Paracoccus rhizosphaerae sp. nov., isolated from the rhizosphere of the plant *Crossostephium chinense* (L.) Makino (Seremban)

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A Gram-negative, coccoid-shaped bacterium, strain CC-CCM15-8^T, was isolated from a rhizosphere soil sample of the plant *Crossostephium chinense* (L.) Makino (Seremban) from Budai Township, Chiayi County, Taiwan. 16S rRNA gene sequence analysis clearly allocated strain CC-CCM15-8^T to the *Paracoccus* cluster, showing highest similarities to the type strains of '*Paracoccus beibuensis*' (98.8 %), *Paracoccus homiensis* (97.6 %), *Paracoccus aestuarii* (97.7 %) and *Paracoccus zeaxanthinifaciens* (97.7 %). The fatty acid profile, comprising C_{18:1ω7c} as the major component and C_{10:0} 3-OH as the characteristic hydroxylated fatty acid, supported the placement of strain CC-CCM15-8^T within the genus *Paracoccus*. The polyamine pattern consisted of putrescine and spermidine as major components. Ubiquinone Q-10 was the major quinone type (95 %); ubiquinone Q-9 was also detected (5 %). The complex polar lipid profile consisted of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylcholine, and unidentified phospholipids, lipids and glycolipids. Levels of DNA–DNA relatedness between strain CC-CCM15-8^T and '*P. beibuensis*' LMG 25871^T, *P. aestuarii* DSM 19484^T, *P. zeaxanthinifaciens* LMG 21993^T and *P. homiensis* KACC 11518^T were 24.9 % (34.8 %, reciprocal analysis), 15.7 % (17.5 %), 17.7 % (23.4 %) and 16.0 % (25.4 %), respectively. Physiological and biochemical test results allowed the phenotypic differentiation of strain CC-CCM15-8^T from its closest relatives in the genus *Paracoccus*. Based on the data presented, it is concluded that strain CC-CCM15-8^T represents a novel species of the genus *Paracoccus*, for which the name *Paracoccus rhizosphaerae* sp. nov. is proposed. The type strain is CC-CCM15-8^T (=LMG 26205^T=CCM 7904^T).

The genus *Paracoccus* was proposed by Davis *et al.* (1969), and subsequent analysis of the 16S rRNA gene sequence of the type species *Paracoccus denitrificans* indicated that this species belongs to the α-3 subgroup of the *Proteobacteria*.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CC-CCM15-8^T is JN662389. A supplementary figure is available with the online version of this paper.

For species of this genus, which generally stain Gram-negative, a high metabolic versatility has been reported. They are chemotaxonomically characterized by fatty acid patterns showing a large amount of C_{18:1ω7c} (often >70 % of the total) and the presence of C_{10:0} 3-OH. The major respiratory quinone is ubiquinone Q-10. Chen *et al.* (2011) described complex polar lipid profiles consisting of the major components diphosphatidylglycerol,

phosphatidylglycerol, phosphatidylcholine and several uncharacterized lipids.

At the time of writing, the genus *Paracoccus* comprised the following recognized species: *P. aestuarii* (Roh *et al.*, 2009), *P. alcaliphilus* (Urakami *et al.*, 1989), *P. alkenifer* (Lipski *et al.*, 1998), *P. aminophilus* and *P. aminovorans* (Urakami *et al.*, 1990), *P. bengalensis* (Ghosh *et al.*, 2006), *P. carotinifaciens* (Tsubokura *et al.*, 1999), *P. chinensis* (Li *et al.*, 2009), *P. denitrificans* (Beijerinck & Minkman, 1910; Davis *et al.*, 1969; Skerman *et al.*, 1980 emend. Nokhal & Schlegel, 1983; Ludwig *et al.*, 1993), *P. fistulariae* (Kim *et al.*, 2010), *P. haeundaensis* (Lee *et al.*, 2004), *P. halodenitrificans* (Robinson & Gibbons, 1952), *P. halophilus* (Liu *et al.*, 2008), *P. homiensis* (Kim *et al.*, 2006), *P. isopora* (Chen *et al.*, 2011), *P. kocurii* (Ohara *et al.*, 1990), *P. kondratievae* (Doronina & Trotsenko, 2000 emend. Doronina *et al.*, 2002), *P. koreensis* (La *et al.*, 2005), *P. marcusii* (Harker *et al.*, 1998), *P. marinus* (Khan *et al.*, 2008), *P. methylutens* (Doronina *et al.*, 1998), *P. pantotrophus* (Robertson & Kuenen, 1984; Rainey *et al.*, 1999), *P. saliphilus* (Wang *et al.*, 2009), *P. seriniphilus* (Pukall *et al.*, 2003), *P. solventivorans* (Siller *et al.*, 1996 emend. Lipski *et al.*, 1998), *P. sphaerophysae* (Deng *et al.*, 2011), *P. sulfuroxidans* (Liu *et al.*, 2006), *P. thiocyanatus* (Katayama *et al.*, 1995), *P. versutus* (Harrison, 1983; Katayama *et al.*, 1995), *P. yeei* corrig. (Daneshvar *et al.*, 2003), *P. zeaxanthinifaciens* (Berry *et al.*, 2003); '*P. beibuensis*' (Zheng *et al.*, 2011) has recently been described but the name has not been validly published. Many of these species have been isolated from marine habitats.

Strain CC-CCM15-8^T was isolated from a rhizosphere soil sample of the plant *Crossostephium chinense* (L.) Makino (Seremban) from Budai Township, Chiayi County, Taiwan, on marine agar 2216 (MA; Difco) at 28 °C and was maintained further on tryptone soy agar at 28 °C. The strain was preserved at -80 °C by mixing well-grown marine broth 2216 (MB; Difco) cultures in a 1:1 ratio with glycerol preservation medium, containing K₂HPO₄ (1.26 %), KH₂PO₄ (0.36 %), MgSO₄·7H₂O (0.01 %), sodium citrate (0.09 %), (NH₄)₂SO₄ (0.18 %) and glycerol (8.8 %). Stock cultures of the isolate in marine broth supplemented with 5 % DMSO were additionally maintained in the vapour phase of liquid nitrogen.

The cellular morphological features and Gram-staining behaviour were observed by phase-contrast microscopy as described previously (Kämpfer & Kroppenstedt, 1996). The 16S rRNA gene was analysed as described by Kämpfer *et al.* (2003).

Multiple sequence alignment and analysis of the data were performed by using the software package MEGA version 4 (Tamura *et al.*, 2007). Genetic distance calculations (distance options according to the Kimura two-parameter model) and clustering with the neighbour-joining (Fig. 1), maximum parsimony (results not shown) and maximum-likelihood (Fig. S1 available in IJSEM Online) methods were determined by using bootstrap values based on 1000

replications. The 16S rRNA gene sequence of strain CC-CCM15-8^T was a continuous stretch of 1390 bp. Highest levels of 16S rRNA gene sequence similarity were found with the type strains of '*P. beibuensis*' (98.8 %), *P. homiensis* (97.6 %), *P. aestuarii* (97.7 %) and *P. zeaxanthinifaciens* (97.7 %); levels of similarity with the type strains of all other *Paracoccus* species were lower than 97.0 %.

Fatty acid analysis was performed according to Kämpfer & Kroppenstedt (1996) with cells grown on MA for 48 h. The fatty acid profile of strain CC-CCM15-8^T was similar to those of closely related *Paracoccus* species, although minor quantitative differences were observed (Table 2). '*P. beibuensis*' LMG 24871^T, *P. aestuarii* DSM 19484^T, *P. zeaxanthinifaciens* LMG 21993^T and *P. homiensis* KACC 11518^T were studied under the same conditions and had C_{18:1ω7c} as the major fatty acid together with the characteristic hydroxylated fatty acid C_{10:0} 3-OH.

For detection of respiratory isoprenoid quinones and polar lipids, cells of strain CC-CCM15-8^T were grown in MB at 28 °C for 48 h. Respiratory quinones were extracted according to the method of Collins *et al.* (1977) and were analysed by HPLC as described by Groth *et al.* (1996). Ubiquinones Q-10 (95 %) and Q-9 (5 %) were detected as isoprenoid quinones. Polar lipids extracted according to the method of Minnikin *et al.* (1979) were identified by two-dimensional TLC as described by Collins & Jones (1980). Strain CC-CCM15-8^T exhibited a complex polar lipid pattern, similar to the data presented by Chen *et al.* (2011). In agreement with polar lipid data for *P. isopora* SW-3^T, *P. aestuarii* JCM 15119^T, *P. homiensis* KACC 11518^T, *P. marinus* NBRC 100637^T, *P. denitrificans* BCRC 12285^T and *P. zeaxanthinifaciens* JCM 21774^T, strain CC-CCM15-8^T contained diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine, an unidentified glycolipid and several unidentified polar lipids, phospholipids and glycolipids (Fig. 2). In contrast to the data presented by Chen *et al.* (2011), however, phosphatidylethanolamine was detected in strain CC-CCM15-8^T rather than an unidentified aminolipid. However, differences in the chromatographic motility (*R_f* values) of the polar lipids could be the result of the different solvent systems used.

Biomass for polyamine analysis was grown in PYE broth (0.3 % peptone from casein, 0.3 % yeast extract, pH 7.2) supplemented with 3.1 % sea salts (Sigma) and harvested at the late exponential growth phase (70 % of the maximum optical density). Polyamines were extracted as described by Busse & Auling (1988) and analysed according to Stolz *et al.*, (2007). The polyamine pattern of strain CC-CCM15-8^T consisted of 23.3 μmol spermidine (g dry weight)⁻¹, 10.4 μmol putrescine (g dry weight)⁻¹, 4.0 μmol cadaverine (g dry weight)⁻¹, 2.2 μmol 1,3-diaminopropane (g dry weight)⁻¹, 0.6 μmol spermine (g dry weight)⁻¹ and 0.2 μmol sym-norspermidine (g dry weight)⁻¹. This polyamine pattern is in good agreement with data published for recognized species of the genus *Paracoccus* but in contrast to strain CC-CCM15-8^T the content of putrescine is higher

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences of strain CC-CCM15-8^T and the type strains of recognized *Paracoccus* species. Numbers at nodes are bootstrap values (percentages of 1000 replications); only values >50 % are shown. Bar, 0.1 substitutions per nucleotide position.

than that of spermidine (Busse & Auling, 1988; Hamana & Matsuzaki, 1992). Also, the presence of *sym*-norspermidine has not been reported previously for *Paracoccus* species, but given the relatively low concentration, we do not attribute any taxonomic relevance to this finding. The diagnostic diamino acid of the peptidoglycan was extracted from PYE broth supplemented with 3.1 % sea salt according to the method reported by Schleifer (1985). In agreement with all *Proteobacteria*, strain CC-CCM15-8^T contained *meso*-diaminopimelic acid as the diagnostic diamino acid. The results of comparative physiological characterization under identical test conditions (Kämpfer *et al.*, 1991) for '*P. beibuensis*' LMG 24872^T, *P. aestuarii* DSM 19484^T, *P. zeaxanthinifaciens* LMG 21993^T and *P. homiensis* KACC 11518^T are shown in Table 2.

DNA–DNA hybridizations between strain CC-CCM15-8^T and '*P. beibuensis*' LMG 24872^T, *P. aestuarii* DSM 19484^T, *P. zeaxanthinifaciens* LMG 21993^T and *P. homiensis* KACC 11518^T were performed as described by Ziemke *et al.* (1998), indicating levels of relatedness of 24.9 % (34.8 %

reciprocal analysis), 15.7 % (17.5 %), 17.7 % (23.4 %) and 16.0 % (25.4 %), respectively.

These data clearly show that strain CC-CCM15-8^T has features that are typical characteristics of the genus *Paracoccus*, such as a quinone system with ubiquinone Q-10 as the major component, a fatty acid profile mainly consisting of C_{18:1ω7c} and the major hydroxylated fatty acid C_{10:0} 3-OH, and a complex polar lipid profile consisting of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine, and several uncharacterized lipids, phospholipids and glycolipids.

Strain CC-CCM15-8^T can be distinguished from its closest phylogenetic relatives in the genus *Paracoccus* based on several physiological and chemotaxonomic traits. The results of DNA–DNA hybridization experiments in addition to differences in 16S rRNA gene sequences suggest that strain CC-CCM15-8^T represents a novel species of the genus *Paracoccus*, for which we propose the name *Paracoccus rhizosphaerae* sp. nov.

Fig. 2. Total polar lipid profile of strain CC-CCM15-8^T after staining with molybdatophosphoric acid. DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PC, phosphatidylcholine; PL1–4, unidentified phospholipids; GL1, GL2, unidentified glycolipids; L1–8, unidentified lipids that did not react with the spray reagents specific for a free amino group, phosphate or sugars.

Description of *Paracoccus rhizosphaerae* sp. nov.

Paracoccus rhizosphaerae (rhi.zo.spha.e'ra.e. Gr. n. *rhiza* a root; L. n. *sphaera* a ball, sphere; N.L. n. *rhizosphaera* the rhizosphere; N.L. gen. n. *rhizosphaerae* of the rhizosphere).

Cells are coccoid-shaped, about 1.5–2.0 µm in diameter. Gram-negative, oxidase-positive, catalase-positive and showing oxidative metabolism. Good growth occurs after 24 h on marine agar 2218 (Oxoid) at 28 °C; moderate growth occurs on tryptone soy agar, nutrient agar and R2A agar (all Oxoid). No growth occurs on MacConkey agar (Oxoid) at 28 °C. Unable to grow at 4 or 40 °C. Cells grow in the presence of 1.0–10.0 % NaCl (optimum, 6.0–7.0 %). Colonies on marine agar are yellow, circular, translucent and shiny with entire edges. The polyamine pattern consists of the major compounds spermidine and putrescine, moderate amounts of cadaverine and 1,3-diaminopropane, and minor amounts of spermine and *sym*-norspermidine. The peptidoglycan diamino acid is *meso*-diaminopimelic acid. The major quinone is ubiquinone Q-10. The polar lipid pattern comprises diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylcholine, four unknown phospholipids, two glycolipids and eight unidentified polar lipids that do not react with the spray reagents specific for a free amino group, phosphate or sugars. Major fatty acids are C_{18:1}ω7c and C_{10:0} 3-OH. Physiological test results (including differential characteristics) are indicated in Table 1. Produces acid from D-glucose, sucrose and lactose (after 7 days of incubation), but not from adonitol,

Table 1. Phenotypic comparison of strain CC-CCM15-8^T with the type strains of closely related species in the genus *Paracoccus*

Taxa: 1, strain CC-CCM15-8^T; 2, '*P. beibuensis*' LMG 24871; 3, *P. aestuarii* DSM 19484^T; 4, *P. homiensis* DD-R11^T; 5, *P. zeaxanthinifaciens* (three strains); 6, *P. carotinifaciens* IFO 16121^T; 7, *P. haendaensis* KCCM 10460^T; 8, *P. marcusii* DSM 11574^T; 9, *P. seriniphilus* DSM 14827^T. Data for taxa 1–4 are from this study. Data for other reference strains are from Berry *et al.* (2003), Pukall *et al.* (2003), Lee *et al.* (2004) and Kim *et al.* (2006). w, Weakly positive; ND, not determined.

Characteristic	1	2	3	4	5	6	7	8	9
Motility	+	–	–	+	–	+	–	–	–
Orange to red pigment	+	+	+	–	+	+	+	+	–
Growth at 40 °C	–	–	–	+	+	–	–	–	–
Growth with 6 % NaCl	+	+	–	+	+	w	+	w	+
Nitrate reduction	–	–	–	–	–	–	+	–	+
Urease	–	–	–	–	+	–	–	–	–
Growth on:									
Acetic acid	+	+	+	+	–	ND	ND	–	+
Adonitol	+	+	+	–	–	+	–	+	+
L-Aspartate	+	+	+	–	+	+	ND	–	+
L-Asparagine	ND	ND	ND	+	+	+	–	–	+
i-Erythritol	ND	ND	ND	+	–	+	ND	+	+
Gentiobiose	ND	ND	ND	–	–	+	ND	+	–
L-Phenylalanine	–	–	–	+	–	ND	ND	–	–
Propionic acid	+	–	–	+	–	ND	ND	+	+
Quinic acid	ND	ND	ND	–	–	+	ND	+	–
L-Rhamnose	+	+	–	+	–	ND	–	–	–
D-Sorbitol	+	+	–	+	–	+	–	+	+
Succinic acid	ND	ND	ND	+	–	ND	ND	+	–
Xylitol	ND	ND	ND	–	–	+	ND	+	+

*Data congruent with those reported for *P. aestuarii* by Roh *et al.* (2009).

†Data congruent with those reported for *P. homiensis* and *P. zeaxanthinifaciens* by Kim *et al.* (2006).

L-arabinose, D-arabitol, dulcitol, erythritol, *i*-inositol, maltose, D-mannitol, melibiose, methyl α-D-glucoside, raffinose, L-rhamnose, salicin, D-sorbitol, trehalose or D-xylose. Negative for urease activity, indole production, hydrolysis of casein, gelatin, starch, DNA and tyrosine, hydrogen sulphide production, and activity of arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and β-galactosidase (ONPG). Positive for hydrolysis of aesculin, *p*-nitrophenyl-α-D-glucopyranoside, *p*-nitrophenyl-β-D-glucopyranoside, 2-deoxythymidine-2'-*p*-nitrophenyl-phosphate and L-alanine-*p*-nitroanilide. The following compounds are not hydrolysed: *p*-nitrophenyl-β-D-galactopyranoside, *p*-nitrophenyl-β-D-xylopyranoside, *p*-nitrophenyl-β-D-glucuronide, bis-*p*-nitrophenyl-phosphate, bis-*p*-nitrophenyl-phenyl-phosphonate, bis-*p*-nitrophenyl-phosphoryl-choline, γ-L-glutamate-*p*-nitroanilide and L-proline-*p*-nitroanilide. The following organic compounds are utilized as sole sources of carbon: L-arabinose, cellobiose, D-fructose, D-galactose, D-glucose, maltose, D-mannose, L-rhamnose, ribose, sucrose, trehalose,

Table 2. Fatty acid composition of strain CC-CCM15-8^T and the type strains of closely related species in the genus *Paracoccus*

Taxa: 1, strain CC-CC-M15-8^T; 2, '*P. beibuensis*' LMG 24871^T; 3, *P. aestuarii* DSM 19484^T; 4, *P. homiensis* DD-R11^T; 5, *P. zeaxanthinifaciens* (mean value from three strains); 6, *P. carotinifaciens* IFO 16121^T; 7, *P. haeundaensis* KCCM 10460^T; 8, *P. marcusii* DSM 11574^T; 9, *P. seriniphilus* DSM 14827^T. Data for taxa 1–5 are from this study. Data in parentheses in columns 3–5 are from the literature (see footnotes). Data for the other strains are from Berry *et al.* (2003), Pukall *et al.* (2003), Lee *et al.* (2004) and Kim *et al.* (2006). Values are percentages of total fatty acids; –, not detected or <1 %.

Fatty acid	1	2	3*	4†	5†	6	7	8	9
C _{10:0} 3-OH	5.2	4.4	2.8 (2.5)	3.2 (2.6)	5.5 (4.9)	3.4	2.1	6.2	7.9
Unidentified									
ECL 11.799	4.6	3.8	2.9 (–)	2.8 (2.4)	5.8 (3.6)	2.8	–	4.9	–
ECL 14959	2.2	–	–	0.8	– (–)	–	–	–	–
ECL 15275	–	–	–	– (–)	– (1.6)	1.1	–	2.9	–
C _{12:1} ω7c	–	–	–	– (–)	– (–)	–	2.0	–	–
C _{12:0} ALDE	1.0	0.6	0.7 (–)	1.4 (1.8)	1.3 (–)	–	–	–	–
C _{14:0} 3-OH	–	–	–	– (–)	– (–)	–	1.5	–	–
C _{18:1} ω7c	73.8	77.7	81.7 (68.9)	75.1 (78.9)	74.6 (80.2)	84.0	84.3	80.3	83.5
C _{17:1} ω8c	–	1.8	–	–	–	–	–	–	–
C _{18:0}	6.4	8.1	7.9 (18.1)	5.6 (4.5)	4.9 (3.6)	5.2	7.8	2.6	2.5
C _{18:0} 3-OH	2.5	–	–	0.9 (1.1)	– (–)	–	–	–	–
11-Methyl C _{18:1} ω7c	–	–	–	3.6 (5.8)	– (–)	–	–	–	1.5
Summed feature 2‡	3.6	3.2	2.6 (2.4)	– (–)	3.5 (2.9)	2.1	–	3.0	–

*Data in parentheses from Roh *et al.* (2009).

†Data in parentheses from Kim *et al.* (2006).

‡Summed feature 2 comprises C_{14:0} 3-OH and/or C_{16:1} iso I.

adonitol, D-mannitol, D-sorbitol, acetate, propionate, *cis*-aconitate, 4-aminobutyrate, citrate, fumarate, glutarate, DL-lactate, L-malate, 2-oxoglutarate, pyruvate, L-alanine, L-aspartate, L-leucine, L-proline and L-serine. The following compounds are not utilized as sole source of carbon in mineral-salt medium (Kämpfer *et al.*, 1991): *N*-acetyl-D-glucosamine, maltose, *N*-acetylgalactosamine, L-arbutin, gluconate, glycerol, maltitol, α-melibiose, salicin, D-xylose, *i*-inositol, putrescine, *trans*-aconitate, adipate, DL-3-hydroxybutyrate, azelate, itaconate, suberate, mesaconate, β-alanine, L-ornithine, L-phenylalanine, L-histidine, L-tryptophan, 3-hydroxybenzoate, 4-hydroxybenzoate and phenylacetate.

The type strain, CC-CCM15-8^T (=LMG 26205^T=CCM 7904^T), was isolated from a rhizosphere soil sample of the plant *Crossostephium chinense* (L.) Makino (Seremban) from Budai Township, Chiayi County, Taiwan.

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