

1 **Supplementary Material**

2 **Genome-based reclassification of *Lentzea roselyniae* (Okoro et al. 2010)**
3 **Nouioui et al. 2018 and *Lentzea terrae* Li et al. 2018 as later heterotypic**
4 **synonyms of *Lentzea atacamensis* (Okoro et al. 2010) Nouioui et al.**
5 **2018 and *Lentzea soli* Li et al. 2018, respectively**

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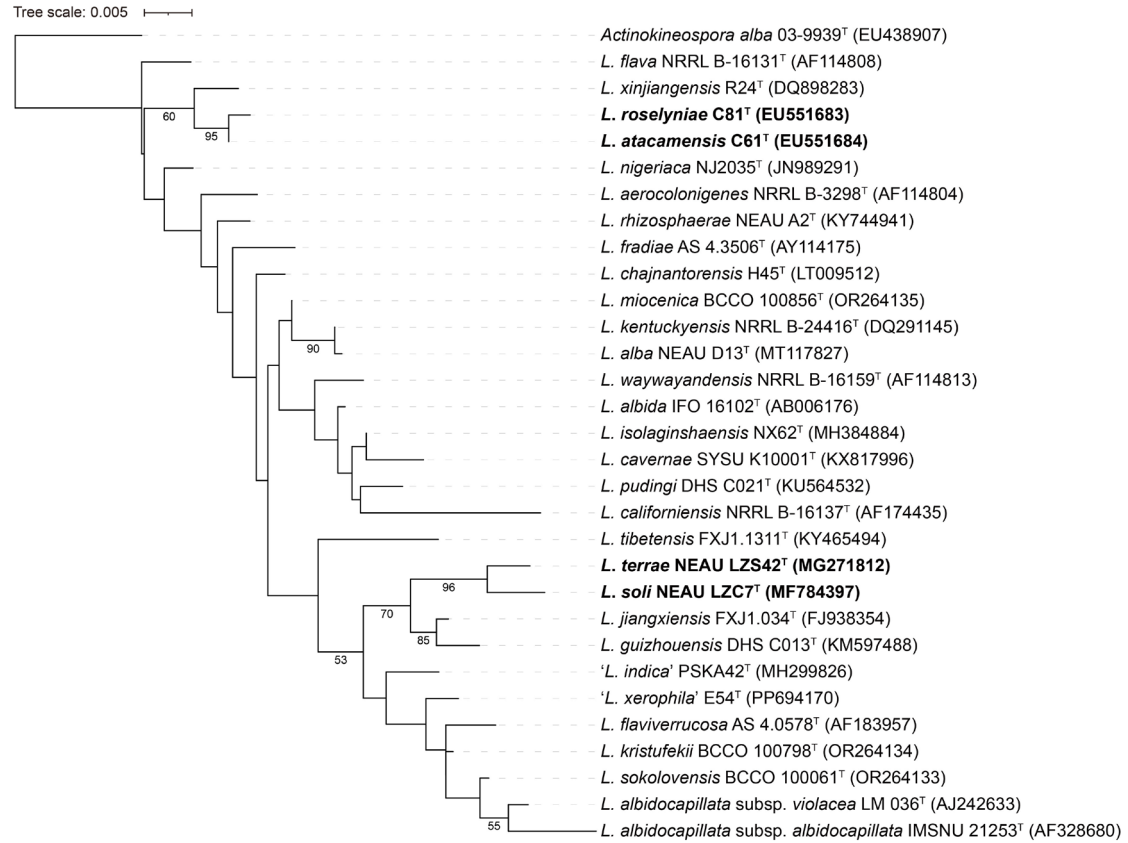
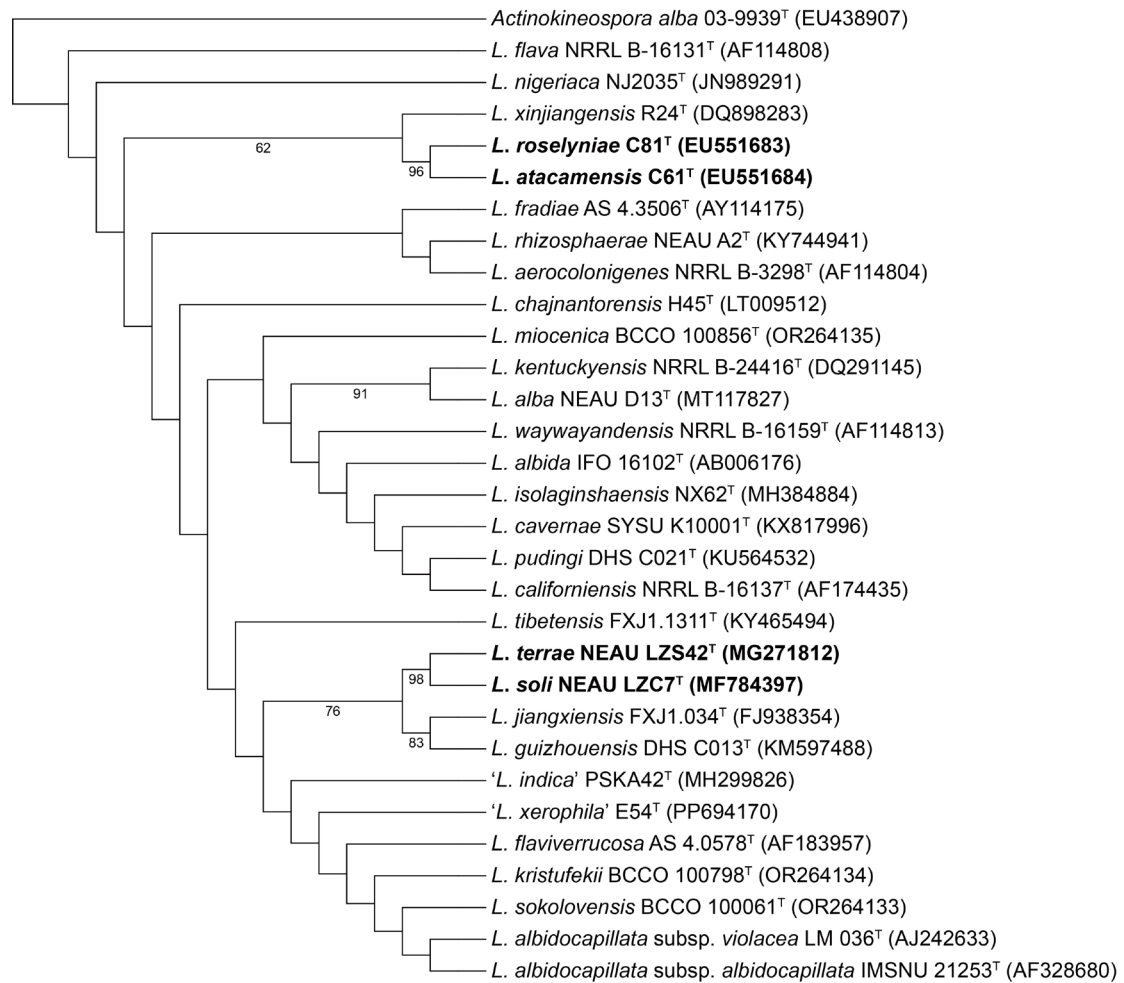


Fig. S1 Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationships among type strains of the genus *Lentzea*. Bootstrap values (%) based on 1,000 replicates are indicated at branch nodes; only values >50% are shown. *Actinokineospora alba* 03-9939^T (EU438907) was used as the outgroup. Bar, 0.002 substitutions per nucleotide position.



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30 **Fig. S2** Maximum-parsimony phylogenetic tree based on 16S rRNA gene sequences
 31 showing the relationships among type strains of the genus *Lentzea*. Bootstrap values
 32 (%) based on 1,000 replicates are indicated at branch nodes; only values >50% are
 33 shown. *Actinokineospora alba* 03-9939^T (EU438907) was used as the outgroup. Bar,
 34 0.002 substitutions per nucleotide position.

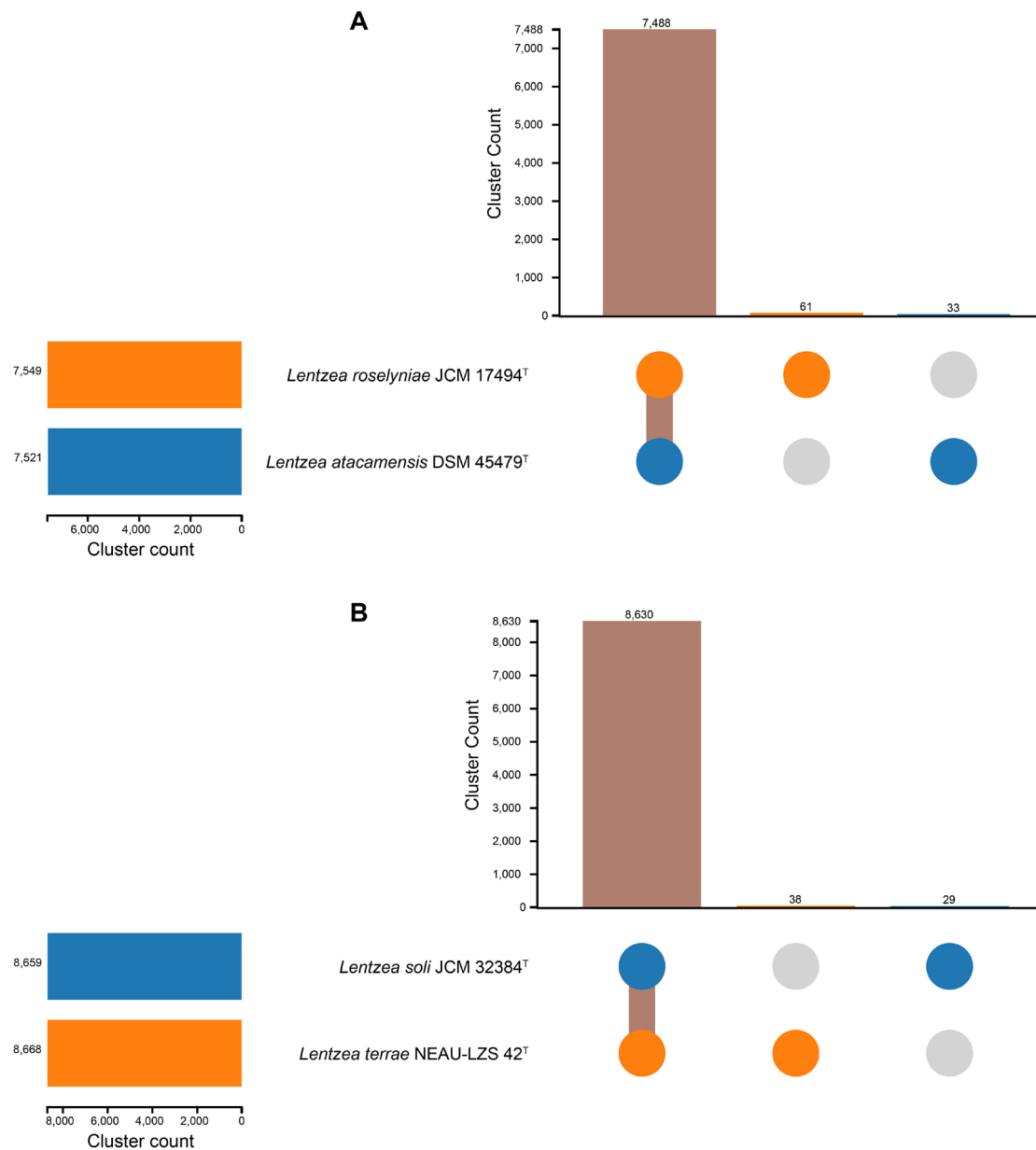


Fig. S3 UpSet plot showing the distribution of orthologous gene clusters inferred by OrthoVenn3 among the two closely related pairs of *Lentzea* type strains: (A) *L. atacamensis* DSM 45479^T and *L. roselyniae* JCM 17494^T, and (B) *L. soli* JCM 32384^T and *L. terrae* NEAU-LZS 42^T. Shared and strain-specific orthologous gene clusters are indicated for each pairwise comparison.

41 **Table S1** Predicted secondary metabolite biosynthetic gene clusters (BGCs) in four *Lentzea* type strains as identified by antiSMASH

Region	Type	From	To	Similarity Confidence	Most similar known cluster	
<i>Lentzea atacamensis</i> DSM 45479 ^T						
Region 1.1	other	2,594	43,427			
Region 1.2	betalactone	471,274	502,655			
Region 1.3	T3PKS	612,417	653,466	Low	loseolamycin A1/loseolamycin A2	PKS
Region 1.4	NRPS-like	890,935	933,334			
Region 1.5	terpene,NRP-metallophore,NRPS	1,417,384	1,502,965	Medium	isorenieratene	terpene
Region 1.6	terpene	1,625,474	1,650,036			
Region 1.7	terpene-precursor	1,663,343	1,684,347			
Region 1.8	lassopeptide	1,798,214	1,820,685	High	citrulassin B	ribosomal:RiPP
Region 3.1	NAPAA	19,965	53,702	High	ε-Poly-L-lysine	NRPS:Type I
Region 3.2	hglE-KS	160,375	210,531			
Region 3.3	terpene	277,038	297,415			
Region 3.4	NRPS	533,796	612,412			
Region 3.5	terpene	707,458	727,976			
Region 3.6	terpene-precursor,T3PKS,terpene	902,641	966,479			
Region 4.1	NI-siderophore,NRPS	307,546	371,722	Low	enduracididine	other:other
Region 4.2	indole,NRPS,T1PKS	532,096	587,907			
Region 4.3	lanthipeptide-class-ii	737,129	759,723			
Region 5.1	terpene	497,311	519,488	High	geosmin	terpene:Sesquiterpene
Region 5.2	NRP-metallophore,NRPS	575,612	631,990	Medium	amychelin	NRPS:Type I
Region 6.1	redox-cofactor	276,480	298,522	Low	lankacidin C	NRPS:Type I+PKS
Region 7.1	lanthipeptide-class-iii	133,406	155,973	Medium	Ery-9/Ery-6/Ery-8/Ery-7/Ery-5/Ery-4/Ery-3	ribosomal:RiPP:Lanthipeptide
Region 7.2	T2PKS,PKS-like,RiPP-like	167,214	239,693	Low	trioxacarin A	PKS
Region 7.3	terpene	255,722	279,322	Low	isorenieratene	terpene
Region 9.1	azole-containing-RiPP	107,147	133,918			
Region 11.1	T1PKS	21,303	66,990	Medium	esperamicin	PKS

Region	Type	From	To	Similarity Confidence	Most similar known cluster	
Region 11.2	terpene	71,318	93,249			
Region 13.1	terpene	261,107	279,694			
Region 15.1	NRPS,T1PKS	104,022	158,053			
Region 19.1	RiPP-like	34,604	45,422			
<i>Lentzea roselyniae</i> JCM 17494^T						
Region 2.1	T3PKS	153,872	194,921	Low	loseolamycin A1/loseolamycin A2	PKS
Region 2.2	betalactone	311,076	342,457			
Region 4.1	redox-cofactor	268,348	290,390	Low	lankacidin C	NRPS:Type I+PKS
Region 5.1	NAPAA	315,594	349,331	High	ϵ -Poly-L-lysine	NRPS:Type I
Region 7.1	terpene-precursor	27,604	48,608			
Region 7.2	terpene	63,794	88,371			
Region 7.3	terpene	241,876	269,524	Medium	isorenieratene	terpene
Region 7.4	terpene	326,406	347,230			
Region 8.1	terpene,azole-containing-RiPP	1	43,541			
Region 9.1	indole,NRPS,T1PKS	195,118	250,916			
Region 10.1	terpene	169,414	190,454			
Region 12.1	lanthipeptide-class-iii	102,868	125,435	Medium	Ery-9/Ery-6/Ery-8/Ery-7/Ery-5/Ery-4/Ery-3	ribosomal:RiPP:Lanthipeptide
Region 12.2	T2PKS,PKS-like,RiPP-like	136,532	209,011	Low	trioxacarcin A	PKS
Region 12.3	terpene	225,134	248,734			
Region 15.1	terpene	204,121	222,910			
Region 16.1	terpene	1,119	22,183	Low	2-methylisoborneol	terpene:Monoterpene
Region 16.2	NRPS	177,519	203,819			
Region 19.1	lanthipeptide-class-ii	27,360	49,954			
Region 20.1	hglE-KS	34,067	84,055			
Region 21.1	NRP-metallophore,NRPS	1	49,701	Medium	amychelin	NRPS:Type I
Region 21.2	terpene	118,011	140,188	High	geosmin	terpene:Sesquiterpene
Region 23.1	T1PKS	29,087	74,774	Medium	esperamicin	PKS
Region 24.1	NI-siderophore,NRPS	37,135	101,313	Low	enduracididine	other:other

Region	Type	From	To	Similarity Confidence	Most similar known cluster		
Region 25.1	lassopeptide	18,447	40,918	High	citrulassin B ribosomal:RiPP		
Region 32.1	T3PKS,terpene	1	36,607	Low	merochlorin A/merochlorin B/deschloro-merochlorin PKS:Type III+terpene:Sesquiterpene A/deschloro-merochlorin B/isochloro-merochlorin B/dichloro-merochlorin B/merochlorin D/merochlorin C		
Region 33.1	NRPS-like	1	34,579				
Region 37.1	T1PKS	54,646	77,306				
Region 38.1	RiPP-like	34,687	45,505				
Region 44.1	NRPS	1	50,051				
Region 45.1	T1PKS	1	32,429				
Region 47.1	terpene-precursor	11,058	32,074				
Region 49.1	hglE-KS	1	35,507				
Region 51.1	T3PKS	7,305	33,394				
Region 62.1	terpene	8,123	18,747				
Region 70.1	terpene	1	13,963				
Region 71.1	terpene	1	13,725	Low	allylmalonyl-CoA		other:other
Region 72.1	terpene	194	12,898				
Region 82.1	T3PKS,terpene	1	8,924				
Region 92.1	terpene	1	5,258				
Region 99.1	terpene	1	3,553				
Lentzea soli JCM 32384^T							
Region 1	betalactone	81,585	112,710				
Region 2	T1PKS,NRPS-like	137,669	196,614	Low	gargantulide B/gargantulide C		PKS
Region 3	terpene	198,751	219,815	Low	2-methylisoborneol		terpene:Monoterpene
Region 4	hglE-KS,T1PKS	688,641	738,775				
Region 5	lanthipeptide-class-ii	820,438	843,212				
Region 6	NRPS-like	883,143	925,509				
Region 7	terpene	1,350,984	1,375,522				
Region 8	terpene-precursor	1,381,957	1,402,946				

Region	Type	From	To	Similarity Confidence	Most similar known cluster	
Region 9	terpene	1,549,410	1,577,399			
Region 10	NI-siderophore	2,002,072	2,032,895			
Region 11	hserlactone	2,110,972	2,131,646			
Region 12	azole-containing-RiPP	2,930,528	2,958,446			
Region 13	arylpolyene	3,481,367	3,522,506			
Region 14	NAPAA	3,704,850	3,738,587	High	ϵ -Poly-L-lysine	NRPS:Type I
Region 15	RiPP-like	4,074,357	4,084,695			
Region 16	redox-cofactor	5,757,142	5,779,184	Low	lankacidin C	NRPS:Type I+PKS
Region 17	NRP-metallophore,NRPS,NRPS-like	6,237,743	6,330,746	Medium	amychelin	NRPS:Type I
Region 18	lanthipeptide-class-iii	6,985,016	7,007,583	Medium	Ery-9/Ery-6/Ery-8/Ery-7/Ery-5/Ery-4/Ery-3	ribosomal:RiPP:Lanthipeptide
Region 19	PKS-like,T2PKS,RiPP-like	7,019,070	7,103,128	Low	LL-D49194 α 1 (LLD)/LL-D49194 β 2	PKS
Region 20	terpene	7,122,901	7,146,487	Low	isorenieratene	terpene
Region 21	RiPP-like	7,366,823	7,377,656			
Region 22	NAPAA,T2PKS	7,552,136	7,655,152	Low	lactonamycin	PKS
Region 23	indole	7,668,518	7,689,612			
Region 24	RRE-containing	7,715,061	7,735,789			
Region 25	T1PKS,NRPS-like	7,820,736	7,992,410	Medium	nystatin A1	PKS:Type I+saccharide:hybrid/tailoring
Region 26	lanthipeptide-class-ii	8,050,536	8,073,118			
Region 27	NRPS	8,529,501	8,577,624			
Region 28	NRPS-like	8,683,941	8,727,903			
Region 29	lanthipeptide-class-ii	9,121,091	9,143,973			
Region 30	ranthipeptide	9,207,076	9,228,684			
Region 31	arylpolyene	9,256,769	9,297,929			
Region 32	azole-containing- RiPP,thioamitides,NRPS- like,T1PKS,HR-T2PKS,NRPS	9,300,240	9,439,097	Low	9-methylstreptimidone	PKS:Type I
Lentzea terrae NEAU-LZS 42 ^T						
Region 5.1	lanthipeptide-class-ii	171,318	193,900			

Region	Type	From	To	Similarity Confidence	Most similar known cluster	
Region 16.1	NRPS-like	197,224	241,186			
Region 16.2	NRPS	347,510	395,627			
Region 20.1	NRPS-like,NRP-metallophore,NRPS	255,160	348,162	Medium	amychelin	NRPS:Type I
Region 22.1	betalactone	40,877	72,002			
Region 23.1	betalactone	4,620	35,745			
Region 25.1	T1PKS,NRPS-like	12,975	100,919	Low	pladienolide B	PKS
Region 26.1	arylpolyene	481,277	510,450			
Region 28.1	hgIE-KS	256,778	306,913			
Region 28.2	lanthipeptide-class-ii	387,600	410,374			
Region 28.3	NRPS-like	450,306	492,672			
Region 29.1	NRPS	1	69,568			
Region 31.1	NAPAA	190,553	224,290	High	ϵ -Poly-L-lysine	NRPS:Type I
Region 32.1	terpene-precursor	150,719	171,708			
Region 32.2	terpene	178,144	202,682			
Region 33.1	NRPS-like,T1PKS	1	41,781	Low	K-41A	PKS
Region 33.2	terpene	43,917	59,980	Low	2-methylisoborneol	terpene:Monoterpene
Region 34.1	redox-cofactor	316,860	338,902	Low	lankacidin C	NRPS:Type I+PKS
Region 35.1	RiPP-like	3,906	14,244			
Region 37.1	T1PKS	1	83,808	Medium	nystatin A1	PKS:Type I+saccharide:hybrid/tailoring
Region 37.2	RRE-containing	130,702	151,430			
Region 37.3	indole	176,802	197,800			
Region 37.4	T2PKS,NAPAA	211,264	315,268	Low	lactonamycin	PKS
Region 37.5	RiPP-like	479,186	490,019			
Region 38.1	azole-containing-RiPP	468,200	496,125			
Region 40.1	terpene	44,059	65,168			
Region 49.1	terpene	1	18,680			
Region 49.2	NI-siderophore	410,017	440,840			
Region 49.3	hserlactone	518,181	538,855			

Region	Type	From	To	Similarity Confidence	Most similar known cluster	
Region 50.1	terpene	174,595	198,181	Low	isorenieratene	terpene
Region 50.2	T2PKS,PKS-like,RiPP-like	217,956	302,014	Low	LL-D49194 α 1 (LLD)/LL-D49194 β 2	PKS
Region 50.3	lanthipeptide-class-iii	313,511	336,078	Medium	Ery-9/Ery-6/Ery-8/Ery-7/Ery-5/Ery-4/Ery-3	ribosomal:RiPP:Lanthipeptide
Region 51.1	lanthipeptide-class-ii	117,663	140,545			
Region 51.2	ranthipeptide	203,647	225,255			
Region 51.3	arylpolyene	253,343	294,503			
Region 51.4	azole-containing- RiPP,thioamitides,NRPS- like,T1PKS,HR-T2PKS,NRPS	296,749	435,607	Low	9-methylstreptimidone	PKS:Type I

43 **Table S2** Shared and strain-specific biosynthetic gene clusters (BGCs) in two pairs of *Lentzea* type strains identified by antiSMASH

Strain pair	Shared BGCs (total no.)	First strain-specific BGCs (total no.)	Second strain-specific BGCs (total no.)
<i>L. atacamensis</i> DSM 45479 ^T (First) vs <i>L. roselyniae</i> JCM 17494 ^T (Second)	15 shared clusters , including terpene (3; e.g., isorenieratene, geosmin), T3PKS (1; loseolamycin A1/A2), betalactone (1), redox-cofactor (1; lankacidin C), NAPAA (1; ϵ -poly-L-lysine), lanthipeptide-class-III (1; Ery-3–Ery-9), T2PKS/PKS-like/RiPP-like (1; trioxacarcin A), T1PKS (1; esperamicin), NRP-metallophore/NRPS (1; amyachelin), and lassopeptide (1; citrulassin B)	4 unique clusters , including NRPS-like (1), terpene-precursor (1), terpene/NRPS/NRP-metallophore hybrid cluster (1), and NI-siderophore (1)	6 unique clusters , including terpene (2), T3PKS/terpene hybrid cluster (1; merochlorin-related), NRPS-like (1), terpene-precursor (1), and terpene/azole-containing RiPP hybrid cluster (1)
<i>L. soli</i> JCM 32384 ^T (First) vs <i>L. terrae</i> NEAU-LZS 42 ^T (Second)	16 shared clusters , including terpene (2; isorenieratene, 2-methylisoborneol), betalactone (1), NAPAA (1; ϵ -poly-L-lysine), NRPS/NRPS-like (3), lanthipeptide-class-II/III (4), and PKS-related clusters (3; e.g., nystatin A1, 9-methylstreptimidone, lactonamycin)	7 unique clusters , including arylpolyene (2), hserlactone (1), lanthipeptide (1), thioamitides-containing hybrid cluster (1), indole (1), and RRE-containing cluster (1)	6 unique clusters , including betalactone (2), pladienolide B-related T1PKS/NRPS-like cluster (1), NRP-metallophore/NRPS-like/NRPS clusters (2), and terpene-precursor (1)

44 Note: Biosynthetic gene clusters (BGCs) were predicted using antiSMASH v8.0.1 with relaxed detection settings. Numbers in parentheses indicate the number of
45 clusters detected within each BGC category. Representative known clusters are shown where applicable.