The biosynthetic pathway for a thousand-year-old natural food colorant and citrinin in *Penicillium marneffei*

Patrick C. Y. Woo^{1,2,3,4*}⁺, Ching-Wan Lam⁵⁺ Emily W. T. Tam¹⁺, Kim-Chung Lee⁵, Karrie K. Y. Yung⁵, Chris K. F. Leung⁵, Kong-Hung Sze^{1,2,3,4}, Susanna K. P. Lau^{1,2,3,4*} and Kwok-Yung Yuen^{1,2,3,4}

¹Department of Microbiology, The University of Hong Kong, Hong Kong, ²State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong, Hong Kong,

³Research Centre of Infection and Immunology, The University of Hong Kong, Hong Kong,

⁴Carol Yu Centre for Infection, The University of Hong Kong, Hong Kong,

⁵Department of Pathology, The University of Hong Kong, Hong Kong



Supplementary Figure S1: Expression of *pks3* and the 14 genes upstream and downstream of *pks3* in the corresponding knockdown mutants of *Penicillium marneffei*.



x104 1.7

1.6

1.5 1.4 1.3

1.2 1.1 0.9 0.8-0.7 0.6

0.5 0.4-

0.3

0.2

0.1 0.



Supplementary Figure S2: Detection of arginine conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of arginine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

300 vs. Mass-to

320 340 o-Charge (m/z)

380

360

400

420 440 540

500

460 480

280 Counts

160

180

200 220 240 260

140

100

120

80



Supplementary Figure S3: Detection of lysine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of lysine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



Supplementary Figure S4: Detection of asparagine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of asparagine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



x103

1.9

1.8 1.7

1.6 1.5 1.4 1.3

1.2 1.1 1 0.9

0.8 0.7

0.6 0.5

0.4

0.3

0.2

0.1 0



Supplementary Figure S5: Detection of serine conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of serine-monascorubrin conjugate detected in wild type P. marneffei but not in pks3 or rp1 to rp4 knockdown mutants.

Counts vs. Mass-to-Charge (m/z)



Supplementary Figure S6: Detection of glutamic acid conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of glutamic-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



Supplementary Figure S7: Detection of tyrosine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of tyrosine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



Supplementary Figure S8: Detection of glycine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of glycine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



а

с



Supplementary Figure S9: Detection of aspartic acid conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of aspartic acid-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



а

b

с



Supplementary Figure S10: Detection of tryptophan conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of tryptophan-monascorubrin conjugate detected in wild type P. marneffei but not in pks3 or rp1 to rp4 knockdown mutants.

280 3 Countr

340 o-Cha





Supplementary Figure S11: Detection of valine conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of valine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.



x103

1.5 1.4 1.3 1.2 1.1

0.9 0.8 0.7 0.6 0.5 0.4

0.3

0.2

0.1



Supplementary Figure S12: Detection of methionine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of methionine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

-Charge (m/z)

Supplementary Figure S13: Detection of leucine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of leucine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

Supplementary Figure S14: Detection of isoleucine conjugated with monascorubrin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of isoleucine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

x10³

1.15 1.1

1.05-1-0.95-0.8-0.8-0.75-0.6-0.55-0.4-0.3-0.3-0.2-0.15-0.2-0.15-0.2-0.15-0.2-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.3-0.4-0.5-0

0.1 0.05 0.

Supplementary Figure S15: Detection of phenylalanine conjugated with monascorubrin in P. marneffei. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of phenylalanine-monascorubrin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

Supplementary Figure S16: Detection of arginine conjugated with rubropunctatin in *P. marneffei.* (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of arginine-rubropunctatin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

x10²

9.5 9

8.5-8-7.5-6.5-5.5-5.5-4.5-3.5-3.5-3.5-2.5-2.5-2.5-1.5-1.5-

0.5

Supplementary Figure S17: Detection of phenylalanine conjugated with rubropunctatin in *P. marneffei*. (a) Extracted ion chromatogram, (b) UV absorption spectrum and (c) MS/MS fragmentation pattern showing the presence of phenylalanine-rubropunctatin conjugate detected in wild type *P. marneffei* but not in *pks3* or *rp1* to *rp4* knockdown mutants.

vs. Mass-to-Charge (m/z)

Counts

390 400 410 420 430 440 450 460 470 480 490 500 510 520 530

90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380

D man offoi atuaina	Relative expression						
P. marnejjel strains	pks3	rp1	rp2	rp3	rp4		
Wild type	1	1	1	1	1		
pks3 KD mutant	< 0.01	0.13	0.08	0.05	0.05		
<i>rp1</i> KD mutant	0.05	0.15	0.12	0.01	0.10		
<i>rp2</i> KD mutant	0.54	0.91	0.23	0.90	0.52		
<i>rp3</i> KD mutant	0.98	1.06	0.30	0.33	0.73		
<i>rp4</i> KD mutant	0.44	0.62	0.22	2.10	0.29		

Supplementary Table S1: Relative expression of all genes involved in biosynthesis of red pigment in different knockdown mutants of *Penicillium marneffei*.

Sample		Absorption maxima		
wild type	373	405	499	553
orfl knockdown	373	411	501	553
orf2 knockdown	373	416	499	556
orf3 knockdown	373	416	500	558
orf4 knockdown	373	404	498	556
orf5 knockdown	372	414	503	558
<i>pks3</i> knockdown				560
rp1 knockdown				559
rp2 knockdown	372	404		561
<i>rp3</i> knockdown	372	404		561
rp4 knockdown	372	411		559
orf6 knockdown	373	417	500	557
orf7 knockdown	372	417	496	553
orf8 knockdown	374	416	499	554
orf9 knockdown	376	417	499	556
orf10 knockdown	373	409	494	557
medium				560

Supplementary Table S2: UV-Vis spectroscopic absorption maxima of culture filtrates in *Penicillium marneffei*.

Supplementary	Table	S3:	Molecul	ar	formula,	mass-to-	-charge	ratio	and
retention time of	of diffe	rent	amino a	cids	conjugat	ed with	monas	corubrin	l or
rubropunctatin	in cu	lture	filtrate	of	Penicilliu	m mari	ieffei d	letected	by
UHPLC-MS ana	alysis.								

Name	Molecular Formula	Mass-to-charge ratio	Retention time (min)
Arginine-monascorubrin	C ₂₉ H ₃₈ N ₄ O ₆	538.2791	16.037
Arginine-rubropunctatin	$C_{27}H_{34}N_4O_6$	510.2478	13.407
Asparagine-monascorubrin	$C_{27}H_{32}N_2O_7$	496.2282	18.901
Aspartic acid-monascorubrin	$\mathrm{C}_{27}\mathrm{H}_{31}\mathrm{NO}_{8}$	497.2050	19.584
Glutamic acid-monascorubrin	C ₂₈ H ₃₃ NO ₈	511.2206	19.205
Glycine-monascorubrin	$C_{25}H_{29}NO_6$	439.1995	19.533
Isoleucine-monascorubrin	C ₂₉ H ₃₇ NO ₆	495.2621	23.197
Leucine-monascorubrin	C ₂₉ H ₃₇ NO ₆	495.2621	22.941
Lysine-monascorubrin	$C_{29}H_{38}N_2O_6$	510.2730	16.913
Methionine-monascorubrin	C ₂₈ H ₃₅ NSO ₆	513.2185	22.279
Phenylalaine-monascorubrin	$C_{32}H_{35}NO_6$	529.2464	23.209
Phenylalaine rubropunctatin	$C_{30}H_{31}NO_{6}$	502.2224	19.730
Serine-monascorubrin	$\mathrm{C}_{26}\mathrm{H}_{31}\mathrm{NO}_{7}$	469.2101	18.901
Tryptophan-monascorubrin	$C_{34}H_{36}N_2O_6$	568.2573	20.696
Tyrosine-monascorubrin	$C_{32}H_{35}NO_7$	545.2414	19.348
Valine-monascorubrin	C ₂₈ H ₃₅ NO ₆	481.2464	22.157

Supplementary Table S4: Primers and plasmids used for gene knockdown experiments in the present study.

Gene	Primer	RE site	F/R	Sequence (5'-3')	Plasmid
orfl LPW1768		XhoI	F	CCGCTCGAGTATGTCCGGGCACAGACAAG	pPW2284
	LPW17687	HindIII	R	CCCAAGCTTGGGAGTGGGACGCAGTTGACACC	
	LPW17688	KpnI	F	GGGGTACCTATGTCCGGGCACAGACAAG	
	LPW17689	<i>Bgl</i> II	R	GAAGATCTAGTGGGACGCAGTTGACACC	
orf2	LPW17690	XhoI	F	CCGCTCGAGGGGGGGAGAACGTGCTTTTGCTC	pPW2285
	LPW17691	HindIII	R	CCCAAGCTTGGGGAAGGAGCCGGTGACTTCAA	
	LPW17692	KpnI	F	GGGGTACCGGGAGAACGTGCTTTTGCTC	
	LPW17693	<i>Bgl</i> II	R	GAAGATCTGAAGGAGCCGGTGACTTCAA	
orf3	LPW17694	XhoI	F	CCGCTCGAGCGACACATACGATCATCCAGCA	pPW2286
	LPW17695	HindIII	R	CCCAAGCTTGGGTGTCGCTACCAGTTGGCTCA	
	LPW17696	KpnI	F	GGGGTACCCGACACATACGATCATCCAGCA	
	LPW17697	<i>Bgl</i> II	R	GAAGATCTTGTCGCTACCAGTTGGCTCA	
orf4	LPW17698	XhoI	F	CCGCTCGAGCGATACTCCGTGTGAAAGACTGC	pPW2287
	LPW17699	HindIII	R	CCCAAGCTTGGGGTGGCTGTGGTCAAGCAGTG	
	LPW17700	KpnI	F	GGGGTACCCGATACTCCGTGTGAAAGACTGC	
	LPW17701	<i>Bgl</i> II	R	GAAGATCTGTGGCTGTGGTCAAGCAGTG	
orf5	LPW17702	XhoI	F	CCGCTCGAGCGTTTTCGTTACCGGAGGTT	pPW2288
	LPW17703	HindIII	R	<u>CCCAAGCTTGGG</u> AGCATGGGTAGGAATGACCG	
	LPW17704	KpnI	F	GGGGTACCCGTTTTCGTTACCGGAGGTT	
	LPW17705	<i>Bgl</i> II	R	GAAGATCTAGCATGGGTAGGAATGACCG	
pks3	LPW9873	XhoI	F	CCGCTCGAGCCTTCTCTTTCGGATCTCTTC	pPW1294
	LPW9874	KpnI	F	GGGGTACCCCTTCTCTTTCGGATCTCTTC	
	LPW9875	<i>Bgl</i> II	R	GAAGATCTGCCTAATGTCAAGCTTTTCG	
rpl	LPW 18206	XhoI	F	CCGCTCGAGCTGCTGGCGATACCGAGTTC	pPW2422
	LPW 18207	HindIII	R	<u>CCCAAGCTTGGG</u> GCAAGGCATCAGCTCAATGA	
	LPW 18208	KpnI	F	GGGGTACCCTGCTGGCGATACCGAGTTC	
	LPW 18209	<i>Bgl</i> II	R	GAAGATCTGCAAGGCATCAGCTCAATGA	
rp2	LPW 17706	XhoI	F	CCGCTCGAGCATGGGCTACTCGGTTTGGA	pPW2289
	LPW 17707	HindIII	R	CCCAAGCTTGGGGTTCGCCTTTGGAGTTCTGC	
	LPW 17708	KpnI	F	GGGGTACCCATGGGCTACTCGGTTTGGA	
	LPW 17709	<i>Bgl</i> II	R	GAAGATCTGTTCGCCTTTGGAGTTCTGC	
rp3	LPW 18210	XhoI	F	CCGCTCGAGGCAGTAATCGGTTGGGTTCG	pPW2423
	LPW 18211	HindIII	R	CCCAAGCTTGGGCGCATGGAACTGAAGGATGA	
	LPW 18212	KpnI	F	GGGGTACCGCAGTAATCGGTTGGGTTCG	
	LPW 18213	<i>Bgl</i> II	R	GAAGATCTCGCATGGAACTGAAGGATGA	
rp4	LPW 18214	XhoI	F	CCGCTCGAGAAAGTCAATGACCCTGCCGA	pPW2424
	LPW 18215	HindIII	R	CCCAAGCTTGGGGGTCAAAGACCTGGCTGGCAC	
	LPW 18216	KpnI	F	GGGGTACCAAAGTCAATGACCCTGCCGA	
	LPW 18217	<i>Bgl</i> II	R	GAAGATCTGTCAAAGACCTGGCTGGCAC	

Gene	Primer	RE site	F/R	Sequence (5'-3')	Plasmid
orf6	LPW18683	XhoI	F	CCGCTCGAGATAGACCTGAAATGGTTCCGATGG	pPW2425
	LPW18684	HindIII	R	<u>CCCAAGCTTGGG</u> GTGATGTAAATCCTCATCGAGCAG	
	LPW18685	KpnI	F	GGGGTACCATAGACCTGAAATGGTTCCGATGG	
	LPW18686	<i>Bgl</i> II	F	GAAGATCTGTGATGTAAATCCTCATCGAGCAG	
orf7	LPW18426	XhoI	R	CCGCTCGAGAGGCTCCTTTCTCCTCCGAT	pPW2426
	LPW18427	HindIII	F	CCCAAGCTTGGGTGAACGTGGATTGTGGGAAG	
	LPW18428	KpnI	R	GGGGTACCAGGCTCCTTTCTCCTCCGAT	
	LPW18429	<i>Bgl</i> II	F	GAAGATCTTGAACGTGGATTGTGGGAAG	
orf8	LPW18430	XhoI	R	CCGCTCGAGCGCTGTGACCGAAATGGAT	pPW2427
	LPW18431	HindIII	F	<u>CCCAAGCTTGGG</u> GGAGTCACACCGCAGATAATGA	
	LPW18432	KpnI	R	GGGGTACCCGCTGTGACCGAAATGGAT	
	LPW18433	<i>Bgl</i> II	F	GAAGATCTGGAGTCACACCGCAGATAATGA	
orf9	LPW18434	XhoI	F	CCGCTCGAGCTGGTTGGAGGTGCCTTGA	pPW2428
	LPW18435	HindIII	R	CCCAAGCTTGGGGCCCATACTGTGCGAATCGTA	
	LPW18436	KpnI	F	GGGGTACCCTGGTTGGAGGTGCCTTGA	
	LPW18437	<i>Bgl</i> II	R	GAAGATCTGCCCATACTGTGCGAATCGTA	
orf10	LPW18438	XhoI	F	CCGCTCGAGGAGGAGGAAATTGACCAGACTGG	pPW2429
	LPW18439	HindIII	R	CCCAAGCTTGGGGGTCAGACCTTCCTTGCCGT	
	LPW18440	KpnI	F	GGGGTACCGAGGAGGAAATTGACCAGACTGG	
	LPW18441	<i>Bgl</i> II	R	GAAGATCTGGTCAGACCTTCCTTGCCGT	