

Supporting Information

Table S1. PKSs and NRPSs in the gene clusters of *S. cellostaticus* NBRC 12849^T pages 2 to 6

Table S1. PKSs and NRPSs in the gene clusters of *S. cellostaticus* NBRC 12849^T.

Gene cluster	Type	Contig	Scel_ ¹	Domain organization	Closest ortholog (I/S ² , Accession no., Source) ³	Predicted product ⁴
Cluster 1	<i>t1pks</i>	sequence02	01580 01590	ACP-KS/AT _{mm} /DH/ACP KS/AT _{mm} /KR/ACP-KS	57/66, MCC4316281, <i>S. malaysiensis</i> HSL-9B 51/61, WEH32272, <i>Streptomyces</i> sp. AM 4-1-1	diketide (a)
Cluster 2	<i>pks/nrps</i>	sequence02 sequence12	04715 ⁵ 87535 ⁵	KS/AT _{mm} /ACP-KS/AT _m /DH/ER/KR... ...KS/AT _{mm} /DH/ACP-C/A _{Cys} /T-TE	84/88, AYN42590, <i>S. dangxiongensis</i> Z022 ^T 83/88, AYN42588, <i>S. dangxiongensis</i> Z022 ^T	tetraketide with Cys (b)
Cluster 3	<i>pks/nrps</i>	sequence06	82410 82420 82430	CoL ACP-KS/AT _{mm} /DH/KR/ACP -KS/AT/DH/KR/ACP-C/FkbH T-TD	90/94, ANP52823, <i>S. griseochromogenes</i> ATCC 14511 ^T (80/87, AOE23577(FoxBI), <i>S. diastatochromogenes</i> Tue6028) 90/92, ANP52822, <i>S. griseochromogenes</i> ATCC 14511 ^T (74/80, AOE23578(FoxBII), <i>S. diastatochromogenes</i> Tue6028) 92/95, ANP52821, <i>S. griseochromogenes</i> ATCC 14511 ^T (77/92, AOE23579(FoxBIII), <i>S. diastatochromogenes</i> Tue6028)	foxicin (c)
Cluster 4	<i>pks/nrps</i>	sequence06	80980 80970 80950 80930 80920 80910 80890 80870	KR A AGly/T KS ACP KS ACP ER	89/94, ANP53435, <i>S. griseochromogenes</i> ATCC 14511 ^T 89/93, ANP53436, <i>S. griseochromogenes</i> ATCC 14511 ^T 86/88, ANP53437, <i>S. griseochromogenes</i> ATCC 14511 ^T 93/95, ANP53439, <i>S. griseochromogenes</i> ATCC 14511 ^T 85/90, ANP53439, <i>S. griseochromogenes</i> ATCC 14511 ^T 92/90, ANP53440, <i>S. griseochromogenes</i> ATCC 14511 ^T 80/87, ANP53441, <i>S. griseochromogenes</i> ATCC 14511 ^T 93/96, ANP52929, <i>S. griseochromogenes</i> ATCC 14511 ^T	unknown
Cluster 5	<i>t3pks</i>	sequence06	77590	KS	97/98, ANP53460, <i>S. griseochromogenes</i> ATCC 14511 ^T (87/93, CAC01488(SCO1206), <i>S. coelicolor</i> A3(2))	flaviolin (d)
Cluster 6	<i>t1pks</i>	sequence06	76540 76550 76560	KS/AT _m /ACP-KR KS/AT _{mx} ACP	76/80, CUW26987, <i>S. reticuli</i> TUE45 84/87, TVZ77481, <i>Streptomyces</i> sp. BK340 98/98, ANP53719, <i>S. griseochromogenes</i> ATCC 14511 ^T	diketide
Cluster 7	<i>t2pks</i>	sequence06	50950 50960 50970	KSα KSβ (CLF) ACP	97/98, SOD85645, <i>Streptomyces</i> sp. Ag109_G2-15 92/96, KUN87591, <i>S. bungoensis</i> DSM 41781 ^T 95/96, ANP55848, <i>S. griseochromogenes</i> ATCC 14511 ^T	spore pigment
Cluster 8	<i>t1pks</i>	sequence06	36700 36690	KS/AT _m /ACP-KS/AT _m /DH/KR/ACP -KS/AT _{mm} /DH/KR/ACP -KS/AT _m /DH/KR/ACP KS/AT _m /DH/KR/ACP -KS/AT _m /DH/KR/ACP-TE	93/95, MBB6174413, <i>Nocardiosis mwathae</i> DSM 46659 ^T (89/92, AGY30676(Ann4), <i>S. calvus</i> ATCC 13382 ^T) 94/95, APD71872, <i>Streptomyces</i> sp. MM13 (89/92, AGY30677(Ann5), <i>S. calvus</i> ATCC 13382 ^T)	an annimycin congener (e)

Cluster 9	<i>pks/nrps</i>	sequence06	26620	KS/AT _{mm} /KR/ACP-KS/AT _{mm} /KR/ACP -KS/AT _m /KR/ACP	91/94, ANP49912, <i>S. griseochromogenes</i> ATCC 14511 ^T	blasticidin A (f)				
			26600	KS/AT _{mm} /KR/ACP-KS/AT _{mm} /KR/ACP	90/93, ANP49913, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			26595 ⁵	KS...	98/98, ANP49914, <i>S. griseochromogenes</i> ATCC 14511 ^T					
		sequence07	84390	...AT _m	91/95, ANP49915, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			84400	KR/ACP-KS/AT _{mm} /DH/KR/ACP -KS/AT _{mm} /KR/ACP	90/93, ANP56409, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			84410	KS/AT _m /KR/ACP -KS/AT _{mm} /DH/KR/ACP -KS/AT _{mm} /DH/KR/ACP -KS/AT _{mm} /DH/ER/KR/ACP	91/94, ANP49915, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			84420	KS/AT _{mm} /DH/ER/KR/ACP -KS/AT _{mm} /DH/KR/ACP-KS/AT _{mm} /ACP	91/93, ANP49917, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			84440	C/A/T	87/91, ANP49919, <i>S. griseochromogenes</i> ATCC 14511 ^T					
		sequence03	84460	ACP	95/96, ANP49921, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			84485	KS/AT _{mm} ...	90/94, WP_261340673, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			04720	...AT _m /DH/ER/KR/ACP	87/90, ANP49925, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			04730	C/A _{Gly} /T	90/93, ANP49926, <i>S. griseochromogenes</i> ATCC 14511 ^T					
			Cluster 10	<i>t1pks</i>	sequence03		06240	KS/AT/DH/KR/ACP	95/97, ANP50132, <i>S. griseochromogenes</i> ATCC 14511 ^T	unknown
			Cluster 11	<i>t1pks</i>	sequence03		09970	KS/AT _m /ACP -KS/AT _{mm} /DH/ER/KR/ACP-KS	89/91, TWF73701, <i>Kitasatospora viridis</i> DSM 44826 ^T	tridecaketide (g)
							09980	AT _{mm} /DH/ER/KR/ACP -KS/AT _{mm} /DH/KR/ACP	89/92, TWF73701, <i>Kitasatospora viridis</i> DSM 44826 ^T	
09990	KS/AT _m /DH...	89/92, TWF73701, <i>Kitasatospora viridis</i> DSM 44826 ^T								
sequence13	88580	...AT _{mm} /DH/ER/KR/ACP -KS/AT _{mm} /DH/ER/KR/ACP -KS/AT _m /DH/ER/KR/ACP			88/91, TWF73702, <i>Kitasatospora viridis</i> DSM 44826 ^T					
	sequence04	10010			...ER/KR/ACP -KS/AT _m /DH/ER/KR/ACP -KS/AT _{mm} /DH/KR/ACP -KS/AT _{mm} /DH/ER/KR/ACP	90/93, TWF73703, <i>Kitasatospora viridis</i> DSM 44826 ^T				
		10020			KS/AT _{mm} /DH/ER/KR/ACP	89/92, TWF73704, <i>Kitasatospora viridis</i> DSM 44826 ^T				
		Cluster 12			<i>t1pks</i>	sequence04	10630	KS/AT _m /ACP-KR	93/94, QRX90474, <i>S. noursei</i> A-2-1	
	Cluster 13	<i>t1pks</i>			sequence04	12810	KS/AT _m /DH/ACP	86/90, OIJ89442, <i>Streptomyces</i> sp. MUSC 14 (81/87, MCD9195255(Pop1), <i>S. albireticuli</i> NRRL B-1670 ^T)	fuelimycins (h)	

		12830	KR		92/95, GHB78300, <i>S. cirratus</i> JCM 4738 ^T (90/93, MCD9195253(Pop3), <i>S. albireticuli</i> NRRL B-1670 ^T)	
Cluster 14	<i>pks/nrps</i>	sequence04	14290 AT _m 14300 KS/KR/ACP 14430 T-C 14440 C/A _{Val} /T		88/93, WP_266794563, <i>Streptomyces</i> sp. NBC_00078 90/95, WP_266794562, <i>Streptomyces</i> sp. NBC_00078 82/88, WP_266794551, <i>Streptomyces</i> sp. NBC_00078 84/87, WP_266802749, <i>Streptomyces</i> sp. NBC_00078	unknown
Cluster 15	<i>nrps</i>	sequence04	23400 T 23390 A/T-TE		89/93, ANP51473, <i>S. griseochromogenes</i> ATCC 14511 ^T 90/92, ANP51472, <i>S. griseochromogenes</i> ATCC 14511 ^T	unknown
Cluster 16	<i>t1pks</i>	sequence04	23720 AT _m /ACP-KS/AT _m /KR/ACP 23710 KS/AT _{mm} /DH/KR/ACP-TE		91/93, ANP51499, <i>S. griseochromogenes</i> ATCC 14511 ^T 91/94, ANP51498, <i>S. griseochromogenes</i> ATCC 14511 ^T	triketide (i)
Cluster 17	<i>t1pks</i>	sequence05	25990 AT/ACP-KS/AT _{mm} /KR/ACP -KS/AT _{mm} /KR/ACP 26000 KS/AT _{mm} /KR/ACP -KS/AT _{mm} /DH/ER/KR/ACP 26010 KS/AT _{mm} /KR/ACP -KS/AT _{mm} /KR/ACP-TE		83/87, MBA9050682, <i>S. murinus</i> DSM 40710 (82/87, BAC76493(LkmAI), <i>S. rochei</i> 7434AN4 pSLA2-L) 89/92, KUM94497, <i>S. yokosukanensis</i> DSM 40224 ^T (85/88, BAC76492(LkmAII), <i>S. rochei</i> 7434AN4 pSLA2-L) 84/88, MBA9050684, <i>S. murinus</i> DSM 40710 (84/88, BAC76491(LkmAIII), <i>S. rochei</i> 7434AN4 pSLA2-L)	lankamycin (j)
Cluster 18	<i>pks/nrps</i>	sequence05	26160 C/A _{Gly} /T-KS 26170 DH 26180 KR/MT/ACP/ACP-KS 26190 AT _m 26210 KR/ACP-KS/KR/ACP-KS 26220 KS/ACP-TE		89/92, KUM95985, <i>S. yokosukanensis</i> DSM 40224 ^T (83/87, BAC76476(LkcA), <i>S. rochei</i> 7434AN4 pSLA2-L) 85/90, KUM95986, <i>S. yokosukanensis</i> DSM 40224 ^T (79/86, BAC76475(LkcB), <i>S. rochei</i> 7434AN4 pSLA2-L) 84/88, ADN64231, <i>S. rochei</i> subsp. <i>volubilis</i> ATCC 21250 (84/88, BAC76474(LkcC), <i>S. rochei</i> 7434AN4 pSLA2-L) 92/96, KUM94156, <i>S. yokosukanensis</i> DSM 40224 ^T (86/94, BAC76473(LkcD), <i>S. rochei</i> 7434AN4 pSLA2-L) 85/89, KUM94154, <i>S. yokosukanensis</i> DSM 40224 ^T (81/85, BAC76471(LkcF), <i>S. rochei</i> 7434AN4 pSLA2-L) 89/92, KUM94153, <i>S. yokosukanensis</i> DSM 40224 ^T (84/89, BAC76470(LkcG), <i>S. rochei</i> 7434AN4 pSLA2-L)	lankacidin (k)
Cluster 19	<i>pks/nrps</i>	sequence05	26550 A 26560 T 26580 C/A/T/E-C/A _{Ala} /T 26590 C/A _{Leu} /T/E-C/A _{Leu} /T		89/92, WP_151484785, <i>S. albicerus</i> RM68295 (86/91, AKJ15823, <i>S. incarnatus</i> NRRL 8089 ^T plasmid) 89/93, ANJ11946, <i>S. parvulus</i> 2297 (plasmid) (88/91, AKJ15824, <i>S. incarnatus</i> NRRL 8089 ^T plasmid) 90/93, KUM99161, <i>S. yokosukanensis</i> DSM 40224 ^T (87/91, AKJ15826, <i>S. incarnatus</i> NRRL 8089 ^T plasmid) 87/91, MCC5480753, <i>S. barringtoniae</i> JA03 ^T	incarnatapeptin congegner (l)

		26595 ^{5,6}	C...	(86/90, AKJ15827, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				89/94, MCC5480753, <i>S. barringtoniae</i> JA03 ^T	
				(87/93, AKJ15828, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
	sequence08	84485 ^{5,6}	...C/A _{Leu} /T	86/90, MCC5480753, <i>S. barringtoniae</i> JA03 ^T	
		84490	C/A _{Thr} /T-TE	(84/89, AKJ15827, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				89/94, MCC5480754, <i>S. barringtoniae</i> JA03 ^T	
		84620	KS/AT/ACP	(88/93, AKJ15828, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				86/89, MCC5480761, <i>S. barringtoniae</i> JA03 ^T	
		84630	KS/AT _{mm} /DH/KR/ACP	(82/87, AKJ15895, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				84/89, RPF24839, <i>Streptomyces</i> sp. TLI_185	
		84640	KS/AT _m /DH/ER/KR/ACP	(76/83, AKJ15835, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				84/89, MCC5480763, <i>S. barringtoniae</i> JA03 ^T	
		84650	KS/AT _{mm} /ACP	(82/88, AKJ15836, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				87/92, WP_267003510, <i>Streptomyces</i> sp. NBC_00526	
		84660	C/A/T	(84/91, AKJ15837, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
				83/89, MCC5480765, <i>S. barringtoniae</i> JA03 ^T	
				(81/87, AKJ15896, <i>S. incarnatus</i> NRRL 8089 ^T plasmid)	
Cluster 20	<i>t1pks</i>	sequence09	86810 CoL/ACP-KS/AT _{mm} /DH/KR/ACP	86/89, KUM00335, <i>S. yokosukanensis</i> DSM 40224 ^T	streptovaricin (m)
			-KS/AT _m /DH/ACP-KS/AT _{mm} /KR/ACP	(76/83, ASZ00147(StvA), <i>S. spectabilis</i> CCTCC M2017417)	
			86815 KS/AT _{mm} ...	94/96, WP_143079278, <i>S. monashensis</i> MUSC 1 ^T	
				(86/91, ASZ00148(StvB), <i>S. spectabilis</i> CCTCC M2017417)	
		sequence10	87375 ⁵ ...KR/ACP-KS/AT _{mm} /DH/KR/ACP	85/89, WP_210583637, <i>Streptomyces</i> sp. GESEQ-35	
				(77/84, ASZ00148(StvB), <i>S. spectabilis</i> CCTCC M2017417)	
			87380 KS/AT _{mm} /DH/KR/ACP	84/89, MCI3150382, <i>Streptomyces</i> sp. GB4-14	
			-KS/AT _{mm} /DH/KR/ACP	(77/85, ASZ00149(StvC), <i>S. spectabilis</i> CCTCC M2017417)	
			87370 KS/AT _{mm} /DH/KR/ACP	89/92, KUM00411, <i>S. yokosukanensis</i> DSM 40224 ^T	
				(77/86, ASZ00150(StvD), <i>S. spectabilis</i> CCTCC M2017417)	
			87360 KS/AT _m /DH/KR/ACP	91/93, KUM00410, <i>S. yokosukanensis</i> DSM 40224 ^T	
			-KS/AT _{mm} /DH/KR/ACP	(78/84, ASZ00151(StvE), <i>S. spectabilis</i> CCTCC M2017417)	
Cluster 21	<i>pks/nrps</i>	sequence10	87080 E-C	90/93, KUM00470, <i>S. yokosukanensis</i> DSM 40224 ^T	unknown
			87050 T/T	74/78, KUM00467, <i>S. yokosukanensis</i> DSM 40224 ^T	
			87010 KS α	95/97, KUM00463, <i>S. yokosukanensis</i> DSM 40224 ^T	
			87000 KS β (CLF)	95/97, KUM00499, <i>S. yokosukanensis</i> DSM 40224 ^T	
			86990 ACP	89/94, KUM00462, <i>S. yokosukanensis</i> DSM 40224 ^T	
			86980 ACP-KS/AT _{mm} /AT _m	74/79, KUM00430, <i>S. yokosukanensis</i> DSM 40224 ^T	

¹ORFs are shown by locus tag; ²Identity/Similarity (%) in amino acid sequences; ³Not the closest but highly similar biosynthetic enzymes, such as FoxB, Ann, Lkm, Lkc and Stv, are also shown in parenthesis; ⁴Chemical structures of **a** to **l** are shown in Figure 2; ⁵ These locus tags are putative, which are encoded at the positions of 511,634-520,186 in sequence02, 1-8,082 in sequence12, 864-1 in sequence06, 57,648-60,470 in sequence07, 140,503-142,299 in sequence05, 1-3,605 in sequence08, 57,784-59,991 in sequence09, and 101,972-94,632 in sequence10, respectively. ⁶These ORFs should be removed as stated in the text. A, adenylation domain; ACP, acyl carrier protein; AT, acyltransferase domain; AT_m, AT for malonyl-CoA, AT_{mm}, AT for methylmalonyl-CoA; AT_{mx}, AT for methoxymalonyl CoA; C, condensation domain; CLF, chain length factor; CoL, CoA ligase domain; DH, dehydratase domain; E, epimerization domain; ER, enoyl reductase domain; KR, ketoreductase domain; KS, ketosynthase domain; mal, residue derived from malonyl-CoA; MT, methyltransferase domain; *nrps*, NRPS gene; *pks/nrps*, hybrid PKS/NRPS gene; T, thiolation domain; TD, termination domain; TE, thioesterase domain, *t1pks*, type-I PKS gene; *t2pks*, type-II PKS gene; *t3pks*, type-III PKS gene. Amino acids incorporated by A domains are indicated as 3-letter abbreviations in subscript just after A.