

Supplementary Material

Polyphasic taxonomic description of *Streptomyces okerensis* sp. nov and *Streptomyces stoeckheimensis* sp. nov. and their pharmaceutical potential.

Imen Nouioui^{1*}, Eveline Derr^{1,2,3}, Alina Zimmermann¹, Marlen Jando¹, Gabriele Pötter¹, Sarah Kirstein¹, Meina Neumann-Schaal^{1,4}, Cathrin Spröer¹, Boyke Bunk¹, Yvonne Mast^{1,4,5}

¹Leibniz-Institut DSMZ – German Collection of Microorganisms and Cell Cultures, Inhoffenstraße 7B, 38124 Braunschweig, Germany.

²Rheinische Friedrich-Wilhelms-University Bonn, Regina-Pacis-Weg 3, 53113 Bonn, Germany.

³Heinrich-Heine-University Düsseldorf, Institute of Pharmaceutical Biology and Biotechnology, Universitätsstraße 1, 40225 Düsseldorf, Germany

⁴Braunschweig Integrated Centre of Systems Biology (BRICS), Rebenring 56, 38106 Braunschweig, Germany.

⁵Technische Universität Braunschweig, Institut für Mikrobiologie, Rebenring 56, 38106 Braunschweig, Germany.

Corresponding author: Imen Nouioui, imen.nouioui@dsmz.de

Section: Actinobacteria

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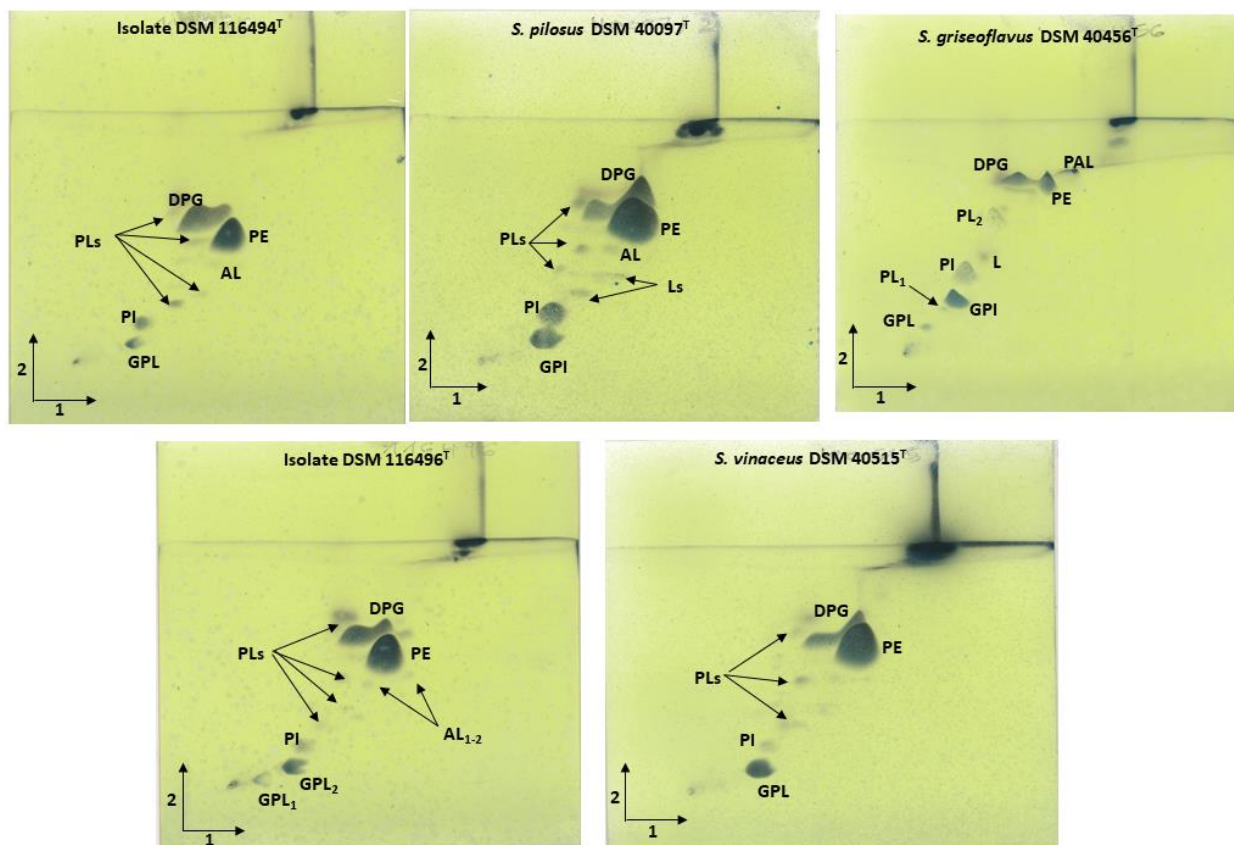
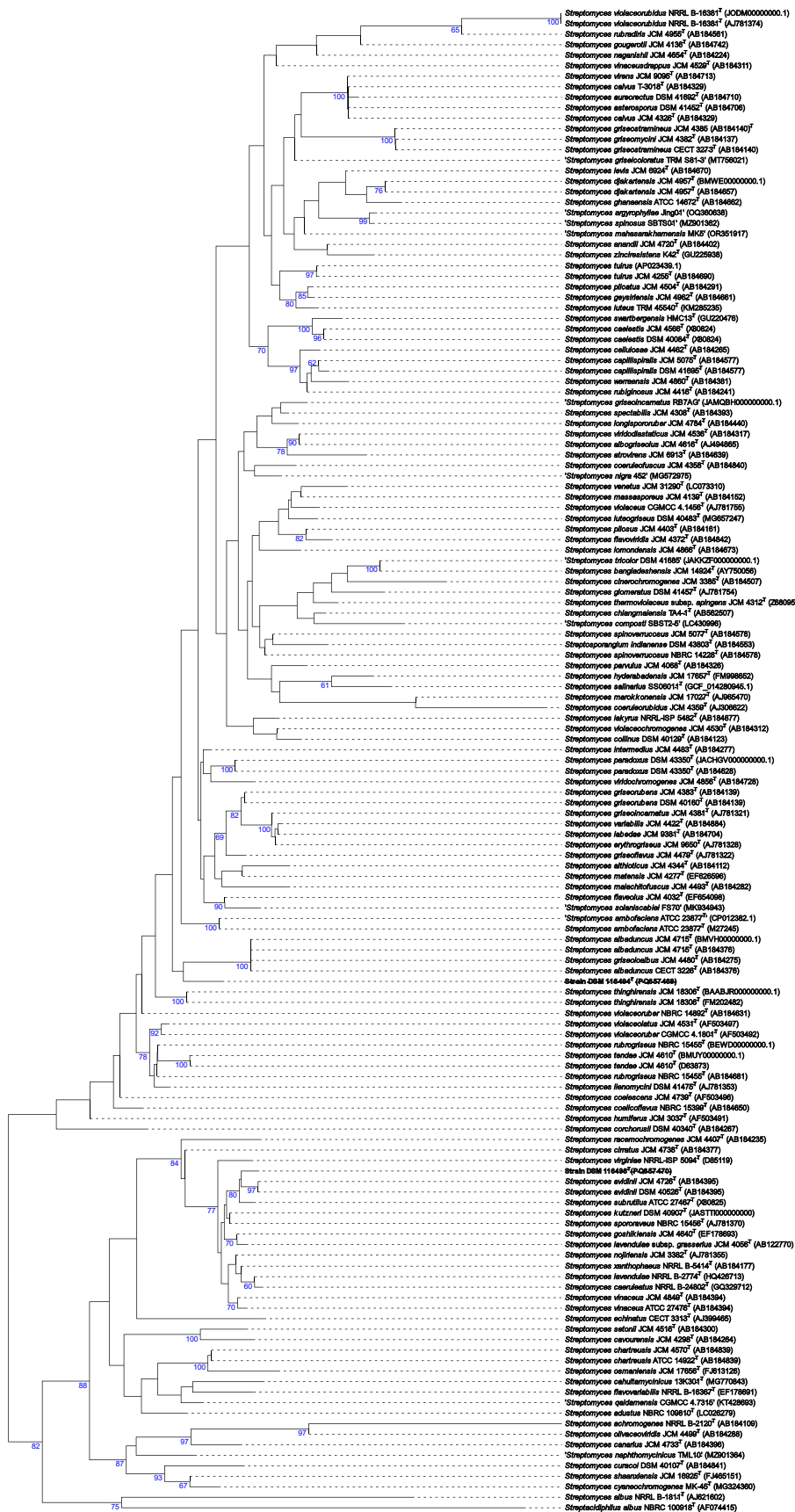


Figure S1. Two-dimensional TLC plate of polar lipids extracted from the strains DSM 116494^T and DSM 116496^T and their close phylogenomic relatives stained with molybdotophosphoric acid (SigmaP1518). Key: DPG diphosphatidylglycerol; PE phosphatidylethanolamine; PI phosphatidylinositol; AL aminolipid; L lipid; GPI glycoposphatidylinositol; GPL glycopospholipid; PAL phosphoaminolipid; PL phospholipid. Solvent1: chloroform: methanol: distilled water (65:25:4 v/v/v); solvent 2: chloroform: glacial acetic acid: methanol: distilled water (80:12:15:4 v/v/v).

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Figure S2. Maximum likelihood phylogenetic tree based on the 16S rRNA gene sequence showing the phylogenetic relatedness of the strains DSM 116494^T and DSM 116496^T to their closest neighbours of *Streptomyces* species validly named.

A

DSM 116494^T chromosome

Region	Type	From	To	Most similar known cluster	Similarity
Region 1.1	lanthipeptide-class-i ⚡, NRPS ⚡ lanthipeptide-class-i ⚡	240,582	305,082	teicoplanin ⚡	NRP:Glycopeptide 5%
Region 1.2	resorcinol ⚡	409,384	450,520	lasaloid ⚡	Polyketide 11%
Region 1.3	NRP-metallophore ⚡, NRPS ⚡	527,565	584,393	peucechin ⚡	NRP 50%
Region 1.4	T2PKS ⚡	866,870	939,379	spore pigment ⚡	Polyketide 83%
Region 1.5	ectoine ⚡	1,736,880	1,747,278	ectoine ⚡	Other 100%
Region 1.6	NRPS-like ⚡	2,461,588	2,505,667	streptozotocin ⚡	Other 23%
Region 1.7	terpene ⚡	2,809,981	2,831,810	desotamide ⚡	NRP 13%
Region 1.8	NH-siderophore ⚡	2,856,505	2,886,277	desferrioxamin Bdesferrioxamine E ⚡	Other 100%
Region 1.9	butyrolactone ⚡	3,910,729	3,921,718		
Region 1.10	RRE-containing ⚡	5,049,461	5,070,534	oryzanaphthopyran A/oryzanaphthopyran B/oryzanaphthopyran C/oryzanthrone A/oryzanthrone B/ chlororyzanthrone A/chlororyzanthrone B ⚡	Polyketide 6%
Region 1.11	terpene ⚡	5,181,972	5,203,057	albaflavonone ⚡	Terpene 100%
Region 1.12	T3PKS ⚡, thiopeptide ⚡	5,274,196	5,349,991	granaticin ⚡	Polyketide:Type II polyketide 16%
Region 1.13	NH-siderophore ⚡	5,907,459	5,937,363	kinamycin ⚡	Polyketide 16%
Region 1.14	terpene ⚡	6,025,560	6,046,384		
Region 1.15	beta-lactone ⚡, T1PKS ⚡	6,163,977	6,208,535	meilingmycin ⚡	Polyketide 6%
Region 1.16	PKS-like ⚡, NRPS ⚡	6,243,118	6,317,279	cadaside A/cadaside B ⚡	NRP 19%
Region 1.17	T1PKS ⚡	6,345,539	6,392,912	enduracidin ⚡	NRP 33%
Region 1.18	RiPP-like ⚡	6,395,911	6,407,224		
Region 1.19	terpene ⚡	6,442,790	6,464,946	geosmin ⚡	Terpene 100%
Region 1.20	NH-siderophore ⚡	6,599,413	6,630,604	paulomyon ⚡	Other 11%
Region 1.21	terpene ⚡	6,635,381	6,661,735	isorenieratene ⚡	Terpene 100%
Region 1.22	hydrogen-cyanide ⚡, lanthipeptide-class-iii ⚡	6,960,166	6,990,137	aboryon ⚡	RiPP 64%
Region 1.23	terpene ⚡	7,045,688	7,072,457	hopene ⚡	Terpene 92%
Region 1.24	hydrogen-cyanide ⚡	7,245,253	7,258,087	aboryon ⚡	RiPP 14%

DSM 116494^T plasmid

Region	Type	From	To	Most similar known cluster	Similarity
Region 2.1	LAP ⚡, thiopeptide ⚡, RRE-containing ⚡	13,322	48,741	streptovaricin ⚡	Polyketide 17%
Region 2.2	RiPP-like ⚡	175,167	185,382	informatipeptin ⚡	RiPP:Lanthipeptide 42%
Region 2.3	NRPS-like ⚡, T1PKS ⚡	447,299	495,491	borrelidin ⚡	Polyketide 11%

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DSM 116496^T chromosome

Region	Type	From	To	Most similar known cluster	Similarity
Region 1.1	NI-siderophore ☒	524,323	555,713	A54145 ☒	NRP 6%
Region 1.2	melanin ☒	635,426	665,346	melanin ☒	Other 100%
Region 1.3	terpene ☒	671,936	692,850	monensin ☒	Polyketide 5%
Region 1.4	terpene ☒ , NRPS ☒	741,140	803,363	azomycin ☒	Other 83%
Region 1.5	CDPS ☒	1,066,662	1,087,381	ibomycin ☒	Polyketide 4%
Region 1.6	CDPS ☒	1,230,194	1,250,934	tetrasin ☒	Polyketide 3%
Region 1.7	thioamides ☒ , thiopeptide ☒	1,295,796	1,332,831		
Region 1.8	lanthipeptide-class-i ☒	1,343,153	1,368,382		
Region 1.9	terpene ☒	1,561,130	1,587,920	hopene ☒	Terpene 61%
Region 1.10	lassopeptide ☒ , lanthipeptide-class-i ☒	1,917,710	1,947,210	citruassin B ☒	RiPP 40%
Region 1.11	lanthipeptide-class-iv ☒	1,988,906	2,011,881	corbomycin ☒	NRP 7%
Region 1.12	terpene ☒	2,034,960	2,057,176	geosmin ☒	Terpene 100%
Region 1.13	RiPP-like ☒	2,144,627	2,156,000		
Region 1.14	hydrogen-cyanide ☒	2,226,071	2,239,280	aborycin ☒	RiPP 21%
Region 1.15	NRPS ☒ , butyrolactone ☒	2,274,768	2,368,737	coelichelin ☒	NRP 100%
Region 1.16	T3PKS ☒ , NI-siderophore ☒	2,448,987	2,520,358	kinamycin ☒	Polyketide 30%
Region 1.17	CDPS ☒	2,870,706	2,891,494		
Region 1.18	T3PKS ☒ , other ☒ , terpene ☒	3,289,549	3,346,577	furaquinocin B ☒	Terpene+Polyketide 39%
Region 1.19	NRPS ☒ , betalactone ☒	3,454,301	3,530,085	enduracidin ☒	NRP 20%
Region 1.20	phenazine ☒	3,826,245	3,846,736	endophenazine A/endophenazine B ☒	Other:Phenazine 38%
Region 1.21	butyrolactone ☒	4,492,090	4,503,079	triacsin C ☒	Other 6%
Region 1.22	NRPS ☒	5,353,401	5,415,283	cinnapeptin ☒	NRP 14%
Region 1.23	NAPAA ☒	7,588,613	7,622,584	ε-Poly-L-lysine ☒	NRP 100%
Region 1.24	NRPS-like ☒	7,889,164	7,931,827	conglobatin ☒	NRP 15%
Region 1.25	terpene ☒	8,194,252	8,215,289		
Region 1.26	lanthipeptide-class-iii ☒	8,322,475	8,345,102	SapB ☒	RiPP:Lanthipeptide 100%
Region 1.27	ectoine ☒	8,422,174	8,432,578	ectoine ☒	Other 100%
Region 1.28	hglE-KS ☒ , T1PKS ☒	8,452,718	8,505,891	hexacosalactone A ☒	Other 6%
Region 1.29	T2PKS ☒	8,593,777	8,666,283	spore pigment ☒	Polyketide 66%
Region 1.30	T1PKS ☒ , lanthipeptide-class-i ☒ , NRPS ☒ , NAPAA ☒	8,830,596	8,914,758	stenothricin ☒	NRP:Cyclic depsipeptide 13%

DSM 116496^T plasmid

Region	Type	From	To	Most similar known cluster	Similarity
Region 3.1	butyrolactone ☒	26,927	37,871	lactonamycin ☒	Polyketide 3%
Region 3.2	lanthipeptide-class-ii ☒ , HR-T2PKS ☒ , thioamides ☒ , arylpolyene ☒ , T2PKS ☒ , butyrolactone ☒	76,959	221,220	prejadomycin/rabelomycin/gaudimycin C/gaudimycin D/UWM6/gaudimycin A ☒	Polyketide:Type II polyketide+Saccharide:Hybrid/ tailoring saccharide 43%

Figure S3. BGCs for strains DSM 116494^T (A) and DSM 116496^T (B) using AntiSMASH webserver.

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Table S1. Growth properties of the isolates DSM 116494^T and DSM 116496^T in the presence of a wide range of agar media.

Strains	ISP-1	ISP-2	ISP-3	ISP-4	ISP-5	ISP-6	ISP-7	GYM	TSA	N-Z Amine	Czapek peptone
DSM 116494 ^T	+++ AM agate grey (RAL7038) / SM light orange brown (RAL8023)	+++ no AM/ SM maize yellow (RAL1006)	++ AM dusty grey (RAL7037) / SM brownish	+++ AM white - greyish / SM saffron yellow (RAL1017)	+++ no AM/ SM golden yellow (RAL1004)	+++ AM white / SM yellow orange (RAL2000) - orange brown (RAL8023)	+ no AM/ SM golden yellow (RAL1004)	+++ AM dusty to platinum grey / SM chrome yellow (RAL1007) - yellow orange (RAL2000)	+++ AM white grey / SM chrome yellow (RAL1007) - yellow orange (RAL2000)	++ no AM/ SM saffron yellow (RAL1017)	+++ AM platinum grey (RAL7036) / SM ochre brown (RAL8001) - orange brown (RAL8023)
DSM 116496 ^T	+++ no AM / SM ochre yellow (RAL1024)	+++ no AM//SM light ivory (RAL 1015)	+++ AM light grey- ivory / SM ochre yellow (RAL1024)	+++ AM light ivory (RAL1015) / SM ochre yellow (RAL1024)	+++ no AM / SM ivory (RAL1014)	+++ no AM / SM light beige (RAL1001)	++ no AM / SM copper brown (RAL8004) / exopigment	+++ warm ivory AM/ SM sand yellow (RAL1002)	+++ no AM / SM ochre yellow (RAL1024)	+ no AM / SM beige (RAL1001)	++ no AM / SM ochre yellow (RAL1024)

+, poor growth; ++, moderate growth; +++ good growth; SM, substrate mycelium; AM, aerial mycelium.

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Table S2. Fatty acid profile of the strains DSM 116494^T and DSM 116496^T and their close phylogenomic relatives *Streptomyces pilosus* DSM 40097^T, *Streptomyces griseoflavus* DSM 40456^T, and *Streptomyces vinaceus* DSM 40515^T.

	Studied strain	Close phylogenetic relatives		Studied strain	Close phylogenetic relative
Fatty acids	Isolate DSM 116494 ^T	<i>S. griseoflavus</i> DSM 40456 ^T	<i>S. pilosus</i> DSM 40097 ^T	Isolate DSM 116496 ^T	<i>S. vinaceus</i> DSM 40515 ^T
C _{12:0}	0.1	NA	0.1	0.1	0.1
<i>iso</i> -C _{13:0}	0.2	NA	0.2	0.3	0.4
<i>anteiso</i> -C _{13:0}	0.2	0.1	0.2	0.2	0.2
C _{13:0}	NA	NA	NA	0.1	NA
<i>iso</i> -C _{14:0}	2.4	3.7	1.4	2.1	2.4
C _{14:0}	0.7	0.8	0.6	1.4	1.0
<i>iso</i> -C _{15:0}	7.3	3.8	7.0	11.0	9.9
<i>anteiso</i> -C _{15:0}	22.3	19.8	13.1	27.5	29.1
C _{15:1} cis 9	0.3	0.4	0.3	0.2	0.1
C _{15:0}	3.0	4.1	2.1	4.0	2.1
<i>iso</i> -C _{16:1} cis 9	2.4	3.5	1.9	0.4	0.3
<i>iso</i> -C _{16:0}	16.9	23.2	16.6	8.1	9.4
C _{16:1} cis 7	NA	NA	NA	0.1	NA
C _{16:1} cis 9	8.8	9.6	7.7	7.0	3.9
C _{16:0}	9.6	9.2	8.0	18.9	15.8
<i>iso</i> -C _{17:1} cis 9	3.0	1.3	5.7	1.2	1.1
<i>anteiso</i> -C _{17:1} cis 9	4.0	4.1	5.0	1.0	1.3
<i>iso</i> -C _{17:0}	2.6	1.2	5.6	3.9	6.4
<i>anteiso</i> -C _{17:0}	12.3	10.2	18.7	8.4	12.4
C _{17:1} cis 9	1.6	2.2	2.1	0.9	0.5
C _{17:1} cis 11	0.2	0.4	NA	NA	NA
C _{17:0} cyclo cis 9	0.1	NA	0.3	0.9	1.1
C _{17:0}	1.0	1.0	1.3	1.5	1.2
<i>iso</i> -C _{18:1} cis 9	0.2	0.3	0.5	NA	NA
<i>iso</i> -C _{18:1} cis 11	0.2	0.4	0.3	NA	NA
<i>anteiso</i> -C _{18:1} cis 9	NA	NA	0.3	NA	NA
<i>iso</i> -C _{18:0}	0.1	0.1	NA	0.1	0.2
C _{18:1} cis 9	0.3	0.2	0.4	0.3	0.2
C _{18:1} cis 11	0.1	0.3	0.3	0.2	0.1
C _{18:1} trans 11	NA	NA	NA	NA	0.1
C _{18:0}	0.2	NA	0.2	0.3	0.5
<i>iso</i> -C _{19:0}	NA	NA	NA	NA	0.1
<i>anteiso</i> -C _{19:0}	NA	NA	0.1	NA	NA

NA, not available.

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Table S3. Pairwise 16S rRNA gene sequence similarity between the strains DSM 116494^T and DSM 116496^T and their closest phylogenetic neighbours.

Isolates	Species validly named	Strain designation	Accession numbers	Pairwise Similarity (%)
DSM 116494 ^T	<i>Streptomyces marokkonensis</i>	Ap1 ^T	AJ965470	99.4
	<i>Streptomyces rubrogriseus</i>	LMG 20318 ^T	AJ781373	99.4
	<i>Streptomyces althioticus</i>	NRRL B-3981 ^T	AY999791	99.4
	<i>Streptomyces malachitofuscus</i>	NBRC 13059 ^T	AB184282	99.3
	<i>Streptomyces lienomycini</i>	LMG 20091 ^T	AJ781353	99.3
	<i>Streptomyces thinghirensis</i>	DSM 41919 ^T	FM202482	99.2
	<i>Streptomyces griseoflavus</i>	LMG 19344 ^T	AJ781322	99.2
	<i>Streptomyces violaceoruber</i>	NBRC 14892	AB184631	99.2
	<i>Streptomyces violaceoruber</i>	NBRC 12826 ^T	AB184174	99.2
	<i>Streptomyces violaceoruber</i>	NBRC 15461	AB184687	99.2
	<i>Streptomyces ambofaciens</i>	ATCC 23877 ^T	CP012382	99.1
	<i>Streptomyces tendae</i>	ATCC 19812 ^T	D63873	99.1
	<i>Streptomyces violaceorubidus</i>	LMG 20319 ^T	AJ781374	99.1
	<i>Streptomyces griseoloalbus</i>	NBRC 13046 ^T	AB184275	99.0
	<i>Streptomyces albaduncus</i>	JCM 4715 ^T	AY999757	99.0
	<i>Streptomyces heliomycini</i>	NBRC 15899 ^T	AB184712	99.0
	<i>Streptomyces djakartensis</i>	NBRC 15409 ^T	AB184657	98.9
	<i>Streptomyces tritolerans</i>	DAS 165 ^T	DQ345779	98.9
	<i>Streptomyces paradoxus</i>	NBRC 14887 ^T	AB184628	98.9
	<i>Streptomyces viridochromogenes</i>	NBRC 3113 ^T	AB184728	98.9
	<i>Streptomyces tuius</i>	NBRC 15617 ^T	AB184690	98.9
	<i>Streptomyces albogriseolus</i>	NRRL B-1305 ^T	AJ494865	98.8
	<i>Streptomyces griseoincarnatus</i>	LMG 19316 ^T	AJ781321	98.8
DSM 116496 ^T	<i>Streptomyces xanthophaeus</i>	NRRL B-5414 ^T	JOFT01000080	99.7

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<i>Streptomyces cirratus</i>	NRRL B-3250 ^T	AY999794	99.7
<i>Streptomyces nojiriensis</i>	LMG 20094 ^T	AJ781355	99.7
<i>Streptomyces spororaveus</i>	LMG 20313 ^T	AJ781370	99.7
<i>Streptomyces subrutilus</i>	DSM 40445 ^T	X80825	99.7
<i>Streptomyces avidinii</i>	NBRC 13429 ^T	AB184395	99.7
<i>Streptomyces vinaceus</i>	NBRC 13425 ^T	AB184394	99.7
<i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i>	NRRL B-2774 ^T	JOEW01000098	99.6
<i>Streptomyces goshikiensis</i>	NBRC 15458	AB184684	99.6
<i>Streptomyces goshikiensis</i>	NBRC 12868 ^T	AB184204	99.6
<i>Streptomyces netropsis</i>	NRRL B-1990	DQ026646	99.5
<i>Streptomyces virginiae</i>	NRRL ISP-5094 ^T	JOAK01000082	99.4
<i>Streptomyces manipurensis</i>	MBRL 201 ^T	JN560156	99.2
<i>Streptomyces spiroverticillatus</i>	NBRC 12821 ^T	AB249921	98.8
<i>Streptomyces adustus</i>	WH-9 ^T	LC026279	98.8
<i>Streptomyces cavourensis</i>	NBRC 13026 ^T	AB184264	98.7
<i>Streptomyces griseus</i>	NRRL ISP-5322	MUNB01000146	98.7

Table S4. Digital DNA-DNA hybridization between the whole genome sequence of strains DSM 116494^T and DSM 116946^T and their close phylogenomic neighbours.

Isolates	Close phylogenetic neighbours	dDDH (d4, in %)
Strain DSM 116494 ^T	<i>Streptomyces griseoflavus</i> JCM 4479 ^T	39.0
Strain DSM 116494 ^T	<i>Streptomyces malachitofuscus</i> JCM 4493 ^T	38.6
Strain DSM 116494 ^T	<i>Streptomyces flavoviridis</i> JCM 4372 ^T	38.5
Strain DSM 116494 ^T	<i>Streptomyces pilosus</i> JCM 4403 ^T	38.5
Strain DSM 116494 ^T	<i>Streptomyces atrovirens</i> JCM 6913 ^T	37.3
Strain DSM 116494 ^T	<i>Streptomyces griseoloalbus</i> JCM 4480 ^T	36.2
Strain DSM 116494 ^T	<i>Streptomyces albaduncus</i> JCM 4715 ^T	36.1
Strain DSM 116494 ^T	<i>Streptomyces capillispiralis</i> DSM 41695 ^T	35.5
Strain DSM 116494 ^T	<i>Streptomyces capillispiralis</i> JCM 5075 ^T	35.3
Strain DSM 116494 ^T	<i>Streptomyces aureorectus</i> DSM 41692 ^T	34.6
Strain DSM 116494 ^T	<i>Streptomyces virens</i> JCM 9095 ^T	34.5
Strain DSM 116494 ^T	<i>Streptomyces asterosporus</i> DSM 41452 ^T	34.4
Strain DSM 116494 ^T	<i>Streptomyces calvus</i> T-3018 ^T	34.4

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Strain DSM 116494 ^T	<i>Streptomyces calvus</i> JCM 4326 ^T	34.3
Strain DSM 116494 ^T	<i>Streptomyces griseomycini</i> JCM 4382 ^T	34.0
Strain DSM 116494 ^T	<i>Streptomyces griseostramineus</i> JCM 4385 ^T	33.9
Strain DSM 116494 ^T	<i>Streptomyces ghanaensis</i> ATCC 14672 ^T	33.3
Strain DSM 116494 ^T	<i>Streptomyces albogriseolus</i> JCM 4616 ^T	31.5
Strain DSM 116494 ^T	<i>Streptomyces albogriseolus</i> JCM 4536	31.5
Strain DSM 116496 ^T	" <i>Streptomyces kutzneri</i> " DSM 40907 ^T	29.4
Strain DSM 116496 ^T	<i>Streptomyces vinaceus</i> ATCC 27476 ^T	29.4
Strain DSM 116496 ^T	<i>Streptomyces goshikiensis</i> JCM 4640 ^T	29.3
Strain DSM 116496 ^T	<i>Streptomycesnojiriensis</i> JCM 3382 ^T	29.2
Strain DSM 116496 ^T	<i>Streptomyces spororaveus</i> NBRC 15456 ^T	29.1
Strain DSM 116496 ^T	<i>Streptomyces subutilus</i> ATCC 27467 ^T	29.0
Strain DSM 116496 ^T	<i>Streptomyces xanthophaeus</i> NRRL B-5414 ^T	29.0
Strain DSM 116496 ^T	<i>Streptomyces avidinii</i> DSM 40526 ^T	28.9
Strain DSM 116496 ^T	<i>Streptomyces avidinii</i> JCM 4726 ^T	28.9
Strain DSM 116496 ^T	<i>Streptomyces lavendulae</i> subsp. <i>grasseri</i> JCM 4056 ^T	28.7
Strain DSM 116496 ^T	<i>Streptomyces virginiae</i> NRRL ISP-5094 ^T	28.7
Strain DSM 116494 ^T	Strain DSM 116496 ^T	22.3

Table S5. Antimicrobial bioassay of strains DSM 116494^T and DSM 116496^T against Gram-positive (multi-resistant *Staphylococcus aureus* DSM 18827 and *Enterococcus faecium* DSM 20477^T) and Gram-negative bacteria (*Escherichia coli* Δ tolC JW5503-1, and *Proteus vulgaris* DSM 2140), as well as yeast (*Candida albicans* DSM 1386). The values in the table correspond to the diameter of the inhibition zone (in mm).

Ethyl acetate extracts	Media	reference strains				
		<i>E. coli</i> Δ tolC JW5503-1	<i>P. vulgaris</i> DSM 2140	<i>S. aureus</i> DSM 18827	<i>E. faecium</i> DSM 20477 ^T	<i>C. albicans</i> DSM 1386
Strain DSM 116494 ^T	NL19	9	-	-	-	-
Strain DSM 116494 ^T	NL800	8	-	-	-	-
Strain DSM 116494 ^T	R5	7	-	28	-	-
Strain DSM 116496 ^T	NL19	7	-	-	-	-
Strain DSM 116496 ^T	NL800	8	-	-	-	-

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Table S6. BCGs of secondary metabolites for the isolates DSM 116494^T and DSM 116496^T and their closest phylogenomic neighbours using the antiSMASH server.

			DSM 11649 4 ^T	S. griseofla vus JCM 4479 ^T	S. pilos us JCM 4403 ^T	DSM 1164 96 ^T	S. vinace us ATCC 27476 ^T
Type	Most similar known cluster		Similarity (%)				
PKS-like,NRPS,other	A54145	NRP		15	-	8	8
hydrogen-cyanide,lanthipeptide-class-iii	aborycin	RiPP	64	57	-	21	21
betalactone,T1PKS	meilingmycin	Polyketide	6	-	-	-	
butyrolactone	lactonamycin	Polyketide	-	-	-	3	
	rubiginone	A2/rubiginone					
	J/rubiginone	K/rubiginone					
butyrolactone	L/rubiginone	M/rubiginone	-	-	-		10
	N/ochromycinone/rubiginone						
	B2						
butyrolactone	triacsin C	Other	-	-	-	6	
CDPS	ibomycin	Polyketide	-	-	-	4	
CDPS	tetronasin	Polyketide	-	-	-	3	
ectoine	ectoine	Other	100	100	100	100	

Supplementary Material

furan, butyrolactone	methylenomycin A	Other	-	23%	-		
hglE-KS, T1PKS	hexacosalactone A	Other	-	-	-	6	9
hydrogen-cyanide, lanthipeptide-class-iii	SapB	RiPP:Lanthipeptide	-	-	100	100	100
lanthipeptide-class-i, NRPS, lanthipeptide-class-ii	teicoplanin	NRP:Glycopeptide	5	-	-	-	
lanthipeptide-class-iii, HR-T2PKS, thioamitides, arylpolyene, T2PKS, butyrolactone	prejadomycin/rabelomycin/gaudimycin C/gaudimycin A	Polyketide:Type II polyketide+Saccharide:Hybrid/tailoring saccharide	-	-	-	43	
lanthipeptide-class-iv	accramycin A	Polyketide		-	-		5
lanthipeptide-class-iv	corbomycin	NRP	-	-	-	7	
LAP	streptamidine	RiPP:Other	-	100	100		
LAP, butyrolactone	esmeraldin	Polyketide+Other:Aminocoumarin	-	-	8		
LAP, thiopeptide, RRE-containing	streptovaricin	Polyketide	17	-	-	-	
lassopeptide	vazabotide A	NRP	-	-	-		13
lassopeptide, lanthipeptide-class-i	citrulassin B	RiPP	-	-	-	40	
linaridin	pentostatine/vidarabine	Other		-	-		9
melanin	melanin	Other	-	-	42	100	28
NAPAA	ϵ -Poly-L-lysine	NRP	-	-	-	100	100
NI-siderophore	desferrioxamin B/desferrioxamine E	Other	100	100	100		100
NI-siderophore	kinamycin	Polyketide	16	13	19	-	13
NI-siderophore	paulomycin	Other	11	11	11	-	-

Supplementary Material

NRP-metallophore,NRPS	peucechelin	NRP	50	-	-	-	-
NRPS	cinnapeptin	NRP	-	-	-	14	-
NRPS	tirandamycin	NRP+Polyketide:Modular type I polyketide	-	66	-		-
NRPS,betalactone	enduracidin	NRP	33	-	-	20	-
NRPS,butyrolactone	coelichelin	NRP	-	-	-	100	-
NRPS,lanthipeptide-class-i,lanthipeptide-class-ii,RiPP-like	jagaricin	NRP	-	-	-		13
NRPS,NRPS-like	zorbamycin	NRP:Glycopeptide+Polyketide: Modular type I polyketide+Saccharide:Hybrid/tacloring saccharide	-	-	91		
NRPS,NRPS-like,blactam	lipopeptide 8D1-1/lipopeptide 8D1-2	NRP	-	-	-		4%
NRPS,T1PKS	antimycin	NRP+Polyketide	-	-	93		
NRPS,terpene	depsibosamycin						
	B/depsibosamycin	NRP	-	-	-		14
	C/depsibosamycin D						
NRPS-like	conglobatin	NRP	-	-	-	15	-
NRPS-like	streptozotocin	Other	23	-	-	-	-
NRPS-like,NRPS	antipain	NRP		-	100	-	-

Supplementary Material

	capreomycin IA/capreomycin						
NRPS-like,NRPS	IB/capreomycin	NRP	9	-	-	-	
	IIA/capreomycin IIB						
NRPS-like,NRPS	friulimicin A/friulimicin	NRP	-	75	-	-	
	B/friulimicin C/friulimicin D						
NRPS-like,T1PKS	amipurimycin	Polyketide+NRP+Saccharide	-	96	-	-	
NRPS-like,T1PKS	borrelidin	Polyketide	11	-	-	-	
NRPS-like,T1PKS	miharamycin B/miharamycin A	Polyketide+NRP+Saccharide	-	-	-	-	89
		Polyketide:Iterative type I					
NRPS-like,T1PKS,butyrolactone	neocarzinostatin	polyketide+Polyketide:Enediyn	-	52	-	-	-
		e type I polyketide					
other	lidamycin	NRP+Polyketide	-	25	-	-	-
phenazine	endophenazine						
	A/endophenazine B	Other:Phenazine	-	-	-	38	-
PKS-like	trioxacarcin A	Polyketide	-	-	7		-
PKS-like,NRPS	cadaside A/cadaside B	NRP	19	-	-	-	-
resorcinol	lasalocid	Polyketide	11	-	-	-	-
RiPP-like	granaticin	Polyketide:Type II polyketide	16	-	8		8
RiPP-like	informatipeptin	RiPP:Lanthipeptide	42	42	42		-
	oryzanaphthopyran						
RRE-containing	A/oryzanaphthopyran	Polyketide	6	-		-	-
	B/oryzanaphthopyran						
	C/oryzanthrone A/oryzanthrone						

Supplementary Material

	B/chlororyzanthrone						
	A/chlororyzanthrone B						
T1PKS,lanthipeptide-class-i,NRPS,NAPAA	stenothricin	NRP:Cyclic depsipeptide	-	-		13	-
T2PKS	spore pigment	Polyketide	83	83	83	66	-
T2PKS,T1PKS	homopiloquinone/piloquinone	Polyketide	-	-	100		-
T3PKS	alkylresorcinol	Polyketide	-	-	-		100
T3PKS,NI-siderophore	kinamycin	Polyketide	-	-	-	30	-
T3PKS,other,terpene	furaquinocin B	Terpene+Polyketide	-	-	-	39	-
terpene	albaflavenone	Terpene	100	100	100	-	-
terpene	avermilol	Terpene	-	-	-	-	100
terpene	desotamide	NRP	13%	-	-	-	-
terpene	geosmin	Terpene	100	100	100	100	-
terpene	hopene	Terpene	92%	92%	92%	61%	61%
terpene	isorenieratene	Terpene	100	87	87	-	-
terpene	monensin	Polyketide	-	-	-	5	5
terpene	oxalomycin B	NRP+Polyketide	-	-	-	-	12
terpene	toxoflavin/ferrenulin	Other	-	-	-	-	14
terpene,NRPS	azomycin	Other	-	-	-	83	-
terpene,T3PKS	flaviolin/1,3,6,8-tetrahydroxynaphthalene	Polyketide	-	-	-	-	100
thiopeptide,LAP	lactazole	RiPP:Thiopeptide	-	-	-	-	66

Supplementary Material