCATATCGTTACACAGCTA	282
Coding region	401 GCCACCGGTGGCGAGCTGTTTCGACCGGATTTGCGAGTATGGCAAGTTCACCGAGAAAGGATGCGTCGCGAGACCATCCGCCAGGTGCTTGATGCTGTGGACT	500
ORF	283 GCCACCGGTGGCGAGCTGTTTCGACCGGATTTGCGAGTATGGCAAGTTCACCGAGAAAGGATGCGTCGCGAGACCATCCGCCAGGTGCTTGATGCTGTGGACT	382
Coding region	501 ATCTACACAAGCGCAACATTGTTTACCGAGGTCGGCTCTTCTTAATGCATTCCGTGCTCTTACATGTAACCTAACCCGCGGAGAACTTGAACCCGAGAAAC	600
ORF	383 ATCTACACAAGCGCAACATTGTTTACCGAGGTCGGCTCTTCTTAATGCATTCCGTGCTCTTACATGTAACCTAACCCGCGGAGAACTTGAACCCGAGAAAC	430
Coding region	601 TCCTCTACCTCACCCGCGCTGCGACTCTCAACTGGTCTTGGCCGATTTTCGGTATTGCGAAGATGCTGCACAGCCCTTCTGAGGTACTGACCAAGCATGGC	700
ORF	431 TCCTCTACCTCACCCGCGCTGCGACTCTCAACTGGTCTTGGCCGATTTTCGGTATTGCGAAGATGCTGCACAGCCCTTCTGAGGTACTGACCAAGCATGGC	530
Coding region	701 CGGCTCCTTTGGATATGCTGCTCCTGAGGTGATGCTCAAGCAGGGCCACGGCAAGGCTGTCGATATGTTGGTGGCTGGTGTATCACCCTATACCCCTCTA	800
ORF	531 CGGCTCCTTTGGATATGCTGCTCCTGAGGTGATGCTCAAGCAGGGCCACGGCAAGGCTGTCGATATGTTGGTGGCTGGTGTATCACCCTATACCCCTCTA	630
Coding region	801 TGTGGCTACTCCCGCTTCGATCCGAGAACTTGACCGACCTCATCGAAGATGCGGAACAGGCGCGATCATCTTCCACGAGCGGTACTGGCGCGAGCTGT	900
ORF	631 TGTGGCTACTCCCGCTTCGATCCGAGAACTTGACCGACCTCATCGAAGATGCGGAACAGGCGCGATCATCTTCCACGAGCGGTACTGGCGCGAGCTGT	730
Coding region	901 CCCAGGACGCCAAAGATTTCATTCTTACCTCTCTGAATACGGACCCACCAAGCGAGTTACCTCTGAGGAAAGCCCTCAAGCACGATGGCTGACCGGAGAA	1000
ORF	731 CCCAGGACGCCAAAGATTTCATTCTTACCTCTCTGAATACGGACCCACCAAGCGAGTTACCTCTGAGGAAAGCCCTCAAGCACGATGGCTGACCGGAGAA	830
Coding region	1001 GACTGCGAGCGACCGTGACTTGTGCTGAAATCCGACCTACATTGACGCTGCGCGCTCGCGCGGAAATCGAGATCGTCAAGCTTGCCAAACCGTATC	1100
ORF	831 GACTGCGAGCGACCGTGACTTGTGCTGAAATCCGACCTACATTGACGCTGCGCGCTCGCGCGGAAATCGAGATCGTCAAGCTTGCCAAACCGTATC	930
Coding region	1101 GAGTCACTCAAGATGCACGAAGAGGACGGGGATGAGGAGGATATCCCAAGTGGCTGGACATGGGCGAGTCAACCAAAGAGTCAAGTGCAGCGGAGCCAT	1200
ORF	931 GAGTCACTCAAGATGCACGAAGAGGACGGGGATGAGGAGGATATCCCAAGTGGCTGGACATGGGCGAGTCAACCAAAGAGTCAAGTGCAGCGGAGCCAT	1030
Coding region	1201 CAGTGCAGGCAACGATGCGAGTCCGCGCCCTGCGCCACACAAAGAAAGAGTCTGTCCGCGCTGCTCGCGGTGCTATTTTCGCTGAAGTTGTTCTGGC	1300
ORF	1031 CAGTGCAGGCAACGATGCGAGTCCGCGCCCTGCGCCACACAAAGAAAGAGTCTGTCCGCGCTGCTCGCGGTGCTATTTTCGCTGAAGTTGTTCTGGC	1130
Coding region	1301 TAAGGTCCTGAGCAGAAAGGAGACTGAGGAGCGGGAGAAAGTTGAACGTGAAGCTCGCGAAAAGGCTGCTTCGCTGCTAG	1379
ORF	1131 TAAGGTCCTGAGCAGAAAGGAGACTGAGGAGCGGGAGAAAGTTGAACGTGAAGCTCGCGAAAAGGCTGCTTCGCTGCTAG	1209

Figure S1. Genomic DNA sequence (coding region) and open reading frame of the PiCaMK1 gene. The underlined sequences indicate introns in the PiCaMK1 gene.

Table S1. Primers applied for gene cloning, knockout, and complementation in the present study.

Primer Name	Sequence (5'→3')	Purpose
PiCaMK1-F	CTCGTATTTCTCTAGTCGC	PiCaMK1 cloning
PiCaMK1-R	AGTACAAGGCAGGATAGAC	PiCaMK1 cloning
PiCaMK1-L-F	TAACGTTCCCGTTGTGGCT	Amplification of left arm
PiCaMK1-L-R	CTAGCTAGCGTGACTAGTCACCATTTCAAGCTCATCGTG	Amplification of left arm
^a Hyg-F	GTGACTAGTCAGAAAGATGATTTGAAGGAGC	^a Hyg cloning
^a Hyg-R	CTAGCTAGCAAAGAAGGATTACCTCTAAACAAG	^a Hyg cloning
PiCaMK1-R-F	GTGACTAGTCAGTCACGCTAGCTAGGCGAAGACTTGAAACCCGA	Amplification of right arm
PiCaMK1-R-R	GCGATGATGGCTTGAATAATTG	Amplification of right arm
PiCaMK1- ^b Ko-F	CATTGTTTCGTTTCGTCGACT	Mutant validation by PiCaMK1 amplification
PiCaMK1- ^b Ko-R	GAATGCATTAAAGACCGACCT	Mutant validation by PiCaMK1 amplification
PiCaMK1- ^c Diag-F	GTACAGCCTCCTTATCGTAG	Mutant validation by ^d L-H-R amplification
PiCaMK1- ^c Diag-R	CATGCTGGTCAGTACCTCA	Mutant validation by ^d L-H-R amplification
PiCaMK1-COM-F	CCCTCGAGGCAAGAAGATCTACGTGCAG	Complementation plasmid construction
PiCaMK1-COM-R	GGACTAGTGATGTCCATTGCCCATTCT	Complementation plasmid construction
^e Sur-F	CTAGAGACTAGATCTGTGCC	^e Sur gene cloning
^e Sur-R	AACTTAACCGTGCAGGCCAT	^e Sur gene cloning
PiCaMK1-Probe-F	TGCAATCACTCCAACATCC	Probe yield for southern blot
PiCaMK1-Probe-R	GGCGGTTAGTTACATGTCA	Probe yield for southern blot

Note: ^aHyg-F/R indicates primers to amplify *hygromycin B* (*hyg*)-resistance cassette. ^bPiCaMK1-Ko-F/R indicates primers to validate knockout fragments. ^cPiCaMK1-Diag-F/R indicates primers to amplify diagnostic fragment. ^dL-H-R indicates the knockout fragment that contains left arm, *hyg*-resistance cassette and right arm. ^eSur-F/R indicates primers to amplify *Sur*-resistance gene that encodes chlorimuron ethyl-degrading enzyme. The underlined sequences indicate restriction sites in the primers (i.e., GCTAGC: *Nhe* I, ACTAGT: *Spe* I, and CTCGAG: *Xho* I).

Table S2. Fungal CaMK genes used in multiple sequence alignments.

Genus and Species	CaMK Gene Accession Number
<i>Penicillium italicum</i>	The present study

<i>Penicillium digitatum</i>	XP_014532050
<i>Penicillium expansum</i>	XP_016598664
<i>Penicillium brasilianum</i>	CEO60329
<i>Penicillium roqueforti</i>	CDM34428
<i>Aspergillus welwitschiae</i>	XP_026623611
<i>Aspergillus flavus</i>	KOC14811
<i>Aspergillus taichungensis</i>	PLN83689
<i>Aspergillus nidulans</i>	XP_660016
<i>Neurospora crassa</i>	AAL14118
<i>Saccharomyces cerevisiae</i>	BAA14383
<i>Saccharomyces cerevisiae</i>	BAA14384

Table S3. Fungal CaMK genes used in phylogenetic tree construction.

Genus and Species	CaMK Gene Accession Number
<i>Penicillium italicum</i>	The present study
<i>Penicillium digitatum</i>	XP_014532050
<i>Penicillium expansum</i>	XP_016598664
<i>Penicillium roqueforti</i>	CDM34428
<i>Penicillium coprophilum</i>	OQE45907
<i>Penicillium arizonense</i>	XP_022485550
<i>Penicillium subrubescens</i>	OKP13003
<i>Aspergillus nidulans</i> FGSC A4	XP_660016
<i>Aspergillus flavus</i> AF70	KOC14811
<i>Aspergillus mulundensis</i>	XP_026603689
<i>Aspergillus welwitschiae</i>	XP_026623611
<i>Aspergillus calidoustus</i>	CEL09411
<i>Aspergillus taichungensis</i>	PLN83689
<i>Aspergillus nomiae</i> NRRL 13137	XP_015409963
<i>Aspergillus japonicus</i> CBS 114.51	XP_025523846
<i>Aspergillus indologenus</i> CBS 114.80	PY134311
<i>Aspergillus brunneoviolaceus</i> CBS 621.78	XP_025445091
<i>Aspergillus costaricensis</i> CBS 115574	XP_025544052
<i>Neurospora crassa</i>	AAL14118

Table S4. Primers used in RT-qPCR.

Gene ID	Gene Function Annotation	Primer	Sequence (5'→3')
EKV13547	DNA primase	F	GAAGGTCCCCGAGTTGATCG
		R	AGCCACCACTGCAGACATAC
EKV11776	DNA replication licensing factor Mcm6	F	GATGCTCGCGGTATGTTCCA
		R	TGGCTTCGTGAATAGCGACC
EKV18089	DNA polymerase δ	F	GAGAAGGACCAGCAATGGGA
		R	CCAGCGAATGGCAAGGACAT
EKV08814	DNA polymerase ϵ	F	TTTCCGTTGACCCTACTGC
		R	CTCCACGATTTGTGCCCTTA
EKV11198	DNA replication licensing factor Mcm3	F	CCGTGGCAAGAATGTGGA
		R	CGAAGAGCAGAATAGGTGGC
EKV17606	Replication factor-a	F	CCCATTCCAAATTGACGG
		R	ACTTCTTGACTTCGCACTCG
EKV16128	DNA replication licensing factor Mcm2	F	GCACTTGTTGCACATTGACCA
		R	TGCCGATGAACGAATCCACA
EKV11033	Nuclear condensing complex	F	ATTGCGAGTGCTACGGGTGT
		R	GCATTTCCGGCTAGAGGCT
EKV17483	Cell-cycle checkpoint protein kinase	F	CGAATGGTTTCCGTCAGC
		R	GAGTCACCGAGGCGTCTTT
EKV19093	Nuclear condensin complex Smc2	F	ATGGAACAGGAACACGAG
		R	GCTCTGTCAAGTTGCGTAGG
EKV04214	Replication checkpoint protein	F	GTCGCATTGCAGCGTTTG
		R	TCGGGTAGGAGATGTTAGGTGT
EKV16186	Mitotic spindle checkpoint protein (Mad2)	F	CGCAGTTGAAGGAATGGATG
		R	GGTTAGTTTCGGACTCGGATG
EKV16749	Condensin complex subunit 1	F	GCCAAGTCAAGGTGAAGGG
		R	GAAGAACATGCGAGCCAGAT
EKV04683	Xanthine dehydrogenase (oxidase)	F	CGTCTTCATCTCCGAGACCG
		R	ATATGGCGTAGCCGTTGAGG
EKV19574	Ribonucleoside-diphosphate reductase	F	ATCAGGGTGGTAACAAGCG
		R	GTCACAAAGCGTAGAAGAGGT
EKV15599	Ribonucleotide reductase RnrA	F	AGCGACCACGAATCAACC
		R	GGAGAATGTGAGACCAGGCA

EKV16890	DNA-directed RNA polymerase III subunit Rpc34	F	TGAAGAACGGCATGACCGAA
		R	GAAGTACTCGCAGGTCTCGG
EKV07940	Adenylate cyclase	F	GACTTCTTTGAACCTCGCC
		R	CAACTTGCCAATCTGAGCC
EKV07761	Uracil phosphoribosyltransferase	F	CATTCCAAGGACACAACGCC
		R	CGGATCGGAGAATTGGCACT
EKV07371	Formamidopyrimidine-DNA glycosylase (H2TH domain)	F	AGGTGCAACTAGTGCCGTTG
		R	CCGTTTGGAATTGGCTGGTG
EKV15299	DNA repair protein RAD1	F	GGGTAAAGTACCCAGCTACA
		R	GAGTGTGACTGTCCGAGG
EKV17484	Phosphatidylinositol 4-kinase (STT4)	F	ACGGAGTATTGCTGGTGAG
		R	GCAACGCAACCAAGTAGTGA
EKV05405	Cytochrome c oxidase assembly protein	F	ATCGGATGTCCTCCCTTGGA
		R	CCTGGCGTGACACTGTATGT
EKV18906	F ₁ /F ₀ -ATP synthase	F	GGAGGGCCACAATGGAGTTT
		R	GGAGGTTGGGATTAGGTGGC
EKV07272	Aldehyde dehydrogenase	F	CATGGGTGGCACTATGGAT
		R	CAAGATGGGGATGAAGGGA
EKV06483	Cysteine synthase	F	CTGTCAAAACGGCGAGGAA
		R	TCACAGCCCCACCAACA
EKV18475	Assimilatory sulfite reductase	F	GCCAGAAAGTGACCCCTACC
		R	GACTTGGAGGGCAGCTTCAT
EKV04855	Oligo-1,6-glucosidase (α -amylase or maltase)	F	TGGTTCAAAGAGTCCCGCTC
		R	TTCTTCTGTTGCCTCGTCCC
EKV05685	Glucosamine-6-phosphate deaminase	F	TACTTGTGCAGCGTCATCGT
		R	TCAGTGGGTGCTTTTCTCCG
EKV11299	NADH-cytochrome b ₅ reductase	F	GTGGGTAGTCTGGCTCCAAG
		R	ATGTTCTTCTCGGCACCCTC
EKV15950	Chitin synthase	F	AGCTCTTTCGGTGGTTCGAG
		R	CAACCCTACCAGCACTCCAG
EKV13467	DnaJ-related protein	F	TTACGATTCTTGGTCGCGCT
		R	TGACGCGGACTTCGCTATAC
EKV14522	Polyubiquitin binding protein	F	TCAGCTGGACAAGACGCAAT
		R	AGACATTGTGACCGTGACCC
EKV14057	HSP90	F	TTCTACTCCGCCTACCTGG
		R	CCTTGAGGGTGAAAGTGCC
EKV13033	HSP70	F	GAGTTCAAGCGCAAGCACAA
		R	AGAGAGAGTTCGCTTGGCAC
EKV13686	Nuclear protein localization protein	F	AGTCAGGTGCTCAACGACTG
		R	AGTGTACACCGTCGACTTC
EKV17406	Catabolic 3-dehydroquinase	F	AGCTATGGTGCCGTCTTG
		R	GGATTGATGATGATCCCGTC
EKV18650	Phospholipase D	F	CACTACCAGGATCGACTCGC
		R	TGATGGCGCAATATGCGTTG
PHI26_NewGene_31	Vacuolar protein sorting-associated protein (VHS domain)	F	ATATCTGTACCGGTGCTGCG
		R	TGGGCTGAACGCTCTTTGAT
PHI26_NewGene_32	Vacuolar protein sorting-associated protein (FYVE-like protein)	F	AGTGTGCCTCAACTCCTTCG
		R	GAAGGCAGTCCTACATCGCA
Internal reference	β -actin	F	TTACCTGATGAAGATCCTCGC
		R	TCTGGATCTCCTGCTCGAAG