Micromonospora profundi sp. nov., isolated from deep marine sediment

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A novel actinobacterial strain, designated DS3010^T, was isolated from a Black Sea marine sediment and characterized using a polyphasic approach. The strain was shown to have chemotaxonomic, morphological and phylogenetic properties consistent with classification as representing a member of the genus *Micromonospora*. Comparative 16S rRNA gene sequence studies showed that the strain was most closely related to the type strains of *Micromonospora saelicesensis* (99.5 %), *Micromonospora chokoriensis* (99.4 %) and *Micromonospora violae* (99.3 %). Similarly, a corresponding analysis based on partial *gyr*B gene sequences showed that it formed a distinct phyletic branch in a subclade that included the type strains of *Micromonosporazamorensis*, '*Micromonospora zeae*', '*Micromonospora jinlongensis*', *M. saelicesensis* and *Micromonospora lupini*. DS3010^T was distinguished from its closest phylogenetic neighbours by low levels of DNA–DNA relatedness and by a combination of chemotaxonomic and phenotypic properties. On the basis of these data, it is proposed that the isolate should be assigned to the genus *Micromonospora* as *Micromonospora profundi* sp. nov. with isolate DS3010^T (=DSM 45981^T=KCTC 29243^T) as the type strain.

The genus *Micromonospora* established by Ørskov (1923) and emended by Gao *et al.* (2014) is the type genus of the family *Micromonosporaceae* (Genilloud, 2012b) which is classified in the order *Micromonosporales* (Genilloud, 2012a). This taxon can be distinguished from other genera assigned to the family *Micromonosporaceae* using a battery of chemotaxonomic, morphological and phylogenetic markers (Genilloud, 2012c; Matsumoto *et al.*, 2014), especially by an ability to form non-motile spores on branched substrate hyphae and to synthesize complex mixtures of fatty acids, menaquinones and sugars (Genilloud, 2012c; Gao *et al.*, 2014; Thawai, 2015). Micromonosporae are widely distributed in the environment, as illustrated by the isolation of *Micromonospora nickelidurans* from a nickel mining site (Lin *et al.*, 2015), '*Micromonospora soli*' from rhizosphere soil (Thawai *et al.*, 2016) and *Micromonospora zhanjiangensis* from mangrove forest soil (Zhang *et al.*, 2015).

The genus *Micromonospora* currently comprises 63 species with validly published names (http://www.bacterio.net/micromonospora.html), the members of which can be separated using a combination of chemotaxonomic, morphological and phenotypic properties (Genilloud, 2012c; Thawai *et al.*, 2016). Members of the genus *Micromonospora*

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Abbreviation: A2pm, diaminopimelic acid.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA and *gyrB* gene sequences of *Micromonospora profundi* DS3010^T (=DSM 45981^T=KCTC 29243^T) are KF494813 and KF818375, respectively.

One supplementary table and three supplementary figures are available with the online Supplementary Material.

tend to feature in bioprospecting campaigns as they are a rich source of novel bioactive compounds of therapeutic value, such as aminoglycoside antibiotics (Kasai *et al.*, 2000; Bérdy, 2005; Genilloud, 2012c). As part of an ongoing programme to discover actinobacteria able to produce novel antibiotics, a strain of a member of the genus *Micromonospora* from a Black Sea sediment was the subject of a polyphasic study designed to establish its taxonomic status. The resultant data showed that the strain, isolate DS3010^T, formed a novel centre of taxonomic variation within the genus *Micromonospora* for which the name *Micromonospora profundi* sp. nov. is proposed.

DS3010^T was isolated from a marine sediment collected at a depth of 45 m using a dredge offshore of the estuary of the river Melet (GPS coordinates 41°00.353′ N 37°57.489′ E). The sediment sample was stored at −20 °C until examined using a standard dilution plate method, as described previously (Veyisoglu *et al.*, 2016). Isolate DS3010^T, *Micromonospora chokoriensis* DSM 45160^T, *Micromonospora lupini* DSM 44874^T, *Micromonospora saelicesensis* DSM 44871^T and *Micromonospora zamorensis* DSM 45600^T were maintained on yeast extract–malt extract agar [International *Streptomyces* Project medium 2 (ISP 2); (Shirling & Gottlieb, 1966)] slopes at room temperature and preserved as suspensions of mycelial fragments and spores in glycerol (20 %, v/v) at −20 and −80 °C.

DNA extraction and 16S rRNA gene amplification and sequencing were achieved following the methods of Chun & Goodfellow (1995). The almost-complete 16S rRNA gene sequence (1460 bp) of DS3010^T was determined and identification of its closest phylogenetic neighbours, using the EzTaxon-e server (Kim *et al.*, 2012), indicated that it represented a member of the genus *Micromonospora.* The sequence of the isolate was aligned and analysed with CLUSTAL W in MEGA6 (Tamura *et al.*, 2013) together with the corresponding sequences of representative type strains of species of the genus *Micromonospora*. Phylogenetic analyses were carried out using the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) algorithms drawn from MEGA version 6.0 software. Evolutionary distances were calculated using the Kimura two-parameter method (Kimura, 1980) and the topologies of the resultant trees were evaluated by bootstrap analyses (Felsenstein, 1985) based on 1000 resamplings. The isolate was found to form a subclade in the *Micromonospora* 16S rRNA neighbour-joining gene tree together with the type strain of *M. saelicesensis*, a relationship that was supported by the corresponding maximum-likelihood and maximum-parsimony analyses (Figs 1 and S1, available in the online Supplementary Material). DS3010^T was most closely related to *M. saelicesensis* Lupac 09^T; these strains shared a 16S rRNA gene sequence similarity of 99.5 %, a value which corresponds to eight nucleotide differences among 1460 locations. Levels of 16S rRNA gene sequence similarity between DS3010^T and *M. chokoriensis* 2–19/6^T, '*Micromonospora lycii*' NEAU-gq11, *Micromonospora violae* NEAU-zh8^T, '*Micromonospora zeae*' NEAU-gq9, *Micromonospora taraxaci* NEAU-P5^T, '*Micromonospora luteifusca*' GUI2^T, '*Micromonospora jinlongensis*' NEAU-GRX11, *M. zamorensis* CR38^T, '*Micromonospora maoerensis*' NEAU-MES19, *Micromonospora coxensis* 2-30-b/28^T, *Micromonospora marina* JSM1-1^T and *M. lupini* Lupac14N^T were 99.4 % (nine nucleotide differences among 1459), 99.3 % (10 nucleotide differences among 1460), 99.3 % (11 nucleotide differences among 1459), 98.9 % (15 nucleotide differences among 1460), 98.9 % (16 nucleotide differences among 1460), 98.8 % (17 nucleotide differences among 1434), 98.8 % (18 nucleotide differences among 1460), 98.7 % (19 nucleotide differences among 1434), 98.6 % (20 nucleotide differences among 1460), 98.6 % (20 nucleotide differences among 1459), 98.6 % (20 nucleotide differences among 1437) and 98.6 % (20 nucleotide differences among 1434), respectively. 16S rRNA gene sequence similarities with the type strains of all of the other species of the genus *Micromonospora* were below 98.50 %.

The partial *gyr*B gene sequence of DS3010^T was amplified and sequenced using primers GYF1 and GYR3B as described by Garcia *et al.* (2010) and the resultant sequence (1124 nt) deposited in the GenBank/EMBL/DDBJ databases as KF818375. Comparative phylogenetic analysis based upon the partial *gyr*B gene sequence of strain DS3010^T and corresponding sequences of type strains of species of the genus *Micromonospora* were found to fall within the range 88.2–96.2 %, similarity values well below those found between strains of members of the genus *Micromonospora* known to belong to distinct genomic species (Carro *et al.*, 2012b). The *gyr*B sequence analysis showed that DS3010^T formed a subclade together with *M. zamorensis* CR38^T, '*M. zeae*' NEAU-pq9^T, '*M. jinlongensis*' NEAU-GRX11^T, *M. saelicesensis* DSM 44871^T, '*M. lycii*' NEAU-gq11^T and *M. lupini* DSM 44874^T a relationship that was supported by the corresponding maximum-likelihood and maximum-parsimony analyses (Fig. 2). DS3010^T was shown to be most closely related to the validly described type strains of *M. zamorensis* (96.0 % similarity; 45 nucleotide differences among 1111 locations), *M. saelicesensis* (95.9 % similarity; 44 nucleotide differences among 1080 locations) and *M. lupini* (95.6 % similarity; 47 nucleotide differences among 1056 locations). In general, good congruence was found between the partial *gyr*B and 16S rRNA gene sequence data though the topologies of the respective trees differed, a result consistent with those of previous studies (Kasai *et al.*, 2000; Kirby & Meyers, 2010; Carro *et al.*, 2012b; Li *et al.*, 2014; Jia *et al.*, 2015).

DNA–DNA hybridization experiments were carried out, in triplicate, between DS3010^T and its closest phylogenetic neighbours, namely the type strains of *M. saelicesensis* DSM 44871^T, *M. chokoriensis* DSM 45160^T and *M. zamorensis* DSM 45600^T. The strains were selected according to the relationships between the isolate and the first two type strains based on 16S rRNA gene phylogeny and the relationship with the last strain based on *gyr*B gene phylogeny. To this end, DNA was extracted from the strains using a French

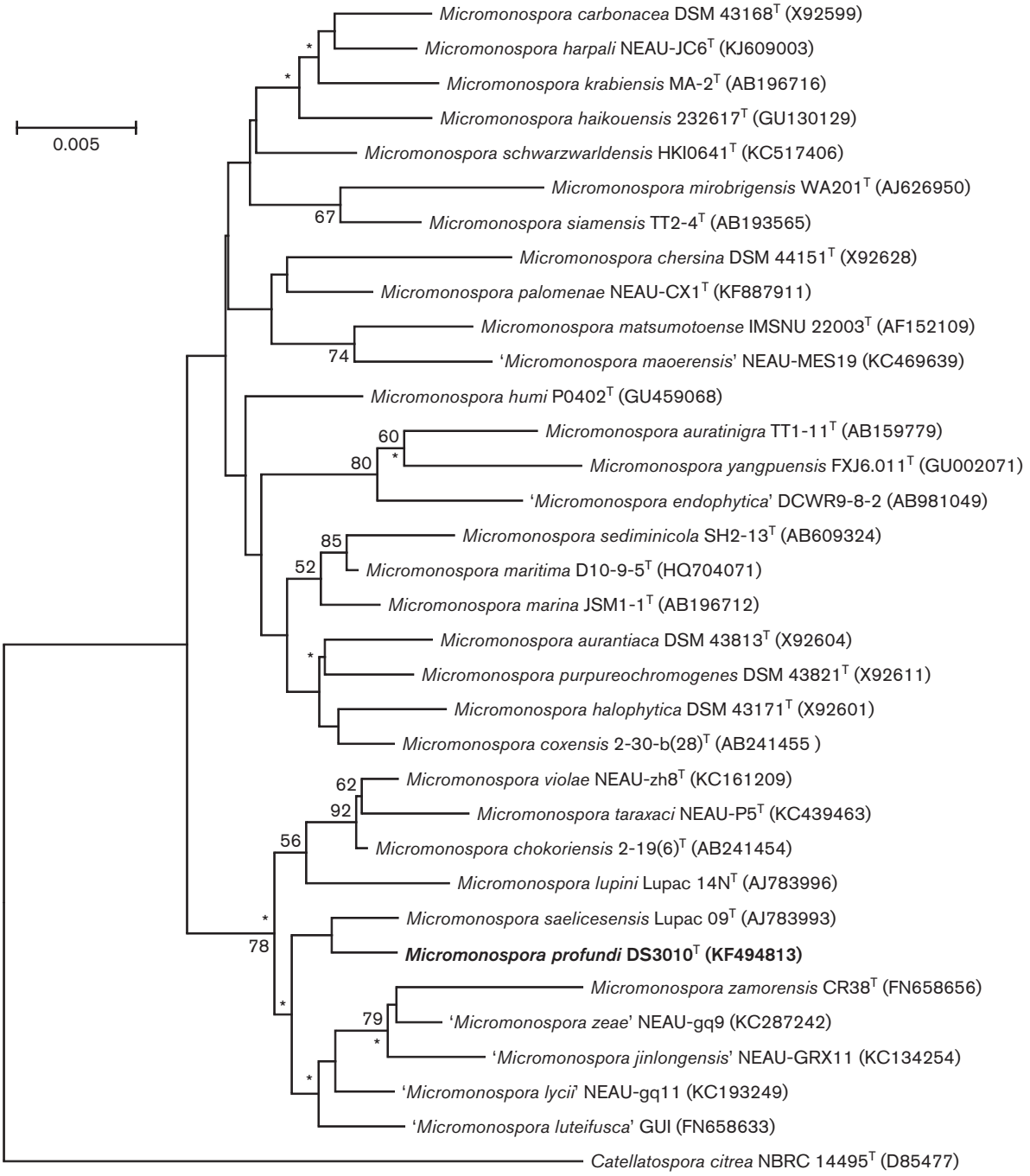

Fig. 1. Neighbour-joining tree (Saitou & Nei, 1987) based on almost complete 16S rRNA gene sequences showing the relationship between strain DS3010^T and its closest phylogenetic neighbours. Asterisks (*) indicate branches of the tree that were also recovered using the maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) tree-making algorithms. Numbers at the nodes indicate the levels of bootstrap support (%); only values ≥50 % are shown. *Catellatospora citrea* NBRC 14495^T (D85477) was used as the outgroup. GenBank accession numbers are given in parentheses. Bar, 0.005 substitutions per site.

pressure cell (Thermo Spectronic) and purified by chromatography on hydroxyapatite, as described by Cashion *et al.* (1977). DNA–DNA hybridization was carried out as described by De Ley *et al.* (1970) using the modifications introduced by Huss *et al.* (1983) on a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-

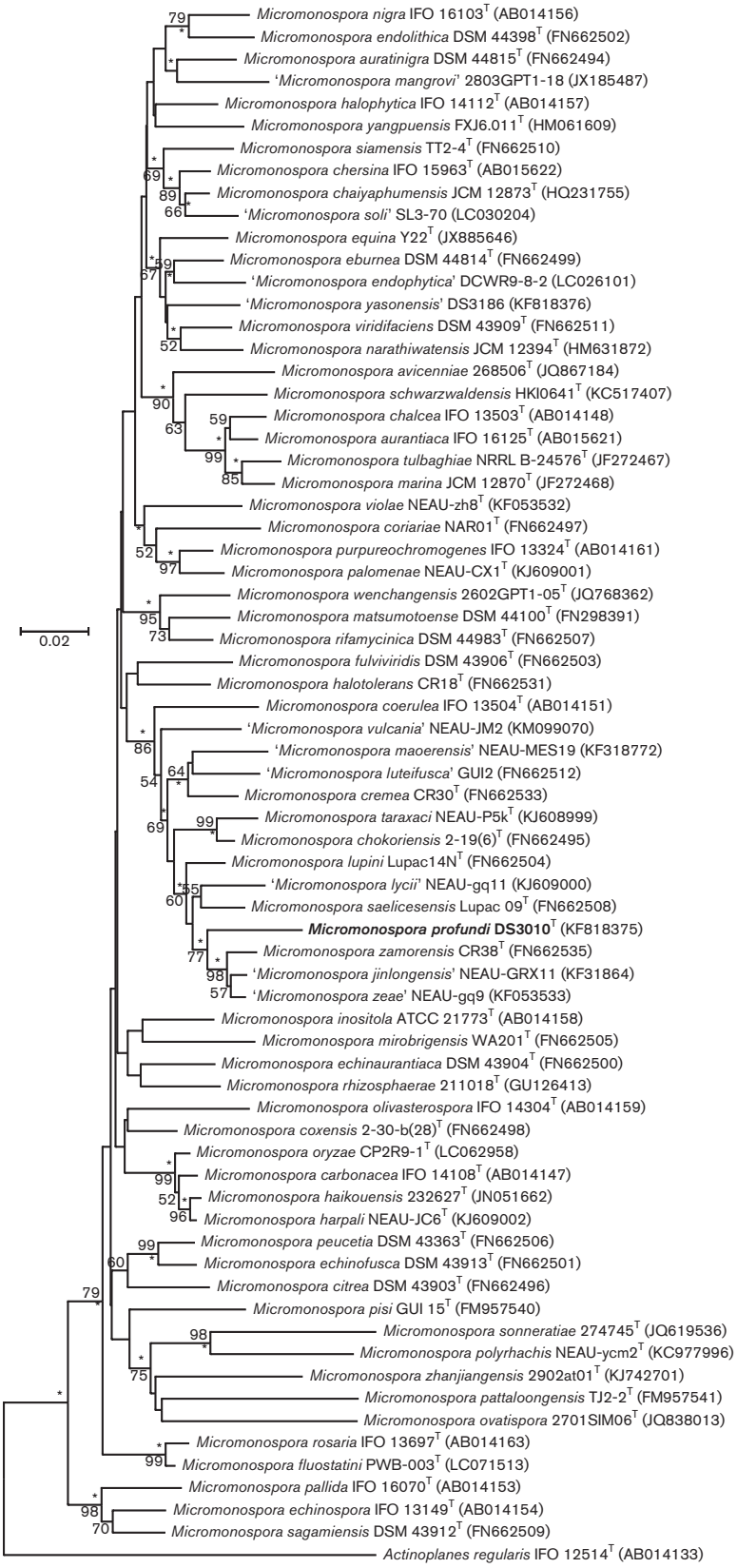

Fig. 2. Neighbour-joining phylogenetic tree (Saitou & Nei, 1987) based on partial *gyr*B gene sequences showing relationships between DS3010^T and its closest phylogenetic neighbours. Asterisks (*) indicate branches of the tree that were also

recovered using the maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) tree-making algorithms. Numbers at the nodes indicate levels of bootstrap support, only values ≥50 % are shown. *Actinoplanes regularis* IFO 12514^T (AB014133) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

thermostat-regulated 6×6 multicell changer and a temperature controller with an *in situ* temperature probe (Varian). DNA–DNA relatedness values between DS3010^T and *M. saelicesensis* DSM 44871^T, *M. chokoriensis* DSM 45160^T and *M. zamorensis* DSM 45600^T were found to be 28.4±2.9 %, 36.7±6.6 % and 42.0±1.1 %, respectively, values well below the 70 % cut-off recommended for assigning bacterial strains to the same genomic species (Wayne *et al.*, 1987).

The G+C content of the genomic DNA of DS3010^T was determined, in triplicate, using the thermal denaturation (T*m*) procedure described by Mandel & Marmur (1968); DNA extracted from *Escherichia coli* JM109 DNA was used as the control. The DNA G+C value of DS3010^T was found to be 73.3±0.5 mol%.

DS3010^T was examined for chemotaxonomic makers considered to be characteristic of strains of members of the genus *Micromonospora* (Genilloud, 2012c). To this end, biomass was obtained by growing the strain in N-Z-Amine broth (DSMZ Medium 554) in shake flasks (160 r.p.m.) for 14 days at 30 °C; cells were harvested by centrifugation, washed twice in distilled water and freeze dried. Isomers of diaminopimelic acid (A_2pm) and sugars in whole-cell hydrolysates prepared after the methods of Lechevalier & Lechevalier (1970) were analyzed by TLC (Staneck & Roberts, 1974). Isoprenoid quinones were prepared and purified using the methods of Collins *et al.* (1977) and analysed by HPLC (Kroppenstedt, 1982) while polar lipids were extracted and analysed as recommended by Minnikin *et al.* (1984) using the modifications of Kroppenstedt & Goodfellow (2006). Fatty acids from DS3010^T and the most closely related type strains were extracted, methylated and analysed by gas chromatography using a 6890N gas chromatography system (Agilent Technologies), fitted with an autosampler and 6783 injector, according to the standard protocol of the Sherlock Microbial identification (MIDI) system (Sasser, 1990; Kämpfer & Kroppenstedt, 1996), the fatty acid methyl esters were quantified using the TSBA database. The muramic acid type was determined according to the protocol of Uchida *et al.* (1999). It is clear from the results that the isolate has chemotaxonomic properties consistent with its classification as a member of the genus *Micromonospora* (Genilloud, 2012c). It contains *meso*-A_2pm in the cell wall peptidoglycan, galactose, glucose, mannose, ribose and xylose in whole-organism hydrolysates, a polar lipid pattern containing diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylinositol and two unidentified phospholipids (Fig. S2); phospholipid type 2 *sensu* Lechevalier *et al.* (1977) and major proportions of tetrahydrogenated menaquinones with ten isoprene units [MK-10(H_4)] (38.0 %) with lesser proportions of MK-10(H_6) (18.0 %), MK-8(H_4) (9.0 %), MK-10(H_8) (5.0 %), MK-9(H_4) (4.0 %), MK-10(H_2) (3.0 %), MK-9(H_6) (2.0 %) and an unidentified menaquinone (14.0 %; ret T 15.197). The fatty acid profile contained major proportions (>10 %) of iso-$C_{15:0}$ (24.1 %), iso-$C_{16:0}$ (13.8 %), $C_{17:1}\omega9c$ (14.3 %) and $C_{16:0}$ 9-methyl (10.3 %) and lesser proportions of iso-$C_{17:0}$ (6.3 %), anteiso-$C_{17:0}$ (5.9 %), $C_{18:1}\omega9c$ (5.3 %) anteiso-$C_{15:0}$ (4.2 %) and $C_{17:0}$10-methyl (3.6 %) (Table S1). The muramic acid moieties were *N*-glycolated.

DS3010^T was examined for a range of cultural and morphological properties using procedures described by Veyisoglu *et al.* (2016). Growth on GPHF agar (DSMZ-medium 553) showed that it had typical characteristics of members of the genus *Micromonospora* (Genilloud, 2012c). The isolate grew well on ISP 2, ISP 3, N-Z-Amine (DSMZ-medium 554) and tryptic soy agar; moderately well on ISP 6 and nutrient agar; but poorly on modified Bennett's, Czapek's and other ISP media. Colony colours varied from light orange to brownish black. Colonies growing on ISP2 were light brown, those on ISP3 brownish black while those growing on ISP 4, ISP 5, ISP 6, ISP 7 and Czapek's agars and on nutrient, N-Z-Amine and tryptic soy agars were light and strong orange, respectively; diffusible pigments were not produced on any of these media. DS3010^T was found to grow at 28–40 °C, optimally at approximately 30 °C but not at 4, 10, 20, 45, 50 or 55 °C, from pH 6.0 to pH 11.0, optimally between pH 7.0 and pH8.0, but not at pH 4.0, 5.0 or 12.0 and was able to tolerate up to 3 % (w/v) NaCl.

The micromorphological properties of the strain were determined by scanning electron microscopy (SEM) after 21-days growth on GPHF agar (DSMZ-medium 553) using a JSM 6060 instrument (JEOL). The strain produced non-motile, single elliptical to oval spores (0.6–0.9×0.8–1.2 μm) with smooth surfaces on branched substrate hyphae, fragmentation was not observed (Fig. S3). DS3010^T and the type strains of its nearest phylogenetic neighbours were examined for a broad range of phenotypic features, as described by Veyisoglu *et al.* (2016). It can be seen from Table 1 that the isolate can be distinguished from all of its phylogenetic neighbours, notably from its closest relatives, *M. saelicesensis* DSM 44871^T, *M. chokoriensis* DSM 45160^T and *M. zamorensis* DSM45600^T using a combination of chemotaxonomic and phenotypic properties. It can be separated from these strains by its ability to grow at pH 11 and 40 °C, but not at 20 °C and from the *M. saelicesensis* strain by its use of D-mannitol as a sole carbon source and by its inability to hydrolyse urea. The *M. chokoriensis* strain was differentiated by its inability to produce α-chymotrypsin, cystine arylamidase and trypsin and degrade starch. The novel isolate can be distinguished from the *M. zamorensis* strain by its capacity to metabolise D-galactose and D-xylose as sole carbon sources. Furthermore, the novel isolate,

Table 1. Phenotypic properties that distinguish isolate DS3010^T from the type strains of closely related species of the genus *Micromonospora*

Data are from this study except where noted. Strains: 1, DS3010^T; 2, *M. chokoriensis* DSM 45160^T; 3, '*M. jinlongensis*' NEAU-GRX11^T [data from Gao *et al.* (2014)] ; 4, *M. lupini* DSM 44874^T; 5, '*M. luteifusca*' GUI2^T [data from Carro *et al.* (2016)]; 6, '*M. lycii*' NEAU-gq11^T [data from Zhao *et al.* (2015)]; 7, *M. saelicesensis* DSM 44871^T; 8, *M. violae* NEAU-zh8^T [data from Zhang *et al.* (2014)]; 9, *M. zamorensis* DSM 45600^T; 10, '*M. zeae*' NEAU-gq9^T [data from Shen *et al.* (2014)]. Abbreviations: PL, unidentified phospholipid; PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; PME, phosphatidylmethylethanolamine; ara, arabinose; gal, galactose; glc, glucose; man, mannose; rham, rhamnose; rib, ribose; xyl, xylose. +, Positive; –, negative; ND, not determined.

Characteristics	1	2	3	4	5	6	7	8	9	10
Major menaquinones (%)	MK-10(H_4), MK-10(H_6)	MK-10(H_4)*	MK-9(H_4) MK-9(H_6)	MK-10(H_4), MK-10(H_6)†	MK-10($H_{2,4,6}$), MK-9($H_{2,4,6}$)	MK-9(H_8) MK-10 (H_6), MK-10(H_2)	MK-10(H_4)†	MK-10(H_4) MK-10(H_2)	MK-10(H_4), MK-9(H_4), MK-10 (H_6)‡	MK-10(H_2), MK-10(H_4), MK-8(H_8), MK-9(H_4)
Polar lipid profile	DPG, PI, PE, 2×PL	DPG, PE, PG, PI, PIMs§	DPG, PME, PE, PI	DPG, PI, PE†	DPG, PE, PI	DPG, PE, PI	DPG, PI, PE†	DPG, PE, PI	DPG, PE, PI‡	DPG, PE, PI
Major fatty acids (>10.0 %)	iso-$C_{15:0}$, $C_{17:1}\omega9c$ iso-$C_{16:0}$, $C_{16:0}$ 9-methyl	iso-$C_{15:0}$, iso-$C_{17:0}$, $C_{17:0}$	$C_{16:0}$, $C_{15:0}$, $C_{17:1}\omega8c$,	iso-$C_{16:0}$, iso-$C_{15:0}$,	iso-$C_{15:0}$, iso-$C_{16:0}$, anteiso-$C_{15:0}$	iso-$C_{16:0}$	iso-$C_{16:0}$, iso-$C_{15:0}$, $C_{17:1}\omega9c$	iso-$C_{15:0}$, $C_{16:0}$, $C_{17:0}$ 10-methyl	iso-$C_{15:0}$, anteiso-$C_{15:0}$, $C_{17:1}\omega8c$	$C_{16:0}$, $C_{17:1}\omega7c$, $C_{15:0}$,
Whole-cell sugars	glc, rib, man, xyl, gal	rib, man, xyl, gal, glc, ara*	rham, xyl, glc	glc, man, ara, xyl, rib†	gal, glc, man, rib, xyl	rham, xyl, glc	glc, man, ara, xyl, rib, rham†	rham, xyl, glc, gal	glc, man, rib, xyl‡	xyl, glc
Growth temperature range °C	28–40	20–37	18–37	20–37	12–37	10–37	20–37	18–37	10–37	18–37
pH range for growth	6.0–11.0	5.0–9.0	6.0–9.0	6.5–9.0	7.0–8.0	6.0–12.0	7.0–9.0	6.0–9.0	6.5–9.0	6.0–9.0
Maximum NaCl tolerance (%, w/v)	3	3	3	1	3	3	2	2	3	3
Biochemical tests:										
Nitrate reduction	–	–	+	–	ND	–	–	–	–	–
Urea hydrolysis	–	–	–	–	–	+	+	+	–	–
Degradation test:										
Starch (1 %, w/v)	+	–	+	+	+	–	+	–	+	–
Sole carbon sources (1.0 %, w/v)										
D-Fructose	+	+	–	+	+	+	+	+	+	+
D-Galactose	+	+	–	+	–	+	+	+	–	+
D-Mannose	+	+	–	+	+	+	+	+	+	+
D-Mannitol	+	+	+	–	ND	+	–	–	+	+
D-Maltose	+	+	+	–	–	+	+	+	+	+
D-Xylose	+	+	–	+	+	+	+	+	–	+
Sole nitrogen source (0.1 %, w/v)										
L-Alanine	+	+	–	+	–	+	+	+	+	+
API ZYM tests										
α-Chymotrypsin	+	–	ND	–	+	ND	+	ND	–	+
α-Fucosidase	–	–	ND	–	–	ND	+	ND	–	–
α-Galactosidase	+	+	ND	–	+	ND	+	ND	+	+
α-Glucosidase	+	+	ND	–	+	ND	+	ND	+	+

Table 1. cont.

Characteristics	1	2	3	4	5	6	7	8	9	10
α-Mannosidase	−	−	ND	−	−	ND	+	ND	−	−
β-Glucosidase	−	+	ND	−	+	ND	+	ND	−	+
β-Glucuronidase	−	+	ND	−	+	ND	−	ND	−	−
Cystine arylamidase	+	−	ND	+	+	ND	+	ND	+	+
Esterase (C4)	−	+	ND	+	+	ND	+	ND	+	+
Esterase lipase (C8)	−	+	ND	+	+	ND	+	ND	+	+
Leucine arylamidase	−	+	ND	+	+	ND	+	ND	+	+
Lipase (C14)	−	+	ND	+	+	ND	+	ND	+	+
N-acetyl-β-glucosaminidase	+	+	ND	−	+	ND	+	ND	−	+
Trypsin	+	−	ND	+	+	ND	+	ND	−	+
Valine arylamidase	−	+	ND	+	+	ND	+	ND	+	+

*Data from Ara & Kudo (2007).
†Data from Trujillo *et al.* (2007).
‡Data from Carro *et al.* (2012a).
§Data from Shen *et al.* (2014).

unlike the *M. saelicesensis* and *M. zamorensis* strains, was characterized by the presence of galactose in whole-cell hydrolysates and two unidentified unknown phopholipids in its polar lipid pattern.

In conclusion, it is evident from the chemotaxonomic, genotypic and phenotypic data that DS3010^T represents a novel species of the genus *Micromonospora* for which the name *Micromonospora profundi* sp. nov. is proposed.

Description of *Micromonospora profundi* sp. nov.

Micromonospora profundi (pro.fun′di. L. gen. n. profundi of the depth of the sea).

Aerobic, Gram-reaction-positive, non-motile actinobacterium that forms elliptical to oval spores (0.6–0.9×0.8–1.2 μm) on well-developed branched substrate hyphae. Aerial hyphae are absent. Growth occurs from pH 6.0 to 11, from 28 to 40 °C and in the presence of 3 % (w/v) NaCl. Optimal growth occurs on GPHF agar (DSMZ-medium 553) and N-Z-Amine agar (DSMZ-medium 554) at 30 °C and pH 7.0–8.0. Allantoin is hydrolysed, but not arbutin or urea. Nitrate reduction is negative. Starch and Tween 80 are degraded, but not adenine, casein, guanine, hypoxanthine, Tween 40, xanthine or xylan. D-Cellobiose, dextrin, D-fructose, D-galactose, D-maltose, D-mannitol, D-mannose, lactose, D-sucrose and D-xylose are used as sole carbon sources, but not adonitol, D-arabinose, dextran, inulin, L-sorbose, D-sorbitol, L-rhamnose or D-ribose. L-Alanine, L-arginine, L-cysteine, α-isoleucine, glycine, L-methionine, L-phenylalanine, L-proline, L-serine, L-tyrosine and L-valine are used as sole nitrogen sources, but not L-histidine or L-hydroxyproline. The characteristic whole-cell sugars are galactose, glucose, mannose, ribose and xylose, the predominant menaquinone is MK-10(H_4), the main polar lipids diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylinositol and the major cellular fatty acids iso-$C_{15:0}$, $C_{17:1}\omega 9c$, iso-$C_{16:0}$ and $C_{16:0}$ 9-methyl.

The type strain, DS3010^T (=DSM 45981^T=KCTC 29243^T) was isolated from a deep Black Sea sediment sample collected off the Yason Peninsula, near Ordu, Turkey. The G+C content of the genomic DNA of the type strain is 73.3 ±0.5 mol%.

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