

**Divergence of pigments in three phylogenetically close *Monascus* species (*M. pilosus*, *M. ruber*, and *M. purpureus*) based on secondary metabolite biosynthetic gene clusters**

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**Table 1 Classification of gene clusters (ID1-54) corresponding to the dendrogram in Figure 4.**

The type of GCs was determined using antiSMASH software. Pi, Ru, and Pu represent the cluster ID in Figure 4. Identical gene organization is denoted by red numbers. The secondary metabolic pathways represent the secondary metabolite information based on DNA sequence homology. Type of ATP-binding cassettes detected in individual groups is represented as ATP-binding cassettes. Gene-cluster groups with both identical gene organization and high DNA sequence similarity are denoted by ‘\*\*’ and groups with only high DNA sequence similarity are denoted by ‘\*’. Two-letter abbreviations used for the Venn diagrams: Pi, *M. pilosus* NBRC 4520; Ru, *M. ruber* NBRC 4483; Pu, *M. purpureus* NBRC 4478.

ID	Type of GCs	Pi	Ru	Pu	Secondary metabolic pathways detected in DNA sequence homology	ATP-binding cassettes	Identity level
1	t1pks	1	4	-	Narbonolide/10-deoxymethynolide ( <i>pikAI – AIV</i> ), Phthiocerol/phenolphthionoceros ( <i>ppsA - E</i> )	-	**
2	t1pks	2	-	-	Phthiocerol/phenolphthionoceros ( <i>ppsA - E</i> )	-	-
3	t1pks	18	19	7	Azaphilone*, Lovastatin (LOVB, LOVF) , Narbonolide/10-deoxymethynolide ( <i>pikAI – AIV</i> ), Phthiocerol/phenolphthionoceros ( <i>ppsA - E</i> )	-	-
4	t1pks	22	-	-	-	-	*
5	t1pks	23	48	17	Lovastatin (LOVB, LOVF) , Narbonolide/10-deoxymethynolide ( <i>pikAI – AIV</i> ), Phthiocerol/phenolphthionoceros ( <i>ppsA - E</i> )	-	*
6	t1pks	19	43	-	Monacolin K*, Compactin, Lovastatin (LOVA, LOVB)	-	*
7	t1pks	-	-	8	Citrinin*, Narbonolide/10-deoxymethynolide ( <i>pikAI– AIV</i> ), Phthiocerol/phenolphthionoceros ( <i>ppsA-C, E</i> )	-	*
8	t1pks	9	-	10	Byssochlamic acid*, Narbonolide/10-deoxymethynolide ( <i>pikAI–AIV</i> ), Phthiocerol/phenolphthionoceros ( <i>ppsA-C, E</i> )	-	*
9	nrps	4	10	19	Neosartoricin*, Fengycin ( <i>fenA–E</i> ), Surfacin( <i>srfAA-AC</i> )	-	**
10	nrps	13	30	20	Brevianamide F ( <i>FTMA</i> )	ABCB	**
11	nrps	7	2	-	Fengycin ( <i>fenA-E</i> ), Surfacin ( <i>srfAA-AC</i> )	ABCC	**
12	nrps	11	23	2	Fengycin ( <i>fenA-D</i> )	ABCC	**
13	nrps	5	22	12	Fengycin ( <i>fenA-D</i> )	-	*
14	nrps	24	21	-	Fengycin ( <i>ppsA-D</i> ), surfacing ( <i>srfAA-AC</i> )	ABCB	*
15	nrps	3	41	-	Fengycin ( <i>fenA–D</i> )	-	*
16	nrps	-	-	9	Fengycin ( <i>fenB, D</i> ), Ferricrocin ( <i>SIDC, SIDD</i> )	-	-
17	t1pks-nrps	8	40	5	NG-391*, Fengycin ( <i>fenA–E</i> ), Surfacin ( <i>surAA-AC</i> )	ABCC	**
18	t1pks-nrps	14	27	14	Gramicidin ( <i>grsA-B</i> ), Fengycin ( <i>fenA–E</i> ), Surfacin ( <i>surAA-AC</i> )	-	*
19	t1pks-nrps	20	13	3	Lovastatin ( <i>LOVB, LOVF</i> ), Fengycin ( <i>fenA-E</i> ), Surfacin ( <i>srfAA-AC</i> )	ABCB	*
20	terpene	12	24	11	Fernesyl-diphosphate ( <i>FDFTI</i> )	-	**
21	terpene	17	12	13	Lupeol ( <i>LUPI,2,4,5</i> ), Arabidiol ( <i>PEN1</i> ), Tinucalladienol ( <i>PEN3</i> ), seco-amyrin ( <i>PEN6</i> )	-	*

ID	Type of GCs	Pi	Ru	Pu	Secondary metabolic pathways detected in DNA sequence homology	ATP-binding cassettes	Identity level
22	terpene	-	-	15	-	-	-
23	others	15	42	18	Fengycin ( <i>fenA, C, E</i> ), Surfactin ( <i>srfAA-AB</i> )	ABCF	**
24	others	6	32	6	Kinesin ( <i>KIDFC1-3</i> )	-	*
25	others	10	5	16	Abscisic aldehyde ( <i>AAO1-4</i> ), Fengycin ( <i>fenA, B, E</i> ), Surfactin ( <i>srfAA, AB</i> )	ABCB	*
26	others	16	33	4	Histidinol ( <i>hisD, IE</i> )	-	*
27	others	21	28	1	-	-	*
28	cf-putative	-	1	-	-	-	-
29	cf-putative	-	3	-	Palmitin ( <i>ZDHHC</i> )	-	-
30	cf-putative	-	6	-	Palmitin ( <i>ZDHHC4</i> )	-	-
31	cf-putative	-	7	-	-	-	-
32	cf-putative	-	8	-	-	-	-
33	cf-putative	-	9	-	-	-	-
34	cf-putative	-	11	-	-	-	-
35	cf-putative	-	14	-	Serine, Threonine ( <i>PPIC, 2C, 4C, 6C</i> )	-	-
36	cf-putative	-	15	-	-	ABCG2	-
37	cf-putative	-	16	-	-	-	-
38	cf-putative	-	17	-	-	-	-
39	cf-putative	-	18	-	Mannan ( <i>ANPI, MNN9</i> )	-	-
40	cf-putative	-	20	-	-	-	-
41	cf-putative	-	25	-	-	-	-
42	cf-putative	-	29	-	-	-	-
43	cf-putative	-	31	-	-	-	-
44	cf-putative	-	34	-	-	-	-
45	cf-putative	-	36	-	-	-	-
46	cf-putative	-	37	-	-	-	-
47	cf-putative	-	38	-	-	-	-

<b>ID</b>	<b>Type of GCs</b>	<b>Pi</b>	<b>Ru</b>	<b>Pu</b>	<b>Secondary metabolic pathways detected in DNA sequence homology</b>	<b>ATP-binding cassettes</b>	<b>Identity level</b>
48	cf-putative	-	39	-	Lovastatin ( <i>LOVB-G</i> ), Phthiocerol/Phenolphthiocerol ( <i>ppsA,C</i> )	-	-
49	cf-putative	-	44	-	-	-	-
50	cf-putative	-	45	-	-	-	-
51	cf-putative	-	46	-	-	-	-
52	cf-putative	-	47	-	-	-	-
53	cf_fatty_acid	-	26	-	-	-	-
54	cf_fatty_acid	-	35	-	Fatty acid ( <i>FAS1,2</i> )	-	-

**Table 2 Comparison of six *M. purpureus*, *M. ruber*, and *M. pilosus* strains based on *Monascus* azaphilone pigment polyketide synthase gene. Mutated nucleotides of the target gene were extracted and summarized in the table.**

		30	
		57	
		88	
		108	
		117	
		123	
		161	
		216	
		219	
		288	
		291	
		321	
		369	
		376	
		392	
		394	
		423	
		442	
		447	
		466	
		471	
		478	
		483	
		516	
		578	
		589	
		606	
		627	
		648	
		663	
		685	
		703	
		748	
		774	
		802	
		820	
		834	
		860	
		939	
		966	
		1022	
		1074	
		1085	
		1112	
		1152	
		1172	
		1180	
		1186	
		1188	
		1193	
<i>M. pilosus</i> NBRC 4520	A	A	A
<i>M. pilosus</i> NCBI	A	A	A
<i>M. ruber</i> NRRP 1597	A	A	A
<i>M. ruber</i> NBRC 4483	A	A	A
<i>M. ruber</i> JF83291.6	C	G	G
<i>M. purpureus</i> NRRP 1596	C	G	G
<i>M. purpureus</i> NBRC 4478	C	G	G
		1204	
<i>M. pilosus</i> NBRC 4520	T	A	G
<i>M. pilosus</i> NCBI	T	A	G
<i>M. ruber</i> NRRP 1597	T	A	G
<i>M. ruber</i> NBRC 4483	T	A	G
<i>M. ruber</i> JF83291.6	C	G	G
<i>M. purpureus</i> NRRP 1596	C	G	G
<i>M. purpureus</i> NBRC 4478	C	G	G
		2681	
<i>M. pilosus</i> NBRC 4520	C	T	C
<i>M. pilosus</i> NCBI	C	T	C
<i>M. ruber</i> NRRP 1597	C	T	C
<i>M. ruber</i> NBRC 4483	C	T	C
<i>M. ruber</i> JF83291.6	T	C	T
<i>M. purpureus</i> NRRP 1596	T	C	T
<i>M. purpureus</i> NBRC 4478	T	C	T
		3919	
<i>M. pilosus</i> NBRC 4520	T	A	A
<i>M. pilosus</i> NCBI	T	A	A
<i>M. ruber</i> NRRP 1597	T	A	A
<i>M. ruber</i> NBRC 4483	T	A	A
<i>M. ruber</i> JF83291.6	C	G	G
<i>M. purpureus</i> NRRP 1596	C	G	G
<i>M. purpureus</i> NBRC 4478	C	G	G
		5492	
<i>M. pilosus</i> NBRC 4520	C	A	T
<i>M. pilosus</i> NCBI	C	A	T
<i>M. ruber</i> NRRP 1597	C	A	T
<i>M. ruber</i> NBRC 4483	C	A	T
<i>M. ruber</i> JF83291.6	T	G	G
<i>M. purpureus</i> NRRP 1596	T	G	G
<i>M. purpureus</i> NBRC 4478	T	G	G
		7189	
<i>M. pilosus</i> NBRC 4520	A	A	G
<i>M. pilosus</i> NCBI	A	A	G
<i>M. ruber</i> NRRP 1597	A	A	G
<i>M. ruber</i> NBRC 4483	A	A	G
<i>M. ruber</i> JF83291.6	G	C	C
<i>M. purpureus</i> NRRP 1596	G	C	C
<i>M. purpureus</i> NBRC 4478	G	C	C

**Table 3 Homologous peptide sequences of the citrinin biosynthetic genes in three *Monascus* species.**

Protein	<i>M. pilosus</i> NBRC 4520		<i>M. ruber</i> NBRC 4483		<i>M. purpureus</i> NBRC 4478		Reference peptide
	length	(%)	length	(%)	length	(%)	sequence
CitA ( <i>mpl1</i> )	249	79.6	249	79.6	312	99.7	313
CitB ( <i>mpl2</i> )	229	69.6	229	69.6	328	99.7	329
CitD ( <i>mpl4</i> )	458	91.4	458	91.4	500	99.8	501
CitE ( <i>mpl6</i> )	231	79.1	231	79.1	284	97.3	292
CitC ( <i>mpl7</i> )	532	85.5	532	85.5	618	99.4	622
CitS ( <i>pksCT</i> )	1525	58.8	1525	58.8	2396	92.4	2593

**Table 4 Homologous peptide sequences of the monacolin biosynthetic genes in three *Monascus* species.**

Protein	<i>M. pilosus</i> NBRC 4520		<i>M. ruber</i> NBRC 4483		<i>M. purpureus</i> NBRC 4478		Reference peptide
	length	(%)	length	(%)	length	(%)	sequence
MokA	1910	100	1910	100	1772	92.8	1910
MokB	1947	100	1947	100	1501	77.1	1947
MokC	339	100	339	100	28	8.3	339
MokD	263	100	263	100	154	58.6	263
MokE	265	100	265	100	231	87.2	265
MokF	258	100	258	100	167	64.7	258
MokG	996	99.0	977	100	322	32.3	977
MokH	487	100	487	100	42	8.6	487
MokI	174	100	174	100	107	61.5	174

