

# Supplementary Materials: Functional Role of *Aspergillus carbonarius* AcOTAbZIP Gene, a bZIP Transcription Factor within the OTA Gene Cluster

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**Table S1.** Location of the putative-OTA-gene cluster in the genome of the *Aspergillus* species and *Penicillium nordicum*.

Species (Strain)	Putative OTA-Gene Cluster	
	Position*	Length (bp)
<i>A. affinis</i> (CBS 129190)	scaffold 263: 13,600–37,157	23,557
<i>A. albertensis</i> (IBT 14317)	scaffold 45: 173,601–196,151	22,550
<i>A. alliaceus</i> (CBS 536.65)	scaffold 38: 62,845–85,005	22,160
<i>A. carbonarius</i> (ITEM 5010)	scaffold 12: 943,452–965,219	21,767
<i>A. cretensis</i> (CBS 112802)	scaffold 236: 237–24,459	24,223
<i>A. elegans</i> (CBS 116.39)	scaffold 6: 221,286–244,294	23,008
<i>A. flocculosus</i> (CBS 112785)	scaffold 15: 210,525–234,022	23,497
<i>A. muricatus</i> (CBS 112808)	scaffold 98: 4,901–29,046	24,145
<i>A. niger</i> ( <i>lacticoffeatus</i> ) (CBS 101883)	scaffold 40: 220,217–241,951	21,734
<i>A. niger</i> (CBS 513.88)	supercontig 15: 1,855,355–1,877,016	21,661
<i>A. niger</i> (ATCC 13496)	scaffold 10: 59,997–82,127	22,130
<i>A. ochraceus</i> (fc-1)	Scaffold 8: 411,427–436,227	24,800
<i>A. pulvericola</i> (CBS 137327)	scaffold 10: 164,973–189,210	24,237
<i>A. roseoglobulosus</i> (CBS112800)	scaffold 81: 55,095–78,939	23,884
<i>A. sclerotiocarbonarius</i> (CBS 121057)	scaffold 107: 8,257–27,296	19,039
<i>A. sclerotioniger</i> (CBS 115572)	scaffold 10: 314,539–335,789	21,250
<i>A. steynii</i> (IBT 23096)	scaffold 3: 425,017–448,672	23,655
<i>A. subramanianii</i> (CBS 138230)	scaffold 42: 121,882–145,732	23,850
<i>A. welwitschiae</i> (CBS139.54b)	scaffold 25: 369,429–391,102	21,673
<i>A. westerdijkiae</i> (CBS 112803)	scaffold 73: 110,154–134,954	24,800
<i>P. nordicum</i> (DAOMC 185683)	scaffold 70: 4,687–26,262	21,575

\*position of OTA-gene cluster in the fungal genome (genome.jgi.doe.gov) identified based on homology with OTA putative gene cluster of *A. carbonarius*.

**Table S2.** Features of BRLZ domains used in the Maximum Likelihood phylogenetic analysis.

Species (Strain)	Protein ID <sup>a</sup>	Sequence of BRLZ Domain <sup>b</sup>
<i>OTAbZIPs</i>		
<i>A. affinis</i> (CBS 129190)	267643	EVKQRRQKYHEKYKERNRLAAGKSRQKQVDLIALLE-AERSDEERRRRRALEDEIQKIQKDLYAIKQELLH
<i>A. albertensis</i> (IBT 14317)	155937	KYHEKYKERNRLAAGRSRQKQVDLIELLEAERREEERRR-KALEEEIQRIQKELLAMKEELRH
<i>A. alliaceus</i> (CBS 536.65)	313480	KYHEKYKERNRLAAGRSRQKQVDLIELLEAERREEERRR-KALEEEIQRIQKELLAMKEELRH
<i>A. carbonarius</i> (ITEM 5010)	7821	KYHEKYKERNRVAAGKSRQKQVDLIELLQAEQREEERRR-KALERELSQIHKELLDLQELQH
<i>A. cretensis</i> (CBS 112802)	260188	EVKQRRQKYHEKYKERNRLAAGKSRQKQVDLIALLE-AERRDEERRRRRALEDEIQKIQKDLYAIKQELLH
<i>A. elegans</i> (CBS 116.39)	385076	KYHEKYKERNRLAAGKSRQKQVDLIALLE-

<i>A. flocculosus</i> (CBS 112785)	228703	AERRDEERRRRRALEDEIRQIQKELYAIKQELLH KYHEKYKERNRLAAGKSRQKQVDLIALLE- AERRDEERRRRRALEDEIQIKQDLYAIKQELLH
<i>A. muricatus</i> (CBS 112808)	167285	KYHEKYKERNRLAAGKSRQKQVDLIALLEAERRDEERRRQAL- EGEIQQIQKELYAIKQELHS
<i>A. niger</i> (ATCC 13496)	368844	KYHEKYKERNRLAAGRSRQKQADLINLLQAEQQEEERRRKALE- LEIANMQKELVDMKQELQH
<i>A. niger</i> (CBS 513.88)	167295	KYHEKYKERNRLAAGRSRQKQADLINLLQAEQQEEERRRKALE- LEIANMQKELVDMKQELQH
<i>A. niger</i> ( <i>lacticoffeatus</i> ) (CBS 101883)	438778	KYHEKYKERNRLAAGRSRQKQADLINLLQAEQQEEERRRKALE- LEIANMQKELVDMKQELQH
<i>A. ochraceus</i> (fc-1)	OTAR1 <sup>c</sup>	KYHEKYKERNRLAAGKSRQKQVDLIALLE- AERRDEERRRRRALEDEIRKIQKDLLAIKQELHS
<i>A. pulvericola</i> (CBS 137327)	431723	KYHEKYKERNRLAAGKSRQKQVDLIALLEAERRDEERRRRRALE- HEIQIKQDLYAMKQELLH
<i>A. roseoglobulosus</i> (CBS 112800)	176400	SEEVKQLRRKYHEKYKERNRLAAGKSRQKQVDLIALLE- AERRDEERRRRRALEDEIQIQRDLYAIKQELHN
<i>A. sclerotii carbonarius</i> (CBS 121057)	328118	KYHEKYKERNRLAAGRSRQKQVDLIELLQAEQREEERRRQALEKEI- AQIQKELEDMKQELQH
<i>A. sclerotioniger</i> (CBS 115572)	593114	KYHEKYKERNRLAAGKSRQKQADLIELLQAEQREEERRRQALEKEI- AQMOKDLVDMKQELQH
<i>A. steynii</i> (IBT 23096)	473593	KYHEKYKERNRLAAGKSRQKQVDLIALLE- AERRDEERRRRRALEDEIRQIQKELYAIKQELLH
<i>A. subramanianii</i> (CBS 138230)	274032	SDEVKQLRRKYHEKYKERNRLAASKSRQKQVDLIALLEAERG- DEERRRRRALEDEIRQIQRDLYAIKQELHN
<i>A. welwitschiae</i> (CBS 139.54b)	172341	KYHEKYKERNRLAAGRSRQKQADLINLLQAEQQEEERRR- KALEQEIANMHKELVDMKQELYH
<i>A. westerdijkiae</i> (CBS 112803)	245987	KYHEKYKERNRLAAGKSRQKQVDLIALLE- AERRDEERRRRRALEDEIRKIQKDLLAIKQELHS
<i>P. nordicum</i> (DAOMC 185683)	11413	KYHEKYKERNRLAAGKSRQKQVDLIALLEAERRDEERRRRVLEEEIQKIK- KDLFAIKQELHH
<i>A. carbonarius</i> bZIPs		
	132388	DSRERRKREHFLERNRVAANKCRK- KKKEHAKQLESRCMVSRQNTLLESEVDHLKGEILNLKNELLR
	203634	TDEEKRNFLERNRVAALKCRQRKKQWLANLQAKVELFTSENDALTAT- VTQLREEIVNLKTLLLA
	204486	LTSEPTSKRKAQNRAAQRAFRRERKEKHLKDLETKVDELQAAS- DNANQENGLLRAQIERLQVELRE
	207072	DSADPAAMKRARNTAARKSRARKLERQGEMERRRIEELEKL- LEESQQREEYWRNVAENG
<i>A. carbonarius</i> (ITEM 5010)	207738	KKLSSKERRQLRNKVSARAFRRRKEYIGQLESEVAAKTNEA- HELRLQNRALFEENARLTDLARM
	208150	EKEQRRIERVLRNRAAAQTSRERKRLE- MEKLENEKIQMEQQNQFLQRLSQMEAENNRNLNQQIAQ EKEESLT-
	208259	PAQSKRKAQNRAAQRAFRRERKERHVRELEEKVSNLENESTSLMADNERL KRELAKFTTENEI
	208905	ATDTPPTKRKAQNRAAQRAFRRERRAARVNELEDQIKKIEDDHEIHVAT- FKDQISTLSLEVEQCRSEMAW
	209595	KRPLSTSKRAAQNRAAQRAFRRQRKESYIRKLEEQVKEFEAT-

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NEALKQLQSENYQLREYIIN  
209790 ADRIKREKFLERNRVAASKCRHKKKLHTEM-  
LQHCHDDLKSKKTELSVLADKLRSELLALKNELLO  
506085 IKELKQQKRLLRNRQAALDSRQRKKLHTEKLEEEKKQFTQVISDLEEEL-  
QNMRLREAELIREKGE

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a: jgi.doe.gov. b: BRLZ domain obtained by using SMART (<http://smart.embl-heidelberg.de/>) and used for the Maximum Likelihood phylogenetic analysis. c: OTAR1 protein sequence obtained from its nucleotide sequence by using ExPaSy translation tool (<http://expasy.org/tools/dna.html>). The OTAR1 nucleotide sequence of *A. westerdijkiae* fc-1 was identified by BLASTn analysis on the assembled genome ([www.ncbi.nlm.nih.gov/assembly/GCA\\_004849945.1](http://www.ncbi.nlm.nih.gov/assembly/GCA_004849945.1)) using the *A. westerdijkiae* CBS 112803 OTAbZIP sequence (ID: 245987, jgi.doe.gov) as query.

**Table S3.** Detail of the Transcription factor binding motif (TFBM) identified by MEME in the OTA-gene cluster upstream, downstream and intergenic sequences.

Fungal Species	Genomic Region*	Strand	Start	p-Value	
<i>A. affinis</i>	OTApks/hp	+	94	6.93×10 <sup>-7</sup>	A T T G A C G T G T A G G A A
<i>A. affinis</i>	OTApks/hp	+	114	4.37× 10 <sup>-6</sup>	C A T G A C G T G T A T T G C
<i>A. affinis</i>	OTAnps/OTAp450	+	323	6.59× 10 <sup>-8</sup>	T A T G A C G T G T A A A T C
<i>A. affinis</i>	OTAnps/OTAp450	+	354	3.44× 10 <sup>-7</sup>	A A T G A G G T G T A G A A C
<i>A. affinis</i>	OTAp450/OTAbZIP	-	714	2.51× 10 <sup>-9</sup>	A A T G A C G T G T A A A A C
<i>A. albertensis</i>	OTApks/hp	-	66	7.53× 10 <sup>-9</sup>	A A T G A C G T G T A G A T C
<i>A. albertensis</i>	OTApks/hp	-	86	6.03× 10 <sup>-6</sup>	G C T G A C G T G G A A A T G
<i>A. albertensis</i>	OTAnps/OTAhah	-	154	3.33× 10 <sup>-8</sup>	A A T G A C G T G T A A A G A
<i>A. albertensis</i>	OTAhah/OTAp450	+	9	1.76× 10 <sup>-6</sup>	A C T G A C G T G T A G G A T
<i>A. alliaceus</i>	OTApks/hp	+	174	7.53× 10 <sup>-9</sup>	A A T G A C G T G T A G A T C
<i>A. alliaceus</i>	OTApks/hp	+	154	6.03× 10 <sup>-6</sup>	G C T G A C G T G G A A A T G
<i>A. alliaceus</i>	OTAnps/OTAhah	+	422	3.33× 10 <sup>-8</sup>	A A T G A C G T G T A A A G A
<i>A. alliaceus</i>	OTAhah/OTAp450	-	1648	2.05× 10 <sup>-6</sup>	A C T G A C G T G T A G G G T
<i>A. alliaceus</i>	OTAhah/OTAp450	-	1668	8.66× 10 <sup>-6</sup>	A A T T A C G T G T A G A T T
<i>A. alliaceus</i>	OTAp450/OTAbZIP	-	706	1.60× 10 <sup>-7</sup>	A A T G A C G T G T A A A A T
<i>A. carbonarius</i>	OTApks/hp	-	100	2.48× 10 <sup>-7</sup>	G C T G A C G T G T A A A T C
<i>A. carbonarius</i>	OTApks/hp	-	79	8.99× 10 <sup>-7</sup>	G T T G A C G T G T A G G G C
<i>A. carbonarius</i>	OTAnps/OTAp450	+	402	1.87× 10 <sup>-7</sup>	A A T G A C G T G T A A C C C
<i>A. carbonarius</i>	OTAp450/OTAbZIP	+	110	1.72× 10 <sup>-8</sup>	A A T G A C G T G T A A A A A
<i>A. carbonarius</i>	OTAhah (UTR-5')	-	408	1.38× 10 <sup>-6</sup>	C T T G A C G T G T A A G C C

<i>A. carbonarius</i>	OTAh <sub>al</sub> (UTR-3')	+	407	5.47 × 10 <sup>-6</sup>	A G T G A G G T G T A A G T G
<i>A. carbonarius</i>	OTAh <sub>al</sub> (UTR-5')	-	428	5.47 × 10 <sup>-6</sup>	T G T G A C G T G T A G G A T
<i>A. cretensis</i>	OTAp <sub>ks</sub> /hp	-	67	6.93 × 10 <sup>-7</sup>	A T T G A C G T G T A G G A A
<i>A. cretensis</i>	OTAp <sub>ks</sub> /hp	-	47	4.37 × 10 <sup>-6</sup>	C A T G A C G T G T A T T G C
<i>A. cretensis</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	134	3.44 × 10 <sup>-7</sup>	T A T G A C G T G T A A C T C
<i>A. cretensis</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	103	3.44 × 10 <sup>-7</sup>	A A T G A G G T G T A G A A C
<i>A. cretensis</i>	OTAp <sub>450</sub> /OTAbZIP	+	85	2.51 × 10 <sup>-9</sup>	A A T G A C G T G T A A A A C
<i>A. cretensis</i>	OTAbZIP/OTAh <sub>al</sub>	-	1720	2.19 × 10 <sup>-7</sup>	G A T G A C G T G T A A G T C
<i>A. elegans</i>	OTAp <sub>ks</sub> /OTAn <sub>ps</sub>	+	697	5.83 × 10 <sup>-7</sup>	A T T G A C G T G T A G G A G
<i>A. elegans</i>	OTAp <sub>ks</sub> /OTAn <sub>ps</sub>	+	717	1.91 × 10 <sup>-6</sup>	C A T G A C G T G T A T C C C
<i>A. elegans</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	+	421	5.18 × 10 <sup>-7</sup>	T A T G A C G T G T A A C T A
<i>A. elegans</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	+	452	5.83 × 10 <sup>-7</sup>	G A T G A G G T G T A G A A C
<i>A. elegans</i>	OTAp <sub>450</sub> /OTAbZIP	-	921	1.38 × 10 <sup>-7</sup>	T A T G A C G T G T A A A G A
<i>A. elegans</i>	OTAbZIP/OTAh <sub>al</sub>	+	171	7.53 × 10 <sup>-9</sup>	A A T G A C G T G T A A A A G
<i>A. elegans</i>	OTAbZIP/OTAh <sub>al</sub>	+	734	6.93 × 10 <sup>-7</sup>	A A T G A C G T G T A A G T T
<i>A. flocculosus</i>	OTAp <sub>ks</sub> /hp	-	211	1.13 × 10 <sup>-6</sup>	T T T G A C G T G T A G G A G
<i>A. flocculosus</i>	OTAp <sub>ks</sub> /hp	-	191	4.37 × 10 <sup>-6</sup>	C A T G A C G T G T A T T G C
<i>A. flocculosus</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	167	4.57 × 10 <sup>-7</sup>	A A T G A G G T G T A G A G C
<i>A. flocculosus</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	198	5.83 × 10 <sup>-7</sup>	T A T G A C G T G T A A C C G
<i>A. flocculosus</i>	OTAp <sub>450</sub> /OTAbZIP	+	119	1.38 × 10 <sup>-7</sup>	T A T G A C G T G T A A A G A
<i>A. flocculosus</i>	OTAbZIP/OTAh <sub>al</sub>	-	2295	1.16 × 10 <sup>-7</sup>	G A T G A C G T G T A A A C A
<i>A. flocculosus</i>	OTAbZIP/OTAh <sub>al</sub>	-	1901	1.91 × 10 <sup>-6</sup>	G G T G A C G T G T A A G A C
<i>A. muricatus</i>	OTAp <sub>ks</sub> /hp	-	135	2.19 × 10 <sup>-7</sup>	A T T G A C G T G T A G A T A
<i>A. muricatus</i>	OTAp <sub>ks</sub> /hp	-	115	2.36 × 10 <sup>-6</sup>	C A T G A C G T G T A T C C A
<i>A. muricatus</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	173	4.57 × 10 <sup>-7</sup>	A A T G A G G T G T A G A G C
<i>A. muricatus</i>	OTAn <sub>ps</sub> /OTAp <sub>450</sub>	-	204	1.91 × 10 <sup>-6</sup>	T A T G A C G T G T A A T T A
<i>A. muricatus</i>	OTAp <sub>450</sub> /OTAbZIP	+	121	1.87 × 10 <sup>-7</sup>	A A T G A C G T G T A G A T T
<i>A. muricatus</i>	OTAbZIP/OTAh <sub>al</sub>	-	1858	2.44 × 10 <sup>-8</sup>	A A T G A C G T G T A A A T A
<i>A. niger</i> (ATCC 13496)	OTAp <sub>ks</sub> /hp	-	144	2.19 × 10 <sup>-7</sup>	A T T G A C G T G T A A A T A

<i>A. niger</i> (ATCC 13496)	OTApks/hp	–	123	3.44×10 <sup>-7</sup>	G T T G A C G T G T A G A G G
<i>A. niger</i> (ATCC 13496)	OTApks/hp	+	107	2.53×10 <sup>-6</sup>	A C T G G C G T G T A G A T G
<i>A. niger</i> (ATCC 13496)	OTAnps/OTAp450	–	114	5.18×10 <sup>-7</sup>	T A T G A C G T G T A A C C C
<i>A. niger</i> (ATCC 13496)	OTAnps/OTAp450	–	94	6.36×10 <sup>-7</sup>	G A T G A G G T G T A G A A G
<i>A. niger</i> (ATCC 13496)	OTAp450/OTAbZIP	+	100	3.33×10 <sup>-8</sup>	G A T G A C G T G T A G A A G
<i>A. niger</i> (ATCC 13496)	after /OTAhal	–	1042	4.37×10 <sup>-6</sup>	C C T G A T G T G T A G A G C
<i>A. niger</i> (CBS 513.88)	OTApks/OTAnps	+	941	2.19×10 <sup>-7</sup>	A T T G A C G T G T A A A T A
<i>A. niger</i> (CBS 513.88)	OTApks/OTAnps	+	962	3.44×10 <sup>-7</sup>	G T T G A C G T G T A G A G G
<i>A. niger</i> (CBS 513.88)	OTApks/OTAnps	–	978	2.53×10 <sup>-6</sup>	A C T G G C G T G T A G A T G
<i>A. niger</i> (CBS 513.88)	OTAnps/OTAp450	+	401	5.18×10 <sup>-7</sup>	T A T G A C G T G T A A C C C
<i>A. niger</i> (CBS 513.88)	OTAnps/OTAp450	+	421	6.36×10 <sup>-7</sup>	G A T G A G G T G T A G A A G
<i>A. niger</i> (CBS 513.88)	OTAp450/OTAbZIP	–	836	3.33×10 <sup>-8</sup>	G A T G A C G T G T A G A A G
<i>A. niger</i> (CBS 513.88)	OTAbZIP/OTAhal	+	152	2.19×10 <sup>-7</sup>	A A T G A C G T G T A A G G A
<i>A. niger</i> (CBS 513.88)	OTAbZIP/OTAhal	+	173	1.52×10 <sup>-6</sup>	C C T G A C G T G T A A C C G
<i>A. niger</i> (CBS 513.88)	after /OTAhal	+	40	4.37×10 <sup>-6</sup>	C C T G A T G T G T A G A G C
<i>A. niger</i> (lacticoffeatus)	OTApks/OTAnps	+	1001	2.19×10 <sup>-7</sup>	A T T G A C G T G T A A A T A
<i>A. niger</i> (lacticoffeatus)	OTApks/OTAnps	+	1022	3.44×10 <sup>-7</sup>	G T T G A C G T G T A G A G G
<i>A. niger</i> (lacticoffeatus)	OTApks/OTAnps	–	1038	2.53×10 <sup>-6</sup>	A C T G G C G T G T A G A T G
<i>A. niger</i> (lacticoffeatus)	OTAnps/OTAp450	+	401	5.18×10 <sup>-7</sup>	T A T G A C G T G T A A C C C
<i>A. niger</i> (lacticoffeatus)	OTAnps/OTAp450	+	421	6.36×10 <sup>-7</sup>	G A T G A G G T G T A G A A G
<i>A. niger</i> (lacticoffeatus)	OTAp450/OTAbZIP	–	836	3.33×10 <sup>-8</sup>	G A T G A C G T G T A G A A G
<i>A. niger</i> (lacticoffeatus)	OTAbZIP/OTAhal	+	152	2.19×10 <sup>-7</sup>	A A T G A C G T G T A A G G A
<i>A. niger</i> (lacticoffeatus)	OTAbZIP/OTAhal	+	173	1.52×10 <sup>-6</sup>	C C T G A C G T G T A A C C G
<i>A. niger</i> (lacticoffeatus)	after /OTAhal	+	7	4.37×10 <sup>-6</sup>	C C T G A T G T G T A G A G C
<i>A. pulvericola</i>	OTAnps/OTAp450	–	168	4.57×10 <sup>-7</sup>	A A T G A G G T G T A G A G C
<i>A. pulvericola</i>	OTAnps/OTAp450	–	199	5.83×10 <sup>-7</sup>	T A T G A C G T G T A A C C G
<i>A. pulvericola</i>	OTAp450/OTAbZIP	+	28	4.57×10 <sup>-7</sup>	T A T G A C G T G T A A G A A
<i>A. pulvericola</i>	OTAbZIP/OTAhal	–	1474	1.91×10 <sup>-6</sup>	G G T G A C G T G T A A G A C
<i>A. roseoglobulosus</i>	OTApks/hp	–	61	5.18×10 <sup>-7</sup>	C A T G A C G T G T A T A A C
<i>A. roseoglobulosus</i>	OTAnps/OTAp450	–	8	5.18×10 <sup>-7</sup>	A A T G A G G T G T A G A A A
<i>A. roseoglobulosus</i>	OTAnps/OTAp450	–	40	7.87×10 <sup>-8</sup>	T A T G A C G T G T A A A T G

<i>A. roseoglobulosus</i>	OTAp450/OTAbZIP	+	55	4.03×10 <sup>-7</sup>	C A T G A C G T G T A A A A T
<i>A. sclerotiiicarbonarius</i>	OTApks/hp	−	145	2.05×10 <sup>-6</sup>	A T T G A C G T G T A G G G T
<i>A. sclerotiiicarbonarius</i>	OTApks/hp	+	128	7.46×10 <sup>-6</sup>	G C T G G C G T G T A T A T C
<i>A. sclerotiiicarbonarius</i>	OTApks/hp	−	165	1.38×10 <sup>-7</sup>	A C T G A C G T G T A A A T C
<i>A. sclerotiiicarbonarius</i>	OTAnps/OTAp450	−	131	1.16×10 <sup>-7</sup>	G A T G A C G T G T A A A C A
<i>A. sclerotiiicarbonarius</i>	OTAnps/OTAp450	−	109	1.13×10 <sup>-6</sup>	A A T G A T G T G T A G A A G
<i>A. sclerotiiicarbonarius</i>	OTAbZIP/OTAhAl	−	475	1.13×10 <sup>-6</sup>	C C T G A C G T G T A A C T G
<i>A. sclerotiiicarbonarius</i>	OTAbZIP/OTAhAl	−	495	1.25×10 <sup>-6</sup>	T G T G A C G T G T A A A T G
<i>A. sclerotioniger</i>	OTApks/hp	+	235	6.36×10 <sup>-7</sup>	A T T G A C G T G T A G G G C
<i>A. sclerotioniger</i>	OTApks/hp	+	215	1.13×10 <sup>-6</sup>	T G T G A C G T G T A A A T C
<i>A. sclerotioniger</i>	OTApks/hp	−	251	8.25×10 <sup>-6</sup>	C T T G G C G T G T A T A T C
<i>A. sclerotioniger</i>	OTAnps/OTAp450	+	526	1.87×10 <sup>-7</sup>	A A T G A C G T G T A A C C C
<i>A. sclerotioniger</i>	OTAnps/OTAp450	+	557	1.91×10 <sup>-6</sup>	G A T G A T G T G T A A A A A
<i>A. sclerotioniger</i>	OTAp450/OTAbZIP	−	515	6.59×10 <sup>-8</sup>	G A T G A C G T G T A G A C C
<i>A. sclerotioniger</i>	OTAbZIP/OTAhAl	+	159	1.76×10 <sup>-6</sup>	C T T G A C G T G T A G C C A
<i>A. sclerotioniger</i>	OTAbZIP/OTAhAl	+	139	3.33×10 <sup>-6</sup>	T G T G A C G T G T A G A G T
<i>A. steynii</i>	OTApks/hp	+	164	5.83×10 <sup>-7</sup>	A T T G A C G T G T A G G A G
<i>A. steynii</i>	OTApks/hp	+	184	1.91×10 <sup>-6</sup>	C A T G A C G T G T A T C C C
<i>A. steynii</i>	OTAnps/OTAp450	+	539	5.18×10 <sup>-7</sup>	T A T G A C G T G T A A C T A
<i>A. steynii</i>	OTAnps/OTAp450	+	570	5.83×10 <sup>-7</sup>	G A T G A G G T G T A G A A C
<i>A. steynii</i>	OTAp450/OTAbZIP	−	922	6.59×10 <sup>-8</sup>	T A T G A C G T G T A A A A G
<i>A. steynii</i>	OTAbZIP/OTAhAl	+	171	7.53×10 <sup>-9</sup>	A A T G A C G T G T A A A A G
<i>A. steynii</i>	OTAbZIP/OTAhAl	+	734	1.38×10 <sup>-7</sup>	A A T G A C G T G T A A G T G
<i>A. subramanianii</i>	OTApks/hp	−	144	1.60×10 <sup>-7</sup>	A T T G A C G T G T A G A T G
<i>A. subramanianii</i>	OTApks/hp	−	124	3.56×10 <sup>-6</sup>	C A T G A C G T G T A T C A T
<i>A. subramanianii</i>	OTAnps/OTAp450	−	173	4.03×10 <sup>-7</sup>	A A T G A G G T G T A G A A G
<i>A. subramanianii</i>	OTAnps/OTAp450	−	204	5.18×10 <sup>-7</sup>	T A T G A C G T G T A A C T A
<i>A. subramanianii</i>	OTAp450/OTAbZIP	+	95	4.03×10 <sup>-7</sup>	C A T G A C G T G T A A A A T
<i>A. subramanianii</i>	OTAbZIP/OTAhAl	−	2118	5.28×10 <sup>-8</sup>	G A T G A C G T G T A A A A A
<i>A. welwitschiae</i>	OTApks/OTAnps	+	949	2.19×10 <sup>-7</sup>	A T T G A C G T G T A A A T A
<i>A. welwitschiae</i>	OTApks/OTAnps	+	970	3.44×10 <sup>-7</sup>	G T T G A C G T G T A G A G G

<i>A. welwitschiae</i>	<i>OTApks/OTAnps</i>	–	986	2.53×10 <sup>−6</sup>	A C T G G C G T G T A G A T G
<i>A. welwitschiae</i>	<i>OTAnps/OTAp450</i>	+	381	5.18×10 <sup>−7</sup>	T A T G A C G T G T A A C C C
<i>A. welwitschiae</i>	<i>OTAnps/OTAp450</i>	+	401	6.36×10 <sup>−7</sup>	G A T G A G G T G T A G A A G
<i>A. welwitschiae</i>	<i>OTAp450/OTAbZIP</i>	–	836	3.33×10 <sup>−8</sup>	G A T G A C G T G T A G A A G
<i>A. welwitschiae</i>	<i>OTAbZIP/OTAhah</i>	+	152	2.19×10 <sup>−7</sup>	A A T G A C G T G T A A G G A
<i>A. welwitschiae</i>	<i>OTAbZIP/OTAhah</i>	+	173	1.76×10 <sup>−6</sup>	C C T G A C G T G T A A C C A
<i>A. welwitschiae</i>	<i>after /OTAhah</i>	+	40	4.37×10 <sup>−6</sup>	C C T G A T G T G T A G A G C
<i>A. westerdijkiae</i>	<i>OTApks/hp</i>	–	164	3.44×10 <sup>−7</sup>	A T T G A C G T G T A G A C A
<i>A. westerdijkiae</i>	<i>OTApks/hp</i>	–	144	1.52×10 <sup>−6</sup>	C A T G A C G T G T A T C A G
<i>A. westerdijkiae</i>	<i>OTAnps/OTAp450</i>	–	16	5.18×10 <sup>−7</sup>	T A T G A C G T G T A A C T A
<i>A. westerdijkiae</i>	<i>OTAp450/OTAbZIP</i>	+	110	1.16×10 <sup>−7</sup>	T A T G A C G T G T A A A T A
<i>A. westerdijkiae</i>	<i>OTAbZIP/OTAhah</i>	–	2726	7.53×10 <sup>−9</sup>	A A T G A C G T G T A A A A G
<i>A. westerdijkiae</i>	<i>OTAbZIP/OTAhah</i>	–	2592	8.99×10 <sup>−7</sup>	A A T G A C G T G T A A T A A
<i>P. nordicum</i>	<i>OTApks/hp</i>	+	174	3.44×10 <sup>−7</sup>	A T T G A C G T G T A G A C A
<i>P. nordicum</i>	<i>OTApks/hp</i>	+	194	6.35×10 <sup>−6</sup>	A A T G A C G T G T A T T G T
<i>P. nordicum</i>	<i>OTAp450/OTAbZIP</i>	–	669	1.16×10 <sup>−7</sup>	C A T G A C G T G T A A A G A
<i>P. nordicum</i>	<i>OTAbZIP/OTAhah</i>	+	548	2.19×10 <sup>−7</sup>	G A T G A C G T G T A A G T C
<i>P. nordicum</i>	<i>OTAbZIP/OTAhah</i>	+	159	5.28×10 <sup>−8</sup>	A A T G A C G T G T A A A C A

\*For each fungal strain, the genomic regions used for the analysis were the intergenic regions between the reported genes, or corresponded to the untranslated regions (UTR) of the specified genes. *OTApks*: polyketide synthase; *OTAnps*: nonribosomal peptide synthase; *OTAp450*: cytochrome P450 monooxygenase; *OTAbZIP*: bZIP transcription factor; *OTAhah*: halogenase; *hp* means the hypothetical protein between the polyketide synthase (*OTApks*) and the nonribosomal peptide synthase (*OTAnps*).



**Table S4.** TOMTOM analysis representing the homology of TFBM identified by MEME with those of *Saccharomyces cerevisiae*.

Name*	Transcription Factor Class	p-Value	E-Value	q-Value
MA0351.1 (DOT6)	Tryptophan cluster factors	4.36×10 <sup>-4</sup>	7.68×10 <sup>-2</sup>	1.51×10 <sup>-1</sup>
MA0409.1 (TYE7)	Basic helix-loop-helix factors (bHLH)	2.21×10 <sup>-3</sup>	3.89×10 <sup>-1</sup>	3.54×10 <sup>-1</sup>
MA0318.1 (HMRA2)	TALE-type homeo domain factors	3.07×10 <sup>-3</sup>	5.41×10 <sup>-1</sup>	3.54×10 <sup>-1</sup>
MA0328.2 (MATAPHA2)	TALE-type homeo domain factors	4.12×10 <sup>-3</sup>	7.25×10 <sup>-1</sup>	3.55×10 <sup>-1</sup>
MA0421.1 (NSI1)	Tryptophan cluster factors	5.32×10 <sup>-3</sup>	9.37×10 <sup>-1</sup>	3.68×10 <sup>-1</sup>
MA0281.1 (CBF1)	Basic helix-loop-helix factors (bHLH)	8.12×10 <sup>-3</sup>	1.43	4.27×10 <sup>-1</sup>
MA0329.1 (MBP1)	APSES-type DNA-binding domain	9.59×10 <sup>-3</sup>	1.69	4.27×10 <sup>-1</sup>
MA0286.1 (CST6)	Basic leucine zipper factors (bZIP)	1.04×10 <sup>-2</sup>	1.83	4.27×10 <sup>-1</sup>
MA0416.1 (YAP3)	Basic leucine zipper factors (bZIP)	1.25×10 <sup>-2</sup>	2.20	4.27×10 <sup>-1</sup>
MA0350.1 (TOD6)	Tryptophan cluster factors	1.42×10 <sup>-2</sup>	2.50	4.27×10 <sup>-1</sup>
MA0310.1 (HAC1)	Basic leucine zipper factors (bZIP)	1.45×10 <sup>-2</sup>	2.55	4.27×10 <sup>-1</sup>

\*Name of transcription factor binding motif (TFBM) according to the JASPAR database.