The forkhead box gene, *MaSep1*, negatively regulates stress tolerances to UV irradiation and heat shock and is required for microcycle conidiation in *Metarhizium acridum*

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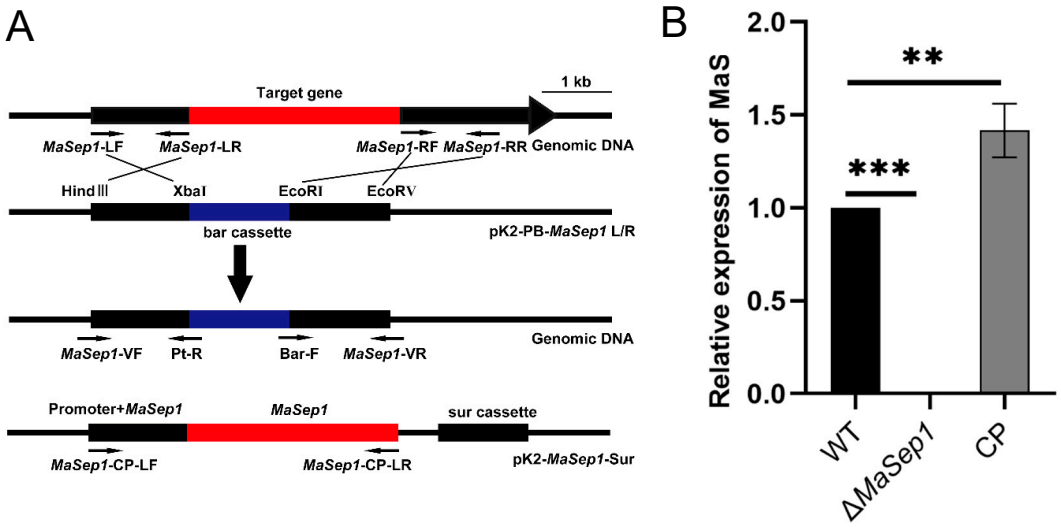


Figure S1. The disruption and complementation of *MaSep1*. (A)The knockout and complement schematic diagram of *MaSep1*. (B) Transcription level analysis of *MaSep1* in WT, Δ*MaSep1* and CP strains. *MaSep1* expression in WT as control.

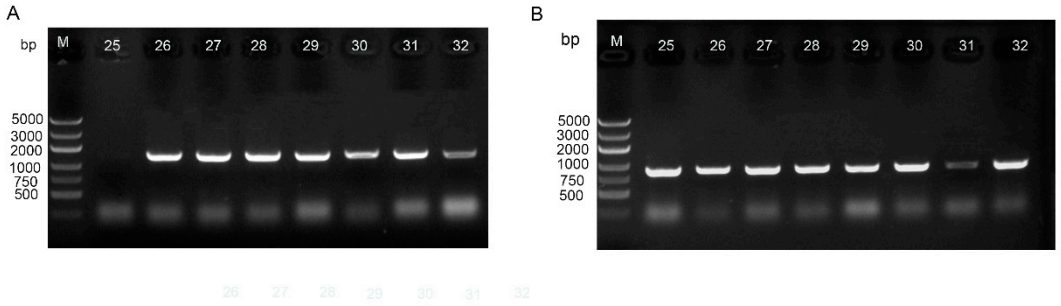


Figure S2. PCR was used to verify the disruption of *MaFkh2*. (A) Fkh2-VF/Pt-R was used to verify the left arm of Δ*MaFkh2*. (B) Fkh2-VR/Bar-F was used to verify the right arm of Δ*MaFkh2*. M: DNA marker. Lanes 25-32: different mutants. Δ*MaFkh2*-27# were used for observation of conidiation pattern.

Table S1. Primers used in this work.

Primers	Sequences (5′- 3′)	Remarks
MaSep1-LF	CTGGCGAAAGTGGTGAATCT	Used to clone the 5′ end of MaSep1
MaSep1-LR	GGTATGACTGCCGAGTGATGT	
MaSep1-RF	GATTTGCCACGGTCTGTTCT	Used to clone the 3′ end of MaSep1
MaSep1-RR	CTCCCGCATGAGGATCTACT	
Pt-R	CAGCCAAGCCCAAAAAGTG	
Bar-F	GCTCTACACCCACCTGCT	Used for screening the MaSep1-disruption transformants
MaSep1-VF	TCTGGAACGTGGAACCCG	
MaSep1-VR	CTTTGCCAACGCCCATAA	
MaSep1-CPF	TGGGCAATGGTCTCCTCTC	Used to form pK2- MaSep1-EGFP-SUR vector
MaSep1-CPR	GAAGGCGGTAGAATAGCTCC	
CP-VF	CGATCCCAATCTCAGACAAC	Used for screening the MaSep1-complement transformants
EGFP-VR	CGATGCGGTTCACCAGG	
MaSep1-qF	AATGGACGACAGTGGTTA	Used to analyze the expression of MaSep1 by qRT-PCR (E=114%)
MaSep1-qR	CGATCAGCCTCAGAAGTA	
MaFkh2-LF	TTTGCCGAGTTGCTGATG	Used to clone the 5’ end of MaFkh2
MaFkh2-LR	CAAGCGTAGCGTGGATGT	
MaFkh2-RF	AGGTGCGGTTGGTTCGTC	Used to clone the 3’ end of MaFkh2
MaFkh2-RR	CTGCTTCAATGCGGAGGG	
MaFkh2-VF	TGGGATTGAATGGGTGTACG	Used for screening the MaSep1-disruption transformants
MaFkh2-RR	GGTGACAAACCCGAGCA	
Rad2-QF	AGGAAGTGGTAGTGGCAACG	Used to verify the transcriptional expression of genes in NER pathway(E=103%)
Rad2-QR	GAGCTGCTGAAACTGAGGGT	
Rad3-QF	ATCACTCCTGACGGCCTAGT	(E=114%)
Rad3-QR	CTTCTGAGACTTTGCCCCGT	
Rad4-QF	AAATGCGAAGGAAGCAGGGA	(E=102%)
Rad4-QR	TCGAACGAGTTGCTGCAGAT	
Rad10-QF	CAGCCCGTACCCCAAAGAAT	(E=106%)
Rad10-QR	GCAGGTTGTGAGTCCCATGA	
Rad14-QF	ACATGATGCTGTTCCTGCGA	(E=116%)
Rad14-QR	TCTGTTCGAGTCTTGCGCTT	
Rad16-QF	AAACACGACTTTTGCCGAGC	(E=109%)
Rad16-QR	ATGCGTTGTCTGAACGGAGT	
Rad23-QF	AGGAAGTGGTAGTGGCAACG	(E=105%)
Rad23-QR	GAGCTGCTGAAACTGAGGGT	
Rad25-QF	CAAGAGGTCACGCACTCCTT	(E=106%)
Rad25-QR	CCACTCTTGGCTCGACCATT	
Hsp40-1-QF	GGCGAAGCGGATCAATTTCC	Used to verify the transcriptional expression of genes (E=107%)
Hsp40-1-QR	CATACCTTCGCCAGCGATCT	

qHSP40-2-F	CACGACCGAGTTTCAGTGGA	(E=106%)
qHSP40-2-R	TGAGAGTGACAGTCGTTGGC	
qHSP70-1-F	TGTCGATTTGGGCACCACTT	(E=105%)
qHSP70-1-R	GTAGACAATGGCGGTTGGGA	
qHSP70-2-F	GCTTGATGTTGCCCCTCTCT	(E=104%)
qHSP70-2-R	TGACGCTCACCCTCAAAGAC	
qHSP70-3-F	AGTCCTACATTGGCCGTGTG	(E=103%)
qHSP70-3-R	CTTAAGGGCAAGCTCCTGCT	
qHSP90-F	AAGAAGGTTGAGGCTGACGG	(E=103%)
qHSP90-R	GAGCTTGTGAATGCGCTCAG	
Cat1-QF	GATACGGTAACAGCAATGG	Used to verify the transcriptional levels of
Cat1-QR	TCGGTCAAGTCAGATACG	genes related to ROS scavenging (E=103%)
Cat2-QF	TTCTCGCCATCCAATCTC	(E=92%)
Cat2-QR	TCGTCGTTATTCCGTCTC	
Cat3-QF	CCTCTACTCTTCATACCTTGT	(E=110%)
Cat3-QR	GTCGCCATTCTCATTCAC	
Cat4-QF	AAGTTCCCGTTGTTCATC	(E=112%)
Cat4-QR	TTCCTGGTGAGTTGAGAG	
Pod-QF	TGTCGTGTCCAACCTGTACG	(E=108%)
Pod-QR	CGCTGTTGGCGATAATGACG	
Sod1-QF	CATGCCTATTACCTACAGTA	(E=102%)
Sod1-QR	CTTCCAGTTGATGACCTT	
Sod2-QF	AGACAAGGACACCAAGAC	(E=108%)
Sod2-QR	GGAGGCGTAGTTGAAGAT	
Sod4-QF	GGTCAAAGCTGTTGCCGTTC	(E=103%)
Sod4-QR	CGCCAAAGGTGTGAATGTGG	
MnSod-QF	CTCCTCTTCTGAACTTCC	(E=111%)
MnSod-QR	CCGAAATCCTCATTGATG	
Gpx-QF	TCGCTGACTACAAGGGCAAG	(E=105%)
Gpx-QR	CTGCATGATGGGGAAGCTGA	

Table S2. Description of these DEGs

Gene ID	log2 (8 h)	log2 (10 h)	log2 (12 h)	Up and Down regulation	GeneBank Description
MAC_00171	1.354849	1.747488	1.254830	Up	acetylcholinesterase precursor
MAC_00187	2.590361	3.037864	5.004447	Up	Maleylacetate reductase, putative
MAC_01539	1.076171	1.318690	1.259298	Up	monooxygenase, putative
MAC_02330	1.722911	1.504425	1.805380	Up	hypothetical protein
MAC_03141	-1.893041	-2.144658	-1.710290	Down	forkhead box protein L2
MAC_04376	4.762802	3.654373	2.797149	Up	hydrophobin
MAC_05784	1.135701	1.550181	1.043445	Up	lipase/esterase family protein, putative
MAC_06623	1.586745	2.585150	2.364665	Up	cytochrome P450 phenylacetate 2-hydroxylase, putative
MAC_07011	1.144803	1.678641	1.240947	Up	dienelactone hydrolase family protein
MAC_07499	2.413438	2.860290	2.764313	Up	hypothetical protein
MAC_08195	1.599824	2.234038	2.051539	Up	zinc-binding oxidoreductase ToxD, putative
MAC_08514	1.173049	1.118032	1.409213	Up	flotillin domain containing protein
MAC_08656	1.448510	2.425115	2.054106	Up	putative glyoxal oxidase precursor
MAC_00180	6.156817	6.210993	0.000000	Up	FAD dependent oxidoreductase family protein
MAC_04005	1.227009	1.320558	0.000000	Up	hypothetical protein
MAC_04635	1.491851	1.189354	0.000000	Up	glutathione-dependent formaldehyde-activating GFA
MAC_05216	1.123938	1.663678	0.000000	Up	hypothetical protein
MAC_06624	1.123938	1.663678	0.000000	Up	DUF636 domain protein
MAC_05447	1.045916	0.000000	1.242190	Up	hypothetical protein
MAC_06937	1.483241	0.000000	2.084351	Up	hypothetical protein
MAC_09524	2.440888	0.000000	2.464496	Up	glutathione S-transferase
MAC_09703	2.753015	0.000000	2.191168	Up	FAD binding domain-containing protein
MAC_00186	0.000000	4.018073	2.672235	Up	C6 transcription factor, putative
MAC_00584	0.000000	1.624207	1.322741	Up	hypothetical protein
MAC_00953	0.000000	1.456978	1.548152	Up	adhesin protein Mad2
MAC_01348	0.000000	1.531687	1.241309	Up	RNA binding protein MSSP-2
MAC_04426	0.000000	1.427538	1.217620	Up	hypothetical protein
MAC_04466	0.000000	2.149804	2.032492	Up	phosphoglycerate mutase family protein, putative
MAC_05897	0.000000	3.785451	3.232837	Up	hypothetical protein

MAC_06625	0.000000	2.000606	1.649035	Up	MFS transporter (Mch2), putative
MAC_06626	0.000000	1.777548	2.138858	Up	hypothetical protein
MAC_07182	0.000000	2.129551	1.360725	Up	hypothetical protein
MAC_07330	0.000000	3.364879	2.168779	Up	Hydrophobin-like rotein ssgA
MAC_07839	0.000000	1.741250	1.222242	Up	hypothetical protein
MAC_08196	0.000000	2.840194	2.490713	Up	hypothetical protein
MAC_08197	0.000000	2.627236	2.391814	Up	MFS monocarboxylate transporter, putative
MAC_08198	0.000000	2.722816	3.352276	Up	pyoverdine/dityrosine biosynthesis protein, putative
MAC_08199	0.000000	2.753592	2.452552	Up	aldehyde dehydrogenase
MAC_08200	0.000000	2.729319	2.409516	Up	tryptophanyl-tRNA synthetase
MAC_08201	0.000000	3.119665	3.269302	Up	hypothetical protein
MAC_08795	0.000000	1.050519	2.024778	Up	hypothetical protein
MAC_09015	0.000000	1.631960	1.308286	Up	integral membrane protein, putative
MAC_09268	0.000000	-1.296967	-1.155283	Down	delta 8-(E)-sphingolipid desaturase, putative
MAC_09686	0.000000	2.006243	1.626963	Up	hscarg dehydrogenase, putative
MAC_00623	1.179172	0.000000	0.000000	Up	beta-glucosidase
MAC_01183	-1.311523	0.000000	0.000000	Down	dihydroxyacetone kinase
MAC_01993	1.097883	0.000000	0.000000	Up	Superoxide dismutase
MAC_03702	-1.454305	0.000000	0.000000	Down	hypothetical protein
MAC_03703	-1.001611	0.000000	0.000000	Down	cryptochrome-2
MAC_05729	1.080103	0.000000	0.000000	Up	hypothetical protein
MAC_05837	2.679246	0.000000	0.000000	Up	GA4 desaturase
MAC_07788	1.149852	0.000000	0.000000	Up	hypothetical protein
MAC_08031	1.287996	0.000000	0.000000	Up	hypothetical protein
MAC_08505	1.206278	0.000000	0.000000	Up	hypothetical protein
MAC_00652	0.000000	-1.169188	0.000000	Down	hypothetical protein
MAC_00672	0.000000	1.277059	0.000000	Up	hypothetical protein
MAC_01449	0.000000	-1.072446	0.000000	Down	hypothetical protein
MAC_02060	0.000000	1.667380	0.000000	Up	hypothetical protein
MAC_02061	0.000000	1.785658	0.000000	Up	GABA permease, putative
MAC_02166	0.000000	1.451026	0.000000	Up	hypothetical protein
MAC_02311	0.000000	-1.562748	0.000000	Down	STF2-like protein
MAC_02602	0.000000	2.484354	0.000000	Up	hypothetical protein
MAC_02867	0.000000	1.793921	0.000000	Up	phosphotransferase enzyme family protein
MAC_03001	0.000000	1.810703	0.000000	Up	ammonium permease MepC
MAC_03043	0.000000	1.300188	0.000000	Up	hypothetical protein

MAC_03050	0.000000	1.070603	0.000000	Up	CFEM domain protein, putative
MAC_03761	0.000000	1.573182	0.000000	Up	cystathionine beta-lyase
MAC_03899	0.000000	1.020697	0.000000	Up	small nucleolar ribonucleoprotein complex subunit Utp15, putative
MAC_04216	0.000000	-1.204446	0.000000	Down	YT521-B-like splicing factor, putative
MAC_04372	0.000000	1.272469	0.000000	Up	ADP-ribose pyrophosphatase
MAC_04525	0.000000	1.742724	0.000000	Up	alpha-glucosidase
MAC_04532	0.000000	-1.817648	0.000000	Down	Quinate permease
MAC_04599	0.000000	1.414678	0.000000	Up	Alternative oxidase
MAC_04678	0.000000	1.086755	0.000000	Up	CipC1 protein, concanamycin induced protein C
MAC_04767	0.000000	1.725920	0.000000	Up	L-PSP endoribonuclease family protein Brt1
MAC_04883	0.000000	1.002398	0.000000	Up	hypothetical protein
MAC_04947	0.000000	1.217463	0.000000	Up	hypothetical protein
MAC_05098	0.000000	1.098380	0.000000	Up	phosphotransferase enzyme family protein
MAC_05253	0.000000	1.133223	0.000000	Up	hypothetical protein
MAC_05446	0.000000	1.165716	0.000000	Up	hypothetical protein
MAC_05716	0.000000	1.847632	0.000000	Up	tyrosinase, putative
MAC_05756	0.000000	1.443539	0.000000	Up	putative zinc finger protein odd-paired-like (opl)
MAC_05828	0.000000	1.577895	0.000000	Up	Cupin family protein
MAC_05875	0.000000	1.353232	0.000000	Up	serine family amino acid catabolism-related protein
MAC_05901	0.000000	1.058562	0.000000	Up	DUF1275 domain protein
MAC_06174	0.000000	1.101550	0.000000	Up	2-deoxyglucose-6-phosphate phosphatase
MAC_06221	0.000000	1.257796	0.000000	Up	WD-repeat containing protein slp1
MAC_06296	0.000000	1.998760	0.000000	Up	NlpC/P60-like cell-wall peptidase
MAC_06320	0.000000	1.112956	0.000000	Up	aspartic proteinase
MAC_06597	0.000000	1.485936	0.000000	Up	hypothetical protein
MAC_06620	0.000000	1.061755	0.000000	Up	zinc-binding dehydrogenase
MAC_06731	0.000000	-1.093226	0.000000	Down	ThiJ/PfpI family protein
MAC_06735	0.000000	-1.067103	0.000000	Down	arrestin
MAC_06779	0.000000	1.123749	0.000000	Up	NADPH-P450 reductase
MAC_07018	0.000000	-1.943428	0.000000	Down	extracellular serine-rich protein
MAC_07302	0.000000	4.444096	0.000000	Up	hypothetical protein
MAC_07323	0.000000	1.084462	0.000000	Up	ThiJ/PfpI family protein
MAC_07691	0.000000	1.136727	0.000000	Up	Hsp70 family chaperone
MAC_08480	0.000000	1.325977	0.000000	Up	copper amine oxidase 1

MAC_08916	0.000000	1.125432	0.000000	Up	cell surface protein
MAC_09371	0.000000	-1.260252	0.000000	Up	reverse transcriptase, putative
MAC_09485	0.000000	1.744783	0.000000	Up	hypothetical protein
MAC_09504	0.000000	1.377220	0.000000	Up	putative glucoamylase GMY2
MAC_00176	0.000000	0.000000	1.074034	Up	DUF895 domain membrane protein
MAC_01184	0.000000	0.000000	-1.651264	Down	ribose 5-phosphate isomerase
MAC_02150	0.000000	0.000000	1.268432	Up	peptidase family T4 protein
MAC_02174	0.000000	0.000000	1.087355	Up	mitochondrial cytochrome b2, putative
MAC_02548	0.000000	0.000000	1.297516	Up	hypothetical protein
MAC_02717	0.000000	0.000000	1.432964	Up	tyrosinase 2
MAC_02882	0.000000	0.000000	1.182703	Up	glycosyltransferase
MAC_03048	0.000000	0.000000	1.399847	Up	Fungal Zn binuclear cluster domain containing protein
MAC_04410	0.000000	0.000000	2.462847	Up	lysine amidinotransferase
MAC_04676	0.000000	0.000000	1.272493	Up	GNAT family acetyltransferase, putative
MAC_04833	0.000000	0.000000	1.191128	Up	hypothetical protein
MAC_05187	0.000000	0.000000	1.118570	Up	L-asparaginase, putative
MAC_05621	0.000000	0.000000	1.486234	Up	hypothetical protein
MAC_05709	0.000000	0.000000	1.930143	Up	uracil permease, putative
MAC_05902	0.000000	0.000000	1.044516	Up	carboxyphosphonoenolpyruvate phosphonomutase, putative
MAC_06568	0.000000	0.000000	2.366885	Up	integral membrane protein, putative
MAC_06676	0.000000	0.000000	-3.475582	Down	hypothetical protein
MAC_06850	0.000000	0.000000	1.081324	Up	cell wall protein
MAC_07250	0.000000	0.000000	1.333144	Up	cysteine synthase A
MAC_07741	0.000000	0.000000	1.323303	Up	putative cytochrome P450 3A7
MAC_08520	0.000000	0.000000	1.119107	Up	hypothetical protein
MAC_08796	0.000000	0.000000	1.755655	Up	exo-1,3-beta-D-glucanase
MAC_08826	0.000000	0.000000	1.148336	Up	serine/threonine-protein kinase Sgk2
MAC_09768	0.000000	0.000000	2.024539	Up	Amino-acid permease inda1

Table S3. 105 putative target genes of MaSep1.

Gene ID	Score	Predicted sequence
MAC_00171	10.83105	ATCAACAA
MAC_00187	9.870977	GTCAACAA
MAC_01539	10.88136	GTAAACAA
MAC_02330	9.492452	TTAAACAA
MAC_04376	9.775361	GAAAACAA
MAC_05784	9.775361	GAAAACAA
MAC_06623	9.203494	CAAAACAA
MAC_08195	9.203494	CAAAACAA
MAC_08514	9.328139	ATAAATAA
MAC_08656	9.299111	CTCAACAA
MAC_04635	10.73543	AAAAACAA
MAC_05216	9.775361	GAAAACAA
MAC_06624	9.203494	CAAAACAA
MAC_05447	10.73543	AAAAACAA
MAC_06937	9.775361	GAAAACAA
MAC_09524	9.725044	AACAACAA
MAC_09703	10.83105	ATCAACAA
MAC_00186	9.701628	ATAAACAG
MAC_00584	9.203494	CAAAACAA
MAC_00953	10.73543	AAAAACAA
MAC_01348	10.83105	ATCAACAA
MAC_04426	9.991104	ATAAACAT
MAC_05897	9.299111	CTCAACAA
MAC_06625	9.245241	ACAAACAA
MAC_06626	9.299111	CTCAACAA
MAC_07182	9.870977	GTCAACAA
MAC_07330	10.73543	AAAAACAA
MAC_07839	10.88136	GTAAACAA
MAC_08196	10.73543	AAAAACAA
MAC_08197	9.299111	CTCAACAA
MAC_08198	9.725044	AACAACAA
MAC_08199	11.84143	ATAAACAA
MAC_08200	11.84143	ATAAACAA
MAC_08201	9.492452	TTAAACAA
MAC_08795	9.299111	CTCAACAA
MAC_00623	9.725044	AACAACAA
MAC_01993	10.83105	ATCAACAA
MAC_03702	11.84143	ATAAACAA
MAC_03703	10.88136	GTAAACAA
MAC_05729	11.84143	ATAAACAA
MAC_05837	9.299111	CTCAACAA

MAC_07788	10.73543	AAAAACAA
MAC_08031	9.203494	CAAAACAA
MAC_08505	10.73543	AAAAACAA
MAC_00652	9.031036	GTAAACAT
MAC_00672	10.83105	ATCAACAA
MAC_01449	10.23209	ATAAACAC
MAC_02061	9.245241	ACAAACAA
MAC_02166	10.83105	ATCAACAA
MAC_02602	9.328139	ATAAATAA
MAC_02867	10.3095	CTAAACAA
MAC_03001	9.725044	AACAACAA
MAC_03043	9.775361	GAAAACAA
MAC_03050	9.203494	CAAAACAA
MAC_03761	9.221707	ATCAACAC
MAC_03899	9.725044	AACAACAA
MAC_04216	10.73543	ATCAACAA
MAC_04372	10.83105	ATCAACAA
MAC_04525	9.775361	GAAAACAA
MAC_04532	9.299111	CTCAACAA
MAC_04599	9.701628	ATAAACAG
MAC_04678	10.23209	ATAAACAC
MAC_04767	9.203494	CAAAACAA
MAC_04883	10.73543	AAAAACAA
MAC_04947	10.88136	GTAAACAA
MAC_05098	11.84143	ATAAACAA
MAC_05253	10.73543	AAAAACAA
MAC_05446	9.245241	ACAAACAA
MAC_05716	10.23209	ATAAACAC
MAC_05756	9.725044	AACAACAA
MAC_05875	9.870977	GTCAACAA
MAC_05901	10.83105	ATCAACAA
MAC_06296	9.203494	CAAAACAA
MAC_06320	10.73543	AAAAACAA
MAC_06597	10.73543	AAAAACAA
MAC_06620	9.725044	AACAACAA
MAC_06735	9.701628	ATAAACAG
MAC_06779	10.73543	AAAAACAA
MAC_07018	9.991104	ATAAACAT
MAC_07302	11.84143	ATAAACAA
MAC_07323	9.701628	ATAAACAG
MAC_07691	9.328139	ATAAATAA
MAC_08480	9.203494	CAAAACAA
MAC_09371	9.328139	ATAAATAA
MAC_09485	11.84143	ATAAACAA

MAC_00176	9.725044	AACAACAA
MAC_02150	10.23209	ATAAACAC
MAC_02174	10.3095	CTAAACAA
MAC_02548	10.73543	AAAAACAA
MAC_02717	9.870977	GTCAACAA
MAC_03048	10.88136	GTAAACAA
MAC_04410	10.23209	ATAAACAC
MAC_04676	9.870977	GTCAACAA
MAC_04833	9.245241	ACAAACAA
MAC_05621	9.299111	CTCAACAA
MAC_05902	10.83105	ATCAACAA
MAC_06568	9.775361	GAAAACAA
MAC_06676	9.328139	ATAAATAA
MAC_06850	9.031036	GTAAACAT
MAC_07250	9.328139	ATAAATAA
MAC_07741	9.870977	GTCAACAA
MAC_08520	9.725044	AACAACAA
MAC_08796	9.870977	GTCAACAA
MAC_08826	9.328139	ATAAATAA
MAC_09768	10.83105	ATCAACAA

Table S4. DEGs involved in conidiation pattern shift.

Gene ID	log2 (8 h)	log2 (10 h)	log2 (12 h)	Functions	References
MAC_06850	0.0000	0.0000	1.0813	Contributed to the integrity of the cell wall	[1]
MAC_04376	4.7628	3.6544	2.7971	Involved in conidial yield	[2]
MAC_07330	0.0000	3.3649	2.1688	Important for fungal growth and conidial yield	[2]
MAC_00623	1.1792	0.8334	0.0000	β-glucosidase is the rate-limiting enzyme for cellulase degradation	[3]
MAC_06625	0.0000	1.7427	0.0000	Involved in hypha morphology	[4]
MAC_08796	0.0000	0.0000	1.7557	Involved in hypha growth and conidial yield	[5]
MAC_06296	0.0000	1.9988	0.0000	Involved in cell cycle	[6]
MAC_04676	0.9276	0.9190	1.2725	Contribute to Chitin metabolism and cell wall rearrangement	[7]
MAC_09768	0.0000	0.0000	2.0245	Inhibition of glucose utilization	[7]
MAC_06568	0.0000	0.0000	2.3669	Contribute to cell division	[8]
MAC_06624	1.0946	2.0173	0.0000	Involved in responses to multiple stresses	[9]
MAC_08514	1.1730	1.1180	1.4092	Related to fungal resistance	[10]
MAC_00186	0.0000	4.0181	2.6722	Involved in hypha growth and conidiation pattern shift	[11]
MAC_03001	0.0000	1.8107	0.9082	Involved in hypha growth	[12]
MAC_08197	0.0000	2.6272	2.3918	Involved in the transport of	[13]

MAC_07250	0.8758	0.0000	1.3331	monocarboxylate contribute to hyphal growth	[14]
MAC_04410	0.0000	0.0000	2.4628	Involved in growth	[15]
MAC_01348	0.0000	1.5317	1.2413	Involved to cell cycle	[16]
MAC_04216	0.0000	-1.2044	0.0000	contribute to hyphal growth and virulence	[17]
MAC_04372	0.0000	1.2725	0.0000	Related to fungal resistance	[18]
MAC_01993	1.0979	0.0000	0.0000	Related to hyphal growth and virulence	[19]
MAC_06623	1.5867	0.0000	2.3647	Involved in growth	[20]
MAC_02061	0.0000	1.3119	0.0000	Important for fungal growth and fungal resistance	[21]
MAC_09524	2.4409	2.9087	2.4645	Contributed to the integrity of the cell wall	[22]
MAC_08199	0.0000	0.0000	2.4526	contribute to conidial yield	[23]

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