Supporting information

Table S1: List of oligonucleotides used in this study.

name	sequence (5‘→ 3‘)
PKS19-KO-for	GGCCCTCCTGCACAAACCTC
PKS19-KO-rev	GAAACTTGGCTACGGTAGGGAAGC
C19OXR1-KO-for	GATGTCCTCGGCCTCAGTCTC
C19OXR1-KO-rev	GCCTTTAGCTCAATGCGTCAG
C19TRF1-KO-for	GCGCGAAAAGAGCAGCAGTGG
C19TRF1-KO-rev	TCGCCGAGGCAGTCAAACAGAGT
C19TRF2-1-KO-for	GGCAGGCATCATTCACCATT
C19TRF2-1-KO-rev	GACTGTAATATCAAGCGTGCGATAG
C19TRF2-2-KO-for	CACAACACAATGGCCTACCA
C19TRF2-2-KO-rev	GCATTCTGAATTACCCAAAGCA
PKS19-comp1-for	CGTACGATGTCCCCAATCTTCCTTGGTG
PKS19-comp1-rev	GTGGTGGTGTCGAGCTTGTGG
PKS19-comp2-for	CTGTTCCTCCACGGACACCCCATC
PKS19-comp2-rev	CAGAAGGCTGCGATATATTTGTGGAATTCTAC
EF1-prom*PKS19*-for	CGTACGCTGAGAGCGAGAAAAAAAAACTCTTC
EF1-prom*PKS19*-rev	CGTACGGGTTTGGTGCTCTCTTTTTGATG
C19OXR1-comp-for	CGGCGCAAGACTAGGAAGAGAAG
C19OXR1-comp-rev	CACCCGGTAAATAATATGCCTGTTGAC
EF1-promOXR1-for	CTGAGAGCGAGAAAAAAAAACTCTTC
EF1-promOXR1-rev	CAAGCTTGGTTTGGTGCTCTCTTTTTGATG
EF1-C19OXR1-for	CAAGCTTATGACCATCAAGTTCGCCTCTC
EF1-C19OXR1-rev	GTCCACTGTCTCGTTACTCTAAAGC
TRF1exHPT-for	ctaggccaccatgttgggcccggcgcgccgGTCGACGTTAACTGATATTGAAGGAGCATTTTTTG
TRF1exHPT-rev	tcgctctcagtcgacGTCGACGTTAACTGGTTCCCGGTCG
TRF1exEF1-for	ccagttaacgtcgacGTCGACTGAGAGCGAGAAAAAAAAACTC
TRF1exEF1-rev	aatctcagtagccatGGTGGCGGTTTGGTGCTCTCTTTTT
C19TRF1ex-for	caccaaaccgccaccATGGCTACTGAGATTAATATGCCCAT
C19TRF1ex-rev	gtcagatctaccatggtggactcctcttaaCCCAAGAGAATCAAGGAAATTCAAC
*EF1-C19TRF2*ex-for	CTCTTCGTCGGATTATCATGC
*EF1-C19TRF2*ex-rev	GCATATTAATCTCAGTAGCCATGGCTCTCTTTTTGATGATAATGT
*C19TRF2*ex-for	ACATTATCATCAAAAAGAGAGCCATGGCTACTGAGATTAATATGC
*C19TRF2*ex-rev	CATCCACACAGCGTCGTAAC
C19TRF2ex-template-for	CCTCCCCTCGTACCCCCTTCAATC
C19TRF2ex-template-rev	CGAGCAACCCAGCGAGTCAGC
RT-actin-for	CCCGACGGACAGGTTATCAC
RT-actin-rev	GAGAGCGAGGCGAGAATGG
RT-EF1-for	CAGGCGATGTGGGCAGTGTG
RT-EF1-rev	GTATCCTCAAGCCCGGTATGGTC
RT-*PKS19*-for	CATTGGAATGGGCTGCCG
RT-*PKS19*-rev	AGTTGCCCACGTAGCAGCC
RT-*C19OXR1*-for	CACGCTCGGCAAGCTAAAGA
RT-*C19OXR1*-rev	TCGAGGGCGTCGATCATCA
RT-*C19OXR2*-for	CTCTCAACACGTTTCACGGCA
RT-*C19OXR2*-rev	TCGCGTTGTACACGTTGAACTG
RT-*C19RED1*-for	GGCGGCCCTTCACCACTG

RT-*C19RED1*-rev	GCCTCTGCACCATAGCCACAA
RT-*C19RED2*-for	AGTTCGAGGCCATGTTCCAAG
RT-*C19RED2*-rev	GACGCTGTTGACACGGATGC
RT-*C19RED3*-for	TCGCCGTCATCTCGTCCAC
RT-*C19RED3*-rev	TCAGCAGCTTGCTCAATCGTC
DIG-*PKS19*-for	CCCAGGCACGTGTGGGAATAC
DIG-*PKS19*-rev	CACCATGAGGGCCTTTTCCAC
DIG-*C19OXR1*-for	GACCCCGGTAACGTGTTTCGC
DIG-*C19OXR1*-rev	TCGCTGGCCCTTGTACTGACTGT
DIG-*C19TRF1*-for	TCGATTTTCTTCGGGTGTTC
DIG-*C19TRF1*-rev	TTCTTGGGTTCTTGGGTGTC
DIG-*C19TRF2*-for	TAGGTGTCCCCAAGTTCCTG
DIG-*C19TRF2*-rev	GTCGGCTTCATCGACTCTTC

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Table S2: **Putative PKS-encoding genes in the *MoWT* genome.** The MGG number of the PKS genes in the 8th annotation of the *M. oryzae* genome is listed. The conserved protein domains were identified using the Interpro database and the PFAM identities were listed. X = domain detected, (X) = insignificant PFAM hit, KS-N = N-terminal ß-ketoacylsynthase, KS-C = C-terminal ß-ketoacylsynthase, AT = acyltransferase, PP = phosphopanthetin-binding sequence, KR = ketoreductase, MT = methyltransferase, ADH/ADHZ = alcohol dehydrogenases, TE = thioesterase.

MGG-nr	gene-name	PKS-form	KS-N (PF00109)	KS-C (PF02801)	AT (PF00698)	PP (PF00550)	KR (PF08659)	MT (PF08242)	ADH/ADHZ (PF08240/ PF00107)	TE (PF00975)
MGG_00241	*MoPKS1*	non-reducing	X	X	X	X				X
MGG_07219	*MoPKS2 (ALB1, Howard and Valent, 1996))*	non-reducing	X	X	X	X				X
MGG_12478	*MoPKS3*	non-reducing	X	X	X	X				X
MGG_00428	*MoPKS5*	non-reducing	X	X	X	X				X
MGG_10011	*MoPKS20*	non-reducing	X	X	X	X				
MGG_13767	*MoPKS7*	reducing-methylating	X	X	X	X	X	X	X	
MGG_00806	*MoPKS8*	reducing-methylating	X	X	X	X	X	X	X	
MGG_08236	*MoPKS9*	reducing-methylating	X	X	X	(X)	X	X	X	
MGG_12214	*MoPKS10*	reducing-methylating	X	X	X	(X)	X	X	X	
MGG_14831	*MoPKS21*	reducing-methylating	X	X	X	X	X	X	X	
MGG_08281	*MoPKS4*	Reducing non-methylating	X	X	X	X	X		X	
MGG_00233	*MoPKS12*	Reducing non-methylating	X	X	X	(X)	X		X	
MGG_04775	*MoPKS13*	Reducing non-methylating	X	X	X	(X)	X		X	
MGG_05589	*MoPKS14*	Reducing non-methylating	X	X	X	X	X		X	
MGG_14945	*MoPKS15*	Reducing non-methylating	X	X	X	(X)	X		X	
MGG_13591	*MoPKS16*	Reducing non-methylating	X	X	X	X	X		X	
MGG_12613	*MoPKS17*	Reducing non-methylating	X	X	X	(X)	X		X	
MGG_18078	*MoPKS18*	Reducing non-methylating	X	X	X	X	X			
MGG_10912	*MoPKS19*	Reducing non-methylating	X	X	X	(X)	X		X	
MGG_11638	*MoPKS22*	Reducing non-methylating	X	X	X	(X)	X			

Table S3: **Putative NRPS and PKS-NRPS encoding genes in the *MoWT* genome.** The MGG number of the genes in the 8th annotation of the *M. oryzae* genome is listed. The conserved protein domains were identified using the Interpro database and the PFAM identities were listed. X = domain detected, (X) = insignificant PFAM hit, KS-N = N-terminal ß-ketoacylsynthase, KS-C = C-terminal ß-ketoacylsynthase, AT = acyltransferase, PP = phosphopanthetin-binding sequence, AMP = AMP-binding sequence, CD = condensation, KR = ketoreductase, MT = methyltransferase, ADH/ADHZ = alcohol dehydrogenases, TE = thioesterase.

MGG-nr	gene-name	PKS-form	KS-N (PF00109)	KS-C (PF02801)	AT (PF00698)	PP (PF00550)	AMP (PF00501)	CD (PF00668)	KR (PF08659)	MT (PF08242)	ADH/ADHZ (PF08240/ PF00107)	TE (PF00975)
MGG_07803	*MoPKSa (TAS1,Yun et al., 2015)*	partial PKS	X	X		X				X	X	
MGG_10202	*MoPKSb*		X	X								
MGG_04118	*MoPKSc*				X							
MGG_14943	*MoPKS-NRPS1*	PKS-NRPS	X	X	X	X	X	X	X	X		
MGG_03810	*MoPKS-NRPS2*		X	X	X	X	X	X	X	X		
MGG_09589	*MoPKS-NRPS3*		X	X	X	X	X	X	X	X		
MGG_12447	*MoPKS-NRPS4 (ACE1, Böhnert et al., 2004))*		X	X	X	X	X	X	X	X		
MGG_15097	*MoPKS-NRPS5*		X	X	X	X	X	X	X	X		
MGG_14897	*MoPKS-NRPS6*		X	X	X	(X)	X	X	X	(X)		
MGG_15100	*MoPKS-NRPSa*	partial PKS-NRPS	X	X	X	(X)		X	X	X	X	
MGG_15272	*MoPKS-NRPSb*		X	X	X	X		X	X		X	
MGG_00022	*MoNRPS1*	NRPS				X	X	X				
MGG_02351	*MoNRPS2*					X	X	X				
MGG_03401	*MoNRPS3*					(X)	X	X				
MGG_07858	*MoNRPS4*					X	X	X				
MGG_12175	*MoNRPS5*					X	X	X				
MGG_14767	*MoNRPS6*					X	X	X				
MGG_14967	*MoNRPS7*					X	X	X				

S1: Construction of gene inactivation, complementation and overexpression vectors

In case of *ΔMopks19* a 4161 bp PCR product was amplified by using the primers *PKS19*-KO-for and *PKS19*-KO-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* (Promega, Mannheim; Germany) giving the vector *pGEMT+PKS19*. *pGEMT+PKS19* was restricted with *Bam*HI and a fragment of the coding sequence was replaced by a *Bgl*II restricted *HPT* cassette from *pCAMB+HPT+Sal* (33) to give *pGEMT+PKS19+HPT*. The

*Eco*RI restricted fragment of *pGEMT+PKS19+HPT* was cloned into *Eco*RI restricted *pCAMBIA-0380* to give the gene inactivation vector *pCAMB+PKS19+HPT*.

For *ΔMopks19/PKS19* a 3246 bp PCR product was amplified by using the primers *PKS19*-comp1-for and *PKS19*-comp1-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+PKS19comp1*. The *EF1α* promoter (gene MGG_03641) of *Magnaporthe oryzae* 70-15 was used to obtain a strong transcription of the *PKS19* since all experiments to complement the strain *ΔMopks19* with its native promoter region were not successful. Therefore, the *EF1α* promoter was amplified by using the primers *EF1*-prom*PKS19*-for and *EF1*-prom*PKS19*-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+EF1prom*. *pGEMT+PKS19comp1* was restricted with *Bsi*WI and was ligated with the *Bsi*WI restricted *EF1α*-fragment from pGEMT+EF1prom to give *pGEMT+EF1+PKS19a*. Furthermore, a 5352 bp PCR product was amplified by using the primers *PKS19*-comp2-for and *PKS19*-comp2-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+PKS19comp2*. *pGEMT+PKS19comp2* was restricted with *Pml*I/*Spe*I and was ligated with the *Pml*I/*Spe*I restricted fragment of *pGEMT+EF1+PKS19a* to give *pGEMT+EF1+PKS19b*. *pGEMT+EF1+PKS19b* was restricted with *Apa*I/*Eco*RI and was ligated into the *Apa*I/*Eco*RI restricted vector *pCAMB+ILV* (33) to give the complementation vector *pCAMB+EF1+PKS19comp+ILV*.

In case of *ΔMoC19ox1* a 4287 bp PCR product was amplified by using the primers *C19OX1*-KO-for and *C19OX1*-KO-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+C19OX1*. *pGEMT+ C19OX1* was restricted with *Bgl*II/*Mfe*I and a fragment of the coding sequence was replaced by a *Bgl*II/*Eco*RI restricted *HPT* cassette from *pCAMB+HPT+Sal* to give *pGEMT+C19OX1+HPT*. The *Not*I restricted fragment of *pGEMT+C19OX1+HPT* was cloned into *Psp*OMI restricted *pCAMBIA-0380* to give the gene inactivation vector *pCAMB+C19OX1+HPT*.

For *ΔMoC19ox1/OX1* a 3796 bp PCR product was amplified by using the primers *C19OX1*-comp-for and *C19OX1*-comp-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+C19OX1comp*. The *Not*I restricted fragment of *pGEMT+C19OX1comp* was cloned into *Psp*OMI restricted *pCAMB+ILV* to give the complementation vector *pCAMB+C19OX1comp+ILV*.

For *MoEF1::C19OX1* a 2116 bp PCR product was amplified by using the primers *EF1-C19OX1*-for and *EF1-C19OX1*-for from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+C19OX1*. A second PCR product was amplified by using the primers *EF1-promOX1*-for and *EF1-*

promOX1-for from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+EF1+promOX1*. *pGEMT+C19OX1* was restricted with *Apa*I/*Hind*III and a *Apa*I/*Hind*III restricted fragment of *pGEMT+EF1+promOX1* was ligated giving *pGEMT+EF1+C19OX1*. The *Eco*RI restricted fragment of *pGEMT+EF1+C19OX1* was cloned into the *Eco*RI restricted *pCAMB+HPT+Sal* to give the expression vector *pCAMB+EF1+C19OX1+HPT*.

For *ΔMoC19tf1* a 3216 bp PCR product was ampflified by using the primers *C19TF1*-KO-for and *C19TF1*-KO-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pGEMTeasy* giving the vector *pGEMT+C19TF1*. *pGEMT+ C19TF1* was restricted with *Bam*HI/*Xho*I and a fragment of the coding sequence was replaced by a *Bam*HI/*Xho*I restricted *HPT* cassette from *pCAMB+HPT+Hind* (33) to give *pGEMT+C19TF1+HPT*. The *Apa*I/*Spe*I restricted fragment of *pGEMT+C19TF1+HPT* was cloned into *Apa*I/*Spe*I restricted *pCAMBIA-0380* to give the gene inactivation vector *pCAMB+C19TF1+HPT*.

MoEF1::C19TF1 was generated using the cloning strategy of Gibson-assembly (Gibson et al., 2009). The required fragments were amplified with the primers *TF1exEF1*-for and *TF1exEF1*-rev (*EF1α* promoter fragment), *C19TF1ex*-for and *C19TF1ex*-rev (coding sequence of *MoC19TF1*+500 bp of terminator region) from genomic DNA of *M. oryzae* 70-15. The *HPT* cassette was amplified with the primers *TF1exHPT*-for and *TF1exHPT*-rev from pCB1003 (Sweigard, Chumley, Carroll, Farrall, & Valent, 1997) and the backbone vector was an *Eco*RI/*Hind*III restricted *pCAMBIA-0380* to give the gene expression vector *pCAMB+EF1::C19TF1+HPT*.

In case of *ΔMoC19tf2* a 976 bp PCR product was amplified by using the primers *C19TF2*-1-KO-for and *C19TF2*-1-KO-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pJET1.2 blunt* (Fermentas GmbH, St. Leon-Roth, Germany) giving the vector *pJET+C19TF2-1*. A second 942 bp PCR product was amplified by using the primers *C19TF2*-2-KO-for and *C19TF2*-2-KO-rev from genomic DNA of *M. oryzae* 70-15 and cloned into *pJET1.2 blunt* giving the vector *pJET+C19TF2-2*. *pJET+C19TF2-1* was restricted with *Bgl*II and cloned into the *Bam*HI restricted *pCAMB+HPT+Sal* to give *pCAMB+C19TF2-1+HPT*. *pJET+C19TF2-2* was restricted with *Bgl*II and cloned into the *Bgl*II restricted *pCAMB+C19TF2a+HPT* to give the gene inactivation vector *pCAMB+C19TF2+HPT*.

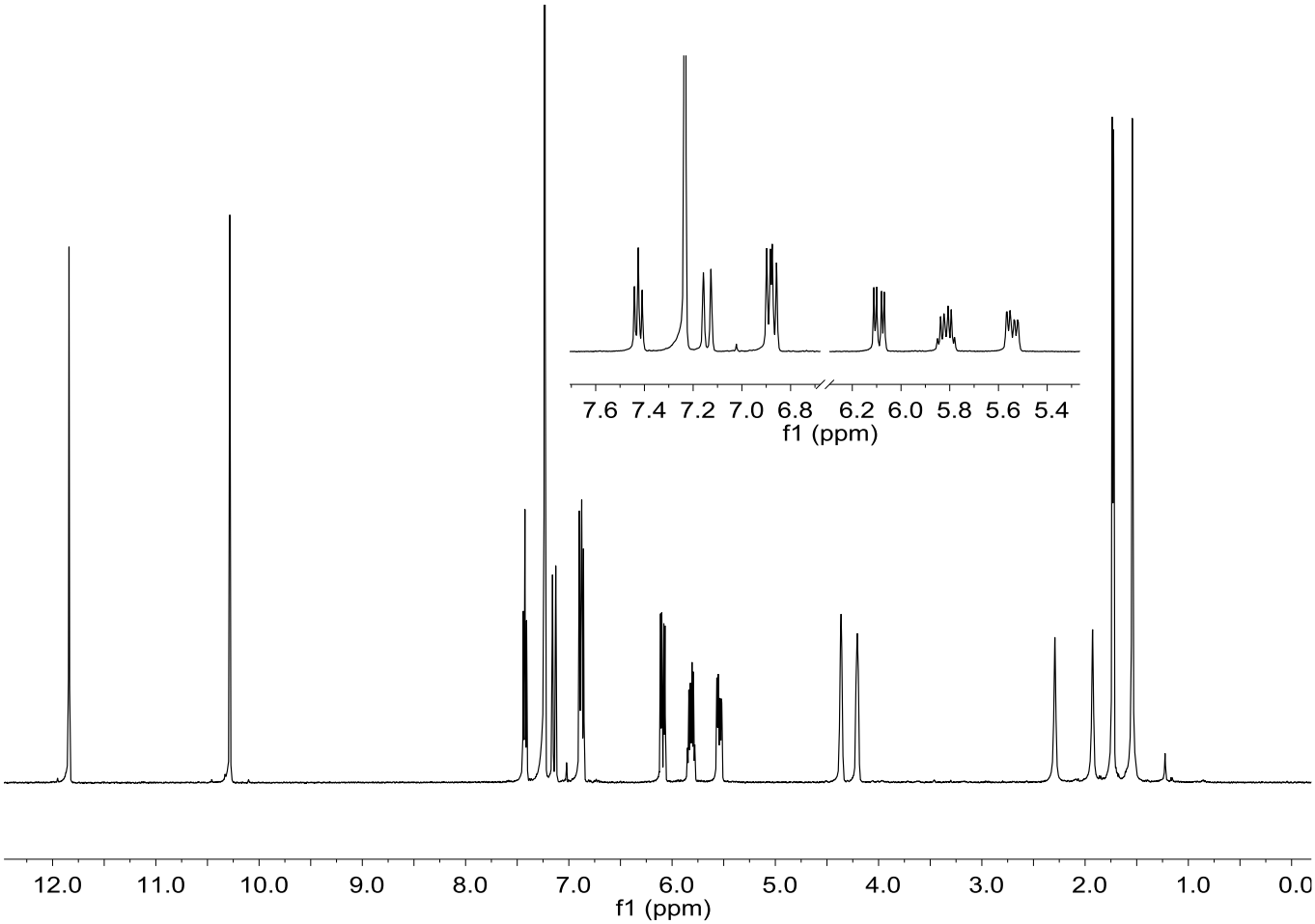
For *MoEF1::C19TF2* a 1137 bp PCR product was amplified by using the primers *EF1-C19TF2*ex-for and *EF1-C19TF2*ex-rev from genomic DNA of *M. oryzae* 70-15. This product was used as a megaprimer for RF-cloning (Bryksin & Matsumura, 2010) (Unger, Jacobovitch, Dantes, Bernheim, & Peleg, 2010). A second 2978 bp PCR product was amplified by using the primers *C19TF2*ex-for and *C19TF2*ex-rev from genomic DNA of *M. oryzae*

70-15. This product was used as a second megaprimer for RF-cloning. The template for RF cloning was the vector *pGEMT+C19TF2(temp)*. *pGEMT+C19TF2(temp)* was given by ligation of the PCR amplificate of the primers *C19TF2ex-template-for* and *C19TF2ex-template-rev* into *pGEMTeasy*. The RF amplificate was cloned into *pJET1.2 blunt* giving *pJET+EF1::C19TF2*. The *Bgl*II restricted fragment of *pJET+EF1::C19TF2* was cloned into *Bgl*II restricted *pCAMB+HPT+Sal* to give the gene expression vector *pCAMB+EF1::C19TF2+HPT*.

S2: NMR-data

1/ PR-70-15-3 was identified as pyriculol based on the comparison with data from the literature (Iwasaki et al., 1973).

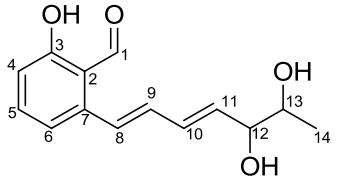
^{1}H NMR (500 MHz, $CDCl_3$) of pyriculol



δ = 11.84 (s, 1H, 3-OH), 10.28 (s, 1H, H-1), 7.43 (pseudo-t, J = 8.0 Hz, 1H, H-5), 7.14 (dd, J = 15.7, 1.6 Hz, 1H, H-8), 6.89 (d, J = 7.8 Hz, 2H, H-6)*, 6.87 (d, J = 8.6 Hz, 2H, H-4)*, 6.09 (dd, J = 15.7, 5.7 Hz, 1H, H-9), 5.81 (dqd, J = 15.7, 6.4, 0.7 Hz, 1H, H-13), 5.54 (ddq, J = 15.7, 7.3, 1.7 Hz, 1H, H-12), 4.36 (br s, 1H, H-10), 4.21 (br

s, 1H, H-11), 2.30 (br s, 1H, OH), 1.30 (br s, 1H, OH), 1.73 (dd, *J* = 6.4, 1.7 Hz, 3H, H-14) ppm. (* = Assignment maybe interchanged.)

2/ AV600-1602A7 was identified as pyriculariol based on the comparison with data from the literature ref Tetrahedron Letters 50 (2009) 4637–4638. The H NMR shows that the sample contains 25% of a related compound.

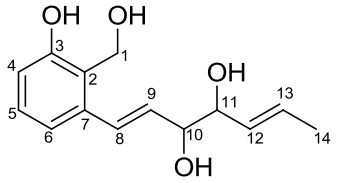


	AV600-1602A7 ($CDCl_3$)		pyriculariol ($CDCl_3$)	
position	H	C	H	C
1	10.3 (1H, s)	195.2	10.3 (1H, s)	
2	-	117.5	-	
3	-	163.0	-	
4	6.88 (1H, d, 8.3)	117.3	6.87 (1H, d, 8.3)	
5	7.45 (1H, pseudo-t, 8.3)	137.3	7.45	
6	6.99 (1H, d, 8.3)	118.5	6.98 (1H, d, 7.8)	
7	-	142.5		
8	7.08 (1H, d, 15.3)	127.0	7.06 (1H, d, 15.3)	
9	6.68 (1H, dd, 10.7, 15.3)	135.0	6.66 (1H, dd, 10.3, 15.3)	
10	6.53 (1H, dd, 10.7, 15.4)	132.3	6.53 (1H, dd, 10.7, 15.1)	
11	5.95 (1H, dd, 6.8, 15.5)	134.1	5.96 (1H, dd, 6.3, 15.1)	
12	4.23 (1H, m)	75.9	4.23 (m)	
13	3.95 (1H, m)	70.4	3.95 (m)	
14	1.19 (3H, d, 6.5)	17.9	1.19 (3H, d, 6.3)	
OH-2	11.9 (1H, s)	-	11.9 (1H, s)	-
OH-12	2.07 (1H, br s)	-	3.49	
OH-13	1.93 (1H, br s)	-	2.31	

AV600-1602A7: ^{1}H NMR ($CDCl_3$, 600 MHz):δ (ppm) 10.3 (1H, s, H-1), 6.88 (1H, d, 8.3, H-4), 7.45 (1H, pseudo-t, 8.3, H-5), 6.99 (1H, d, 8.3 H-6), 7.08 (1H, d, 15.3, H-8), 6.68 (1H, dd, 10.7, 15.3, H-9), 6.53 (1H, dd, 10.7, 15.4, H-10), 5.95 (1H, dd, 6.8, 15.5, H-11), 4.23 (1H, m, H-12), 3.95 (1H, m, H-13), 1.19 (3H, d, 6.5, H-14), 11.9 (1H, s, OH-2), 2.07 (1H, br s, OH-3), 1.93 (1H, br s, OH-13) ^{13}C NMR ($CDCl_3$, 150 MHz):δ (ppm) 195.2 (C-1), 117.5 (C-2), 163.0 (C-3), 117.3 (C-4), 137.3 (C-5), 118.5 (C-6), 142.5 (C-7), 127.0 (C-8), 135.0 (C-9), 132.3 (C-10), 134.1 (C-11), 75.9 (C-12), 70.4 (C-13), 17.9 (C-14).

$[\alpha]_D^{22}$ = +1.8 (c = 0.11, $CHCl_3$).

3/ AV600-1602A8 was identified as epidihydropyriculol or dihydropyriculol based on the comparison with data from the literature Ref: Agricultural and Biological Chemistry Vol. 55 (1991) No. 11 P 2785-2791.

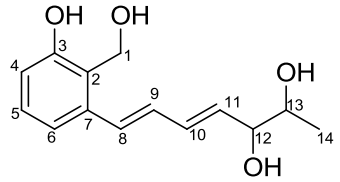


	AV600-1602A8 (MeOD)		Related to dihypyricullariol ($CDCl_3$+CD_3OD)	
position	H	C	See ref	C
1	4.78 (1H, d, 14.0) 4.76 (1H, d, 14.0)	56.6		
2	-	125.3		
3	-	157.3		
4	6.71 (1H, dd, 1.0, 8.0)	115.4		
5	7.07 (1H, pseudo-t, 7.9)	129.7		
6	6.99 (1H, d, 8.3)	118.7		
7	-	139.7		
8	6.95 (1H, d, 15.9)	130.5		
9	6.15 (1H, dd, 6.8, 15.9)	132.6		
10	4.15 (1H, ddd, 1.3, 5.0, 6.5)	77.0		
11	4.04 (1H, dd, 5, 6.1)	77.1		
12	5.59 (1H, m)	131.8		
13	5.75 (1H, m)	129.2		
14	1.73 (3H, dd, 0.8, 6.5)	18.1		

AV600-1602A8: ^{1}H NMR (CD_3OD, 600 MHz):δ (ppm) 4.78 (1H, d, 14.0, H-1a), 4.76 (1H, d, 14.0, H-1b), 6.71 (1H, dd, 1.0, 8.0, H-4), 7.07 (1H, pseudo-t, 7.9, H-5), 6.99 (1H, d, 8.3, H-6), 6.95 (1H, d, 15.9, H-8), 6.15 (1H, dd, 6.8, 15.9, H-9), 4.15 (1H, ddd, 1.3, 5.0, 6.5, H-10), 4.04 (1H, dd, 5, 6.1, H-11), 5.59 (1H, m, H-12), 5.75 (1H, m, H-13), 1.73 (3H, dd, 0.8, 6.5, H-14) ^{13}C NMR (CD_3OD, 150 MHz):δ (ppm) 56.6 (C-1), 125.3 (C-2), 157.3 (C-3), 115.4 (C-4), 129.7 (C-5), 118.7 (C-6), 139.7 (C-7), 130.5 (C-8), 132.6 (C-9), 77.0 (C-10), 77.1 (C-11), 131.8 (C-12), 129.2 (C-13), 18.1 (C-14).

$[\alpha]_D^{22}$ = +5.7 (c = 0.11, MeOH).

4/ AV600-1602A9 was identified as dihydropyricullariol based on the comparison with data from the literature Ref: European Journal of Organic Chemistry Volume 2011, Issue 31, pages 6276–6280.

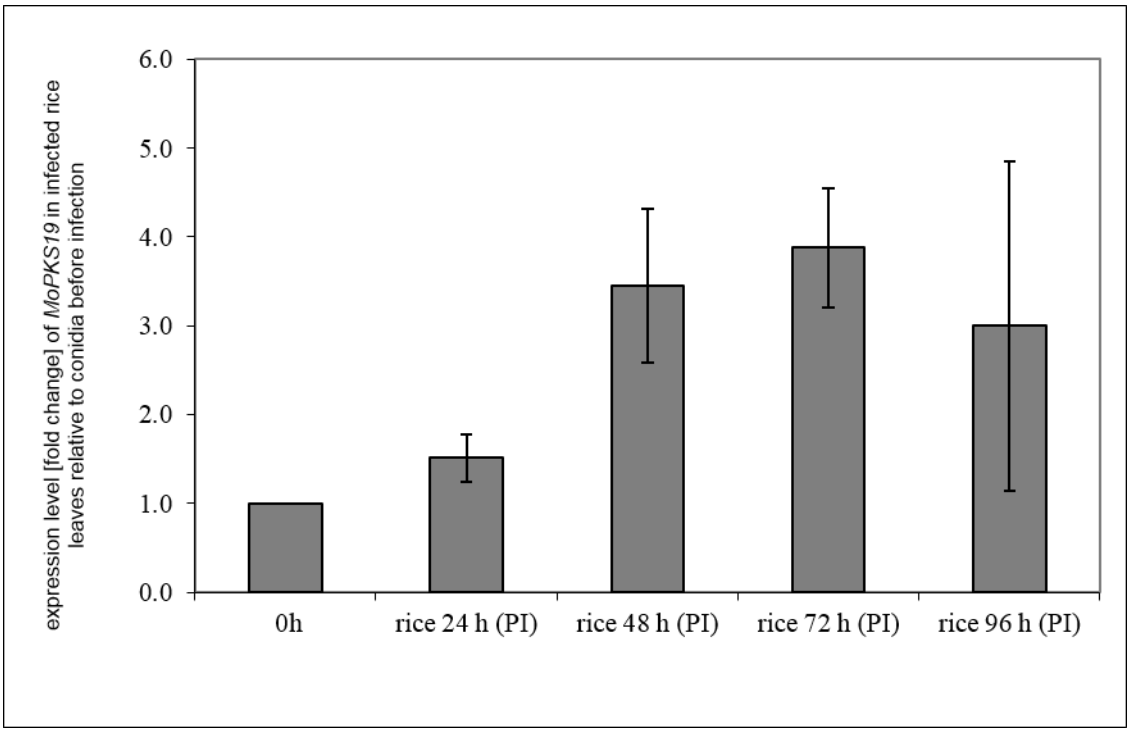


	AV600-1602A9 (MeOD)			
position	H	C		C
1	4.77 (2H, s)	56.3		
2	-	125.3		
3	-	157.4		
4	6.70 (1H, d, 7.0)	115.4		
5	7.08 (1H, pseudo-t, 8.0)	129.7		
6	6.99 (1H, d, 7.0)	118.0		
7	-	139.6		
8	6.97 (1H, d, 15.2)	131.0		
9	6.76 (1H, dd, 10.6, 15.2)	131.8		
10	6.49 (1H, dd, 10.6, 15.3)	133.7		
11	5.90 (1H, dd, 7.0, 15.3)	134.5		
12	4.00 (1H, ddd, 1.0, 5.0, 6.2)	77.6		
13	3.71 (1H, m)	71.7		
14	1.19 (3H, d, 6.5)	18.7		

AV600-1602A9 ^{1}H NMR (CD_3OD, 600 MHz):δ (ppm) 4.77 (2H, s, H-1), 6.70 (1H, d, 7.0, H-4), 7.08 (1H, pseudo-t, 8.0, H-5), 6.99 (1H, d, 7.0, H-6), 6.97 (1H, d, 15.2, H-8), 6.76 (1H, dd, 10.6, 15.2, H-9), 6.49 (1H, dd, 10.6, 15.3, H-10), 5.90 (1H, dd, 7.0, 15.3, H-11), 4.00 (1H, ddd, 1.0, 5.0, 6.2, H-12), 3.71 (1H, m, H-13), 1.19 (3H, d, 6.5, H-14) ^{13}C NMR (CD_3OD, 150 MHz):δ (ppm) 56.3 (C-1), 125.3 (C-2), 157.4 (C-3), 115.4 (C-4), 129.7 (C-5), 118.0 (C-6), 139.6 (C-7), 131.0 (C-8), 131.8 (C-9), 133.7 (C-10), 134.5 (C-11), 77.6 (C-12), 71.7 (C-13), 18.7 (C-14).

$[\alpha]_D^{22}$ = +8.9 (c = 0.07, MeOH).

154 **Fig.S1: MoPKS19 expression in planta**
155



156

157 **Figure S1:** **qRT-PCR analysis of the *in planta* expression level from the *MoPKS19* gene.** Conidia of *M. oryzae*
158 cultures were harvested and used for plant infection as stated in methods section. Samples were taken after
159 24 h, 48 h, 72 h and 96 h. The RNA was isolated from rice leaves and the results of transcript abundance in
160 were given relative to quantification in the conidia pre infection. Three replicates were made of each.

161

Fig.S2: Phylogenetic analysis of MoPks19p and tree visualization

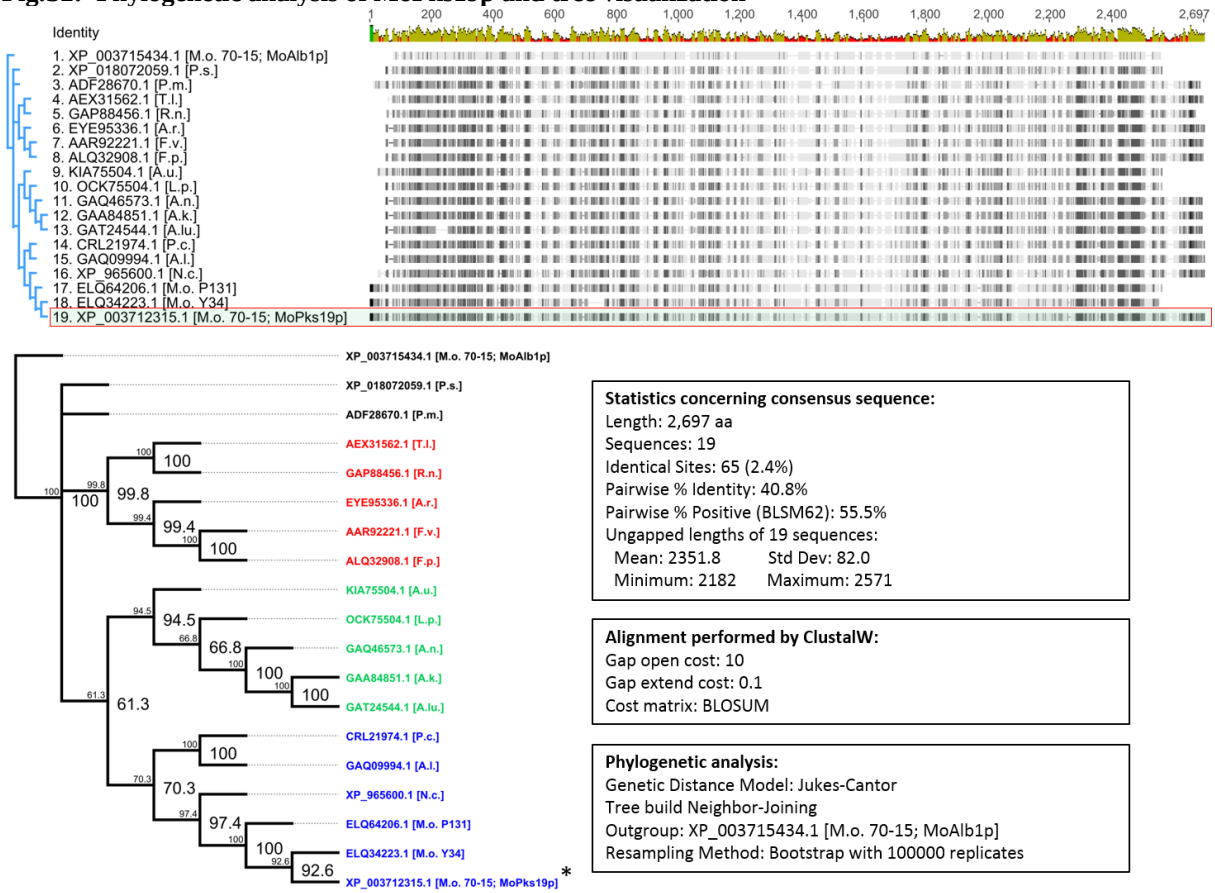


Figure S2: Phylogenetic analysis of amino acid sequences of MoPks19 from *Magnaporthe oryzae* and selected fungal species. The GeneBank accession numbers of the analyzed proteins or the gene name from the JGI database are shown and trivial names were shown in square brackets. Related clades of the dendrogram have the same colour. MoAlb1p was used as *Magnaporthe*-internal PKS-control. P.s. (*Phialocephala scopiformis*), N.c. (*Neurospora crassa*), R.n. (*Rosellinia necatrix*), A.n. (*Aspergillus niger*), P.m. (*Peltigera membranacea*), F.v. (*Fusarium verticillioides*), A.l. (*Aspergillus lentulus*), M.o. (*Magnaporthe oryzae*), A.k. (*Aspergillus kawachii*), A.lu. (*Aspergillus luchuensis*), A.r. (*Aspergillus ruber*), P.c. (*Penicillium camemberti*), L.p. (*Lepidopterella palustris*), T.l. (*Trichoderma lixii*), L.p. (*Lepidopterella palustris*)

Fig.S3: qPCR results from selected putative PKS19 clustered genes.

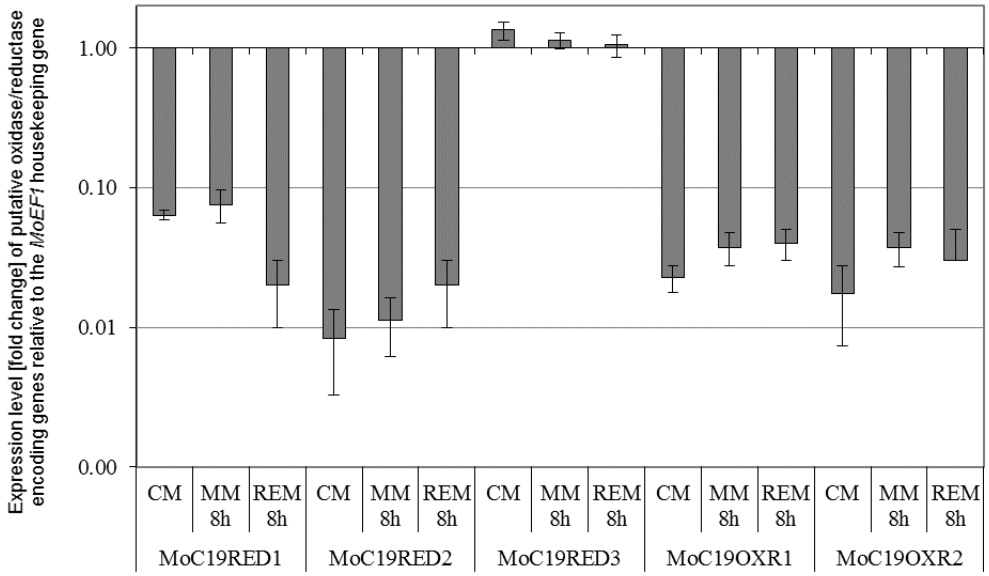


Figure S3: **qRT-PCR analysis of the expression level from selected putative PKS19 clustered genes.** The *M. oryzae* cultures were grown for 72 h in CM at 26 °C and 120 rpm. The mycelium was transferred for further submersed cultivation to MM or REM at 26 °C and 120 rpm. Samples were taken after 8 h. The RNA was isolated from the mycelium samples and the results of transcript abundance in MM or REM were given relative to EF1 alpha expression. Three replicates were made of each.

Fig.S4: Pathogenicity assay

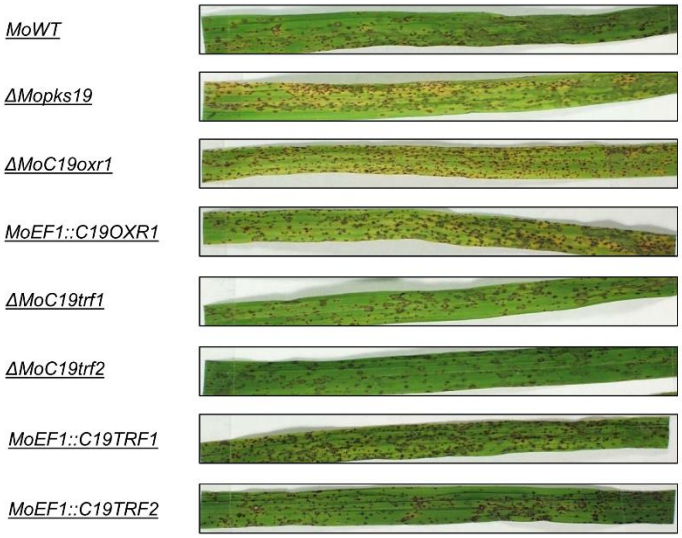


Figure S4: **Rice leaves of cultivar CO-39 infected with the *Magnaporthe oryzae* 70-15 (*MoWT*) strain and the mutant strains.** The plant infection assays were carried out as described in experimental procedures. Conidial suspensions were adjusted to 5×10^4 conidia/mL in H_2O containing 0.2% gelatin. The intact rice plants were spray-inoculated with each 5 mL of conidial suspension and were incubated in plastic bags in a test chamber for 5 days at 28°C.