

Supplementary material

Genomic analysis of a novel heavy metal resistant isolate from a Black sea contaminated sediment with the potential to degrade alkanes: *Plantactinospora alkalitolerans* sp. nov.

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Table S1 dDDH values of strain S1510^T and type strains used in the phylogenomic reconstruction of *Plantactinospora* and *Micromonospora* genera. Values in brackets indicate the confidence intervals obtained using formula d4 in TYGS server (equivalent to GGDC formula 2)

	S1510 ^T	
<i>P. soya</i> DSM 46832 ^T	41.1	[38.7 - 43.7]
<i>P. veratri</i> CGMCC 4.7143 ^T	35.8	[33.3 - 38.3]
<i>P. mayteni</i> NBRC 109088 ^T	28.9	[25.7 - 32.7]
<i>P. endophytica</i> NBRC 110450 ^T	28.6	[27.1 - 34.1]
<i>M. cremea</i> DSM 45599 ^T	23.3	[21.0 - 25.8]
<i>M. pallida</i> DSM 43817 ^T	23.0	[20.7 - 25.4]
<i>M. viridifaciens</i> DSM 43909 ^T	23.0	[20.7 - 25.5]
<i>M. chalcea</i> DSM 43026 ^T	22.6	[20.3 - 25.0]
<i>M. nigra</i> DSM 43818 ^T	22.5	[20.3 - 25.0]

Table S2 Differential characteristics of strain *Plantactinospora* sp. S1510^T and close related type strains. *Data from Guo et al. 2016 [43] and Li et al. 2018 [44]. +: positive; -: negative; DPG: diphosphatidylglycerol; PE: phosphatidylethanolamine; PEM: phosphatidylmethylethanolamine; PG: phosphatidylglycerol; PI: phosphatidylinositol; PIM: phosphatidylinositol mannoside; MK: menaquinone.

Characteristics	<i>Plantactinospora</i> sp. S1510 ^T	<i>Plantactinospora soyae</i> NEAU-gxj3 ^T *	<i>Plantactinospora solaniradicis</i> NEAU-FJL1 ^T *
Colony colour on ISP 2	Brilliant Orange	Strong Orange Yellow	Light Orange Yellow
Colony colour on ISP 3	Light Orange	Light yellow to pale greenish yellow	Brilliant Orange Yellow
Colony colour on ISP 6	Light Salmon	Light Orange Yellow	Moderate Orange Yellow
pH tolerance			
5	-	-	+
6	-	+	+
10	+	+	-
11	+	-	-
Temperature (°C)			
20	-	+	+
28	+	+	+
37	-	-	+
40	-	-	+
Degradation of (% w/v)			
Starch (1 %)	+	-	+
Urea Hydrolysis	-	+	-
Cellulose	+	+	-
Utilisation as sole carbon source			
L-arabinose	+	-	+
D-fructose	+	-	+
D-mannitol	-	+	-
<i>myo</i> -inositol	-	+	-
D-sorbitol	-	+	+
Sucrose	+	-	+
Utilisation as sole nitrogen source			
L-threonine	-	+	+
L-tyrosine	-	+	-
Whole-cell sugars	glucose, mannose, ribose, xylose	galactose, glucose, xylose	arabinose, galactose, glucose, xylose
Polar lipids	DPG, PE, PI, PEM, PG	DPG, PI, PIM, PE	DPG, PI, PE
Major fatty acids (> 10%)	<i>iso</i> -C _{15:0} , <i>anteiso</i> -C _{15:0} , <i>iso</i> -C _{16:0} , <i>anteiso</i> -C _{17:0}	<i>anteiso</i> -C _{17:0} , <i>iso</i> -C _{16:0} , <i>iso</i> -C _{15:0} , C _{15:0}	C _{15:0} , <i>iso</i> -C _{16:0} , <i>iso</i> -C _{17:0} , C _{17:0} , <i>iso</i> -C _{15:0}
Predominant menaquinones (> 10%)	MK-10(H ₆), MK-10(H ₈)	MK-10(H ₆), MK-9(H ₈), MK-10(H ₂), MK-10(H ₄)	MK-10(H ₆), MK-10(H ₄)
DNA G+C content (mol%)	70.5	70.3	69.5

Table S3 Fatty acids profile of strain S1510^T

Fatty acids	S1510 ^T
Saturated	
C _{15:0}	2.2
C _{16:0}	1.1
C _{17:0}	9.5
C _{18:0}	1.2
C _{19:0}	0.8
Unsaturated	
C _{17:1} <i>cis</i> 9	7.2
C _{18:1} <i>cis</i> 9	2.5
Branched	
<i>iso</i> C _{14:0}	1.3
<i>iso</i> C _{15:0}	22.6
<i>iso</i> C _{15:1} G	1.5
<i>iso</i> C _{16:0}	13.1
<i>iso</i> C _{16:1} G	2.4
<i>iso</i> C _{17:0}	2.7
<i>iso</i> C _{18:0}	0.4
<i>anteiso</i> C _{15:0}	14.4
<i>anteiso</i> C _{17:0}	10.0
<i>anteiso</i> C _{15:1} A	0.4
<i>anteiso</i> C _{17:1} A	1.1
Hydroxi	
C _{16:1} 2OH	4.4

Table S4 Biosynthetic gene clusters detected with antiSMASH 5.1.2 tool for strain S1510^T

		Similarity	%	Nucleotides	Location	
Type					Contig	Position
Cluster 1	NRPS-like	bicornutin A1, rhizomide A, anabaenopeptin NZ857, xenotetrapeptide, luminmide	100	1272	493	1 - 1272
Cluster 2	NRPS	-	-	6010	358	1 - 6010
Cluster 3	Terpene	isorenieratene, carotenoid	28, 25	20990	10	41207 - 62196
Cluster 4	Terpene	phosphonoglycans, amycolamycin A	3, 2	17398	102	12506 - 29903
Cluster 5	NRPS/Bacteriocin	-	-	53779	21	2905 - 56683
Cluster 6	NRPS	JBIR-78, feglymycin	44,31	24990	137	1 - 24990
Cluster 7	NRPS	-	-	28816	109	1 - 28816
Cluster 8	NRPS/T3PKS	kistamicin A	40	53344	28	1 - 53344
Cluster 9	Terpene	-	-	10611	33	38262 - 48872
Cluster 10	NRPS	-	-	26814	7	1 - 26814
Cluster 11	Other/phosphonate	phosphinothricintripeptide	34	40969	7	38506 - 79474
Cluster 12	Bacteriocin	hygromycin A, apramycin, lividomycin	6	10816	138	9780 - 20595
Cluster 13	Lasso peptide	-	-	14615	96	1 - 14615
Cluster 14	NRPS	-	-	1843	468	1 - 1843
Cluster 15	T1PKS	hygrocine A, hygrocine B	9	16624	215	1 - 16624
Cluster 16	Bacteriocin	lymphostin, neolymphostinol B, lymphostinol, neolymphostinol B	33	10822	6	39763 - 50584
Cluster 17	NRPS-like	-	-	32841	15	32649 - 65489
Cluster 18	Siderophore	scabichelin	20	13310	1	3861 - 17170
Cluster 19	NRPS/PKS-like	kistamicin A, feglymycin	32, 31	33771	81	1 - 33771
Cluster 20	Indole	fortimycin	11	14230	177	5429 - 19658
Cluster 21	NRPS	-	-	35834	26	1 - 35834
Cluster 22	Ladderane	MS-271, aborycin	14	31574	60	8377 - 39950
Cluster 23	T3PKS	alkyl-O-dihydrogeranyl-methoxyhydroquinones	71	29483	74	1 - 29483
Cluster 24	NRPS/T1PKS	buryrolactol A	46	41135	56	1 - 41135
Cluster 25	Lanthipeptide	-	-	18093	18	43345 - 61437
Cluster 26	T2PKS	frankiamicin	28	42270	8	1 - 42270
Cluster 27	Terpene	hopene	38	12352	253	1 - 12352
Cluster 28	NRPS	-	-	12238	254	1 - 12238
Cluster 29	NRPS	-	-	10418	283	1 - 10418
Cluster 30	Tfua-related	thiovarsolin a, b, c, d	33	22024	32	28410 - 50433
Cluster 31	NRPS	-	-	5419	369	1 - 5419
Cluster 32	NRPS	-	-	5096	377	1 - 5096
Cluster 33	NRPS	-	-	3544	414	1 - 3544
Cluster 34	NRPS	sarpeptin A, B	25	4381	389	1 - 4381
Cluster 35	NRPS	-	-	2325	448	1 - 2325
Cluster 36	NRPS	-	-	3144	422	1 - 3144
Cluster 37	NRPS	-	-	2172	455	1 - 2172

Table S5 Capacity of S1510^T to grow in the presence of several concentrations of different metals after 14 days on M65 medium. + good growth (similar to the positive control); w weak growth; - no growth

	1 ppm	10 ppm	100 ppm	300 ppm	500 ppm	1000 ppm	2000 ppm	5000 ppm
Cd	+	w	-	-	-	-	-	-
Co	+	+	w	-	-	-	-	-
Cr	+	+	+	+	-	-	-	-
Cu	+	+	+	+	+	+	+	-
Hg	w	-	-	-	-	-	-	-
Pb	+	+	+	+	+	+	+	-
Zn	+	+	+	+	+	+	+	w

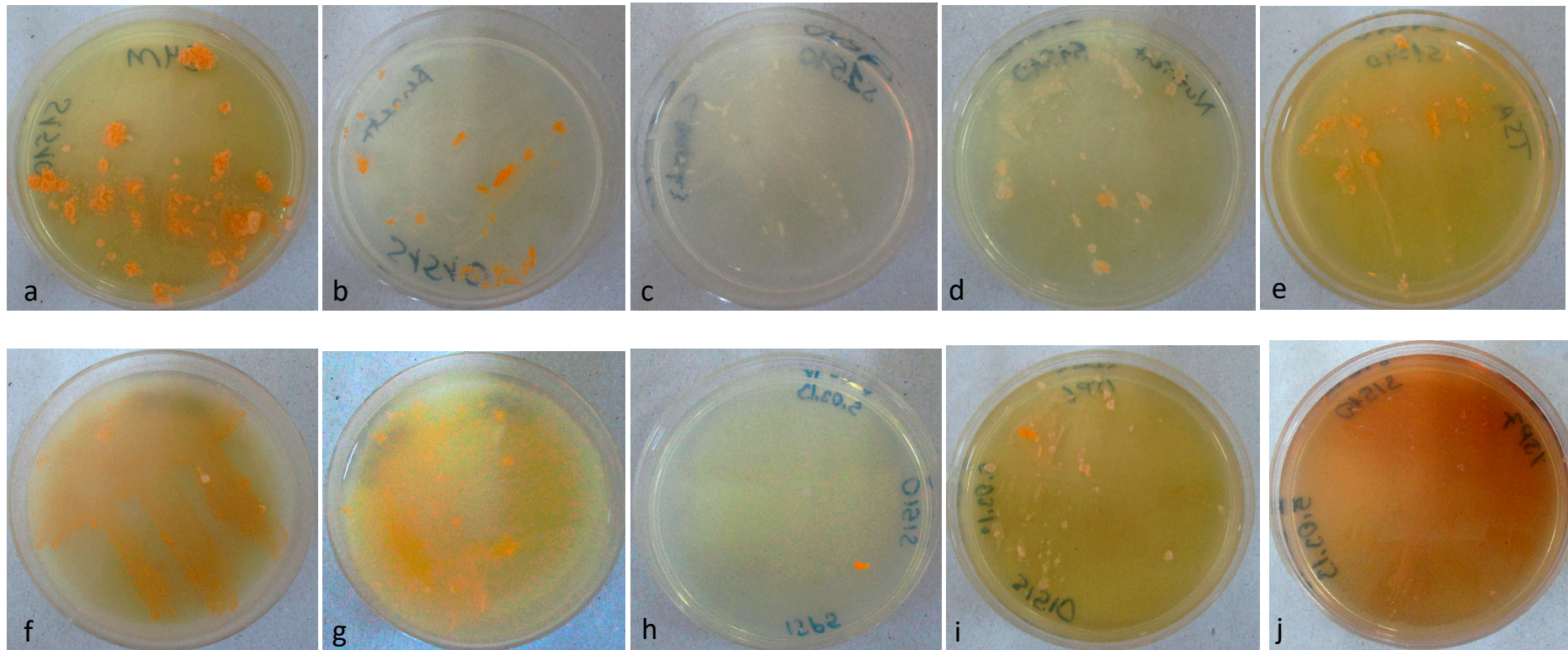


Figure S1 Cultural characteristics of the strain S1510^T after growth on different media. (a) ISP 2 agar; (b) Bennett's agar; (c) Czapek's agar; (d) Nutrient agar; (e) TSA agar; (f) ISP 3 agar; (g) ISP 4 agar; (h) ISP 5 agar; (i) ISP 6 agar; (j) ISP 7 agar.

Figure S2 Polar lipid profile of strain S1510^T after spraying with molybdatophosphoric acid. DPG: diphosphatidylglycerol; PE: phosphatidylethanolamine; PEM: phosphatidylmehtylethanolamine; PG: phosphatidylglycerol; PI: phosphatidylinositol

