

Table S1: Prediction of Biosynthetic Gene Clusters encoding for secondary metabolites in *Nocardiopsis sp.* ZS3416R2A antiSMASH (version 7.1.0.1).

antiSMASH Region id	Begin	End	Length	Region type	MIBiG	Completion	Product
1	94414	150433	56020	T1PKS	BGC0000018	0.6	Angolamycin
2	728815	802708	73894	NRPS	BGC0002691	0.25	amphibactin B/amphibactin C/amphibactin D/amphibactin E/amphibactin H/amphibactin S/amphibactin T/amphibactin V
3	994804	1016006	21203	terpene	BGC0000657	0.5	2-methylisoborneol
5	2059372	2091027	31656	NI-siderophore	BGC0000244	0.333333	Nonactin/monactin/dinactin/trina ctin/tetranactin
7	2191112	2227679	36568	thiopeptide	BGC0002115	0.166667	Streptamidine
8	2336207	2382032	45826	T1PKS	BGC0002545	0.129032	sungeidine C/sungeidine B/sungeidine D/sungeidine H/sungeidine A/sungeidine E/sungeidine F/sungeidine G
9	2930417	2978632	48216	PKS-like, T1PKS	BGC0001283	0.56	Arsono-polyketide
12	3392002	3417123	25122	lanthipeptide-class-i	BGC0001846	0.0869565	valinomycin/montanastatin
13	3426186	3451727	25542	terpene	BGC0000664	0.857143	Isorenieratene
14	4155016	4219899	64884	NRPS	BGC0001561	0.230769	Curacomycin
15	4399303	4475221	75919	lanthipeptide-class-v, NRPS	BGC0000876	0.25	Neopolyoxin C
17	4920511	4992999	72489	T2PKS	BGC0001960	0.724138	Hiroshidine
19	5744840	5755241	10402	Ectoine	BGC0002052	0.75	Ectoine

Table S2: Prediction of Biosynthetic Gene Clusters encoding potentially novel secondary metabolites in *Nocardiopsis* sp. ZS3416R2A.

antiSMASH Region id	Begin	End	Length	Region type
4	1099202	1123430	24229	Lanthipeptide-class-i
6	2148767	2171454	22688	Lanthipeptide-class-iii
10	3114525	3124833	10309	RiPP-like
11	3251041	3284241	33201	Ranthipeptide, lanthipeptide-class-i
16	4479398	4507504	28107	Thiopeptide, LAP
18	5216394	5227323	10930	RiPP-like

Table S3: Prediction of Biosynthetic Gene Clusters encoding for secondary metabolites in strain *Nocardiopsis terrae* DSM 45157 antiSMASH (version 7.1.0.1).

antiSMASH Region id	Begin	End	Length	Region type	MIBiG	Completion	Product
2	160070	236306	76237	NRPS, oligosaccharide, other	BGC0000898	0.888889	Desosamine/Pikromycin /Neomethymycin/Narbomycin
3	1122633	1148174	25542	Terpene	BGC0000664	1	Isorenieratene
4	1227485	1250145	22661	Lanthipeptide-class-iii	BGC0000551	1	SapB
5	1256955	1372938	115984	NRPS, Transat-PKS, Arylpolyene	BGC0001116	0.722222	Virginiamycin S1
6	2349906	2400066	50161	NRPS, RiPP-like	BGC0000202	0.111111	Azicemicin B
7	2539885	2571540	31656	NI-siderophore	BGC0000244	0.333333	Nonactin/monactin/dinactin /trinactin/tetranactin
8	2623640	2687840	64201	T1PKS, NRPS-like	BGC0002128	0.222222	5-dimethylallylindole-3-acetonitrile
9	2870374	2892068	21695	Terpene	BGC0000242	0.0434783	lysolipin I
10	3592100	3613302	21203	Terpene	BGC0000657	0.5	2-methylisoborneol
11	4429284	4487423	58140	T1PKS	BGC0000067	0.75	Geldanamycin
13	5024471	5034872	10402	Ectoine	BGC0002052	0.75	Ectoine
14	5208472	5228969	20498	Phenazine	BGC0000936	0.857143	Pyocyanine
16	5777235	5809718	32484	Phosphonate	BGC0000926	0.428571	Rhizocticin A

Table S4: Prediction of Biosynthetic Gene Clusters encoding potentially novel secondary metabolites in *Nocardiopsis terrae* DSM 45157.

antiSMASH Region id	Begin	End	Length	Region type
1	131108	159205	28098	Thiopeptide, LAP
12	4506242	4517024	10783	Butyrolactone
15	5570084	5581010	10927	RiPP-like

Table S5: Comparative Analysis of CAZyme Families and Their Functional Profiles in *Nocardiopsis sp. ZS3416R2A* and *Nocardiopsis terrae* DSM 45157

Famille CAZyme	Principal function	<i>Nocardiopsis sp. ZS3416R2A</i>	<i>Nocardiopsis terrae</i> DSM 45157
AA (Auxiliary Activities)	Oxidation, lignocellulose degradation	AA3(3),AA4(2),AA6(1),AA7(3),AA10(3)	AA3(2),AA4(2),AA6(1),AA7(4),AA10(3)
CBM (Carbohydrate Binding Modules)	Binding to polysaccharides	CBM2(4), CBM4(1), CBM6(1), CBM13(1),CBM48(2)	CBM2(5), CBM4(1), CBM13(1), CBM48(2), CBM67(2)
CE (Carbohydrate Esterases)	Deacylation, modification of polysaccharides	CE1(1), CE3(2),CE4(4),CE9(1)	CE1(1), CE3(3), CE4(4), CE9(1), CE14(5)
GH (Glycoside Hydrolases)	Hydrolysis of glycosidic bonds	GH1(3), GH2(2), GH3(4), GH5(3), GH6(1), GH10(2), GH11(1), GH13(8), GH15(3), GH16(1), GH18(3), GH20(2), GH23(2),GH26(1),GH31(1),GH42(1), GH43(1),GH51(2),GH74(1),GH77(1), GH(81),GH89(1),GH95(1),GH178(1), GH179(3),GH184(1),GH188(4)	GH1(3), GH2(2), GH3(5), GH5(3), GH6(1), GH10(2), GH11(1), GH13(8), GH15(2), GH16(1), GH18(3), GH20(2), GH23(1),GH26(1),GH31(1),GH42(1), GH43(1),GH51(2),GH74(1),GH77(1), GH(81),GH89(1),GH95(1),GH178(1), GH179(2),GH184(2),GH188(4)
GT (Glycosyltransferases)	Biosynthesis and modification of polysaccharides	GT1(3), GT2(10), GT4(15), GT20(1), GT28(2), GT39(1), GT51(4), GT81(1), GT9(1)	GT1(6), GT2(11), GT4(17), GT20(1), GT28(2), GT39(1), GT51(51), GT81(1), GT119(4)
PL (Polysaccharide Lyases)	Non-hydrolytic cleavage of polysaccharides	PL1 (3), PL11(1),PL9(1)	PL1(3), PL9(1)

Table S6 : Comparative table of cultural characteristics between *Nocardiopsis sp.* ZS3416R2A and *Nocardiopsis terrae DSM 45157* on ISP Media

ISP Medium	Strain	Growth ^a	Aerial mycelium ^b	Substrate mycelium ^c	Diffusible pigment ^d
Tryptone-Yeast Extract agar (ISP 1)	<i>N. terrae DSM 45157</i>	Abundant	White	Light brown	Strong yellowish brown
	<i>Nocardiopsis sp. ZS3416R2A</i>	Abundant	Pale yellow	Light orange yellow	Strong orange yellow
Yeast extract-malt extract agar (ISP 2)	<i>N. terrae DSM 45157</i>	Good	yellowish white	Deep brown	Strong brown
	<i>Nocardiopsis sp. ZS3416R2A</i>	Abundant	Pale yellow	Strong brown	Strong brown
Oatmeal agar (ISP 3)	<i>N. terrae DSM 45157</i>	Moderate	Absent	Strong orange yellow	Moderate yellow
	<i>Nocardiopsis sp. ZS3416R2A</i>	Moderate	White	Pale yellow	Moderate orange yellow
Inorganic salt-starch agar (ISP 4)	<i>N. terrae DSM 45157</i>	Good	White	Dark orange yellow	Moderate yellow
	<i>Nocardiopsis sp. ZS3416R2A</i>	Abundant	Pale yellow	Moderate brown	Moderate orange yellow
Glycerol-asparagine agar (ISP 5)	<i>N. terrae DSM 45157</i>	Abundant	White	Pale gray	Light yellow
	<i>Nocardiopsis sp. ZS3416R2A</i>	Abundant	White	Light brown	Light yellow
Peptone-yeast extract agar (ISP 6)	<i>N. terrae DSM 45157</i>	Abundant	White	Yellowish white	Strong yellowish brown
	<i>Nocardiopsis sp. ZS3416R2A</i>	Abundant	Pale greenish yellow	Deep brown	Deep yellowish brown
Tyrosine agar (ISP7)	<i>N. terrae DSM 45157</i>	Moderate	Yellowish withe	yellowish withe	Strong yellowish brown
	<i>Nocardiopsis sp. ZS3416R2A</i>	Moderate	Yellowish white	Light brown	Strong yellowish brown

All media were supplemented with 4% (w/v) NaCl; ISP: International *Streptomyces* Project (**Shirling and Gottlieb 1966**).

^a **No growth:** No visible colonies or mycelium; **Poor growth :** Limited colony formation and colonies underdeveloped; **Moderate growth :** Colonies with typical actinobacterial features, less dense than optimal; **Good growth :** Distinct colonies with sporulation ; **Abundant growth :**Extensive colony formation with dense sporulation.

^{b, c, d} Colours of both substrate and aerial mycelia and any soluble pigments produced were determined by comparison with chips from the colour charts of the Inter-Society Color Council National Bureau of Standards (**Kelly ,1964**).

Table S7 : Growth responses of *Nocardiosis sp.* ZS3416R2A and *Nocardiosis terrae* DSM 45157 under different salinity ,temperature and pH conditions after 14 days of incubation.

Condition		<i>Nocardiosis sp.</i> ZS3416R2A	<i>Nocardiosis terrae</i> DSM 45157
Salinity (%)	0	++++	++++
	5	++++	++++
	10	++++	++++
	15	+	-
	20	-	-
Temperature (°C)	5	-	-
	16	++++	++
	28	++++	+++
	30	++++	+++
	37	++++	+
	50	-	-
pH	5	-	-
	6	-	-
	7	+++	-
	8	++++	++
	9	-	-
	10	-	-

Growth code legend: (-): No growth ; (+) Poor growth ; (++) Moderate growth ; (+++) : Good growth ; (++++): Abundant growth

Supplementary Table S8. List of accession numbers of 16S rRNA gene sequences employed for phylogenetic analysis within the genus *Nocardiopsis*.

Scientific name	Strain	16S rRNA accession numbers	Taxonomy	Database
<i>Nocardiopsis terrae</i>	YIM 90022	DQ387958	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis exhalans</i>	ES10.1	AY036000	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis eucommiae</i>	HDS5	OM368591	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis valliformis</i>	DSM 45023	ANAZ01000070	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis ganjiahuiensis</i>	DSM 45031	ANBA01000044	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis prasina</i>	DSM 43845	X97884	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis metallicus</i>	KBS6	AJ420769	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis oceani</i>	10A08A	KF270094	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis algeriensis</i>	B32	KJ470139	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis aegyptia</i>	DSM 44442	AJ539401	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis lucentensis</i>	DSM 44048	ANBC01000932	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis tropica</i>	VKM Ac-1457	AF105971	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis sinuspersici</i>	HM6	EU410476	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis quinghaiensis</i>	YIM 28A4	EF597511	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis umidischolae</i>	66/93	AY036001	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis alkaliphila</i>	DSM 44657	AY230848	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis flavescens</i>	CGMCC 4.5723	jgi.1085022	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis dassonvillei subsp. crassaminis</i>	D1	LR606207	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis;Nocardiopsis dassonvillei	EzBioCloud 16S database
<i>Nocardiopsis deserti</i>	H13	VWVS01000045	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis nikkonensis</i>	YU1183-22	AB491226	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis halotolerans</i>	DSM 44410	ANAX01000410	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis fildesensis</i>	GW9-2	FJ853144	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis salina</i>	YIM 90010	AY373031	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis coralli</i>	HNM0947	MT947107	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis rhizosphaerae</i>	EGI 80674	KU992916	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis kunsanensis</i>	DSM 44524	ANAY01000063	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis xinjiangensis</i>	YIM 90004	ANBE01000070	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis ansamitocini</i>	EGI 80425	KR605109	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Marinactinospora thermotolerans</i>	DSM 45154	FUWS01000037	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Marinactinospora	EzBioCloud 16S database
<i>Marinactinospora endophytica</i>	YIM 690053	KP277099	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Marinactinospora	EzBioCloud 16S database
<i>Nocardiopsis rhodophaea</i>	YIM 90096	AY619714	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis halophila</i>	KCTC 9825	AF195411	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis suaedae</i>	LSu2-4	OQ181232	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Streptomonospora halophila</i>	YIM 91355	EF423989	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Streptomonospora	EzBioCloud 16S database
<i>Actinorugispora endophytica</i>	YIM 690008	KM925046	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Actinorugispora	EzBioCloud 16S database
<i>Nocardiopsis endophytica</i>	RSe5-2	OQ181233	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Nocardiopsis composta</i>	KS9	AF360734	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database
<i>Streptomonospora arabica</i>	S186	EF095149	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Streptomonospora	EzBioCloud 16S database
<i>Nocardiopsis coralliiicola</i>	SCSIO 10427	JN006759	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	EzBioCloud 16S database

Supplementary Table 9. List of whole-genome assemblies employed in the study, including scientific names, strain designation, assembly information, accession numbers, taxonomic details, and source database.

Scientific name	Strain	Assembly	Genome Assembly Accession	Taxonomy	Database
<i>Nocardiopsis terrae</i>	DSM 45157	ASM1465169v1	GCA_014651695.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Nocardiopsis eucommiae</i>	HDS5	BGI_Neuc_01	GCA_965344335.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Nocardiopsis ganjiahuensis</i>	DSM 45031	SOAPdenovo v1.06	GCA_000341085.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Nocardiopsis metallicus</i>	DSM 44598	ASM1420111v1	GCA_014201115.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Nocardiopsis algeriensis</i>	CECT 8712	ASM1420369v1	GCA_014203695.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Nocardiopsis aegyptia</i>	DSM 44442	ASM1341075v1	GCA_013410755.1	Bacteria;Actinobacteria;Actinomycetia;Streptosporangiales;Nocardiopsaceae;Nocardiopsis	NCBI database
<i>Streptomyces albidoflavus</i>	DSM 40455	ASM419573v1	GCA_004195735.1	Bacteria;Actinomycetota;Actinomycetia;Streptomycetales;Streptomycetaceae;Streptomyces	NCBI database