

Supplementary Table S1. Chemotaxonomic characteristics of strain CC 0387^T and recognized species of the genus *Promicromonospora*

Strains: 1, *Promicromonospora flava* sp. nov. CC 0387^T; 2, *P. vindobonensis* V45^T; 3, *P. aerolata* V54A^T; 4, *P. sukumoe* NBRC 14650^T; 5, *P. citrea* NBRC 12397^T; 6, *P. kroppenstedtii* RS16^T. DPG, Diphosphatidylglycerol; GL, glycolipid; PG, phosphatidylglycerol; PGL, phosphoglycolipid; PI, phosphatidylinositol. ND, No data available.

Characteristic	1	2	3	4	5	6
Menaquinone composition (%)	MK-9(H ₄) (86), MK-8(H ₄) (7), MK-9(H ₂) (5), MK-9 (3)	MK-9(H ₄) (92), MK- 9(H ₂) (4), MK-9(H ₆) (4)	MK-9(H ₄) (93), MK-9(H ₂) (7)	MK-9(H ₄), MK-9, MK- 9(H ₂), MK- 9(H ₆)	MK-9	MK-9(H ₄) (64), MK-9(H ₆) (15), MK-8(H ₄) (10), MK-9(H ₂) (2)
Polar lipids	DPG, PG, PL, GL	DPG, PG, unknown GL, unknown PGL	DPG, PG, an unknown PL	PI, DPG	PG, PI, unidentified glucosamine- phospholipid	PG, DPG, PI, GL, PGL
Cell-wall composition	Lys:Ala (A3α)	Glu:Gly:Ala:Lys (0.98:0.69:2.88:1.0) (A3α)	Glu:Gly:Ala:Lys (1.05:0.43:3.4:1. 0) (A3α)	Lys (A3α)	Lys:Ala (A3α)	Ala:Glu:Lys (2.3:2.0:1.0) (A4α)
Cell-wall sugars	Rha, Gal, Glu	Rha, Gal, Glu	ND	Gal	Gal, Rha	Rib, Gal, Glu, Rha
Fatty acids						
C _{13:0}	0	1.0	0	0	0	0.17
C _{14:0}	1.87	1.5	0.8	1.3	0.6	1.78

Characteristic	1	2	3	4	5	6
iso-C _{14:0}	2.34	0	0.3	0.9	1.2	1.46
iso-C _{15:1} G	0	0	0.4	3.4	0	0.54
anteiso-C _{15:1} A	0	0	0.4	4.4	0	1.21
iso-C _{15:0}	16.26	36.7	30.8	36.6	40.6	39.7
anteiso-C _{15:0}	57.20	46.5	51.1	38.0	38.9	43.2
C _{15:0}	0	0	0	1.6	1.0	0.95
C _{16:0} N alcohol	0	0	0	0.4	0	0
iso-C _{16:0}	9.08	2.2	2.2	3.9	4.0	4.41
C _{16:0}	3.89	6.0	3.8	2.4	0.8	1.93
iso-C _{17:0}	0.87	1.3	1.5	2.0	3.1	1.21
anteiso-C _{17:0}	8.48	3.8	6.7	4.6	9.7	3.4
C _{18:1} ω9c	0	0	0.5	0	0	0
C _{18:3} ω6c (6,9,12)	0	0	0	0.4	0	0
Summed feature 5*	0	2.0	1.4	0	0	0

*Summed feature 5 contains iso-C_{17:1} I and/or anteiso-C_{17:1} B.

Jiang, Y., Wiese, J., Cao, Y.-R., Xu, L.-H., Imhoff, J. F. & Jiang, C.-L. (2009). *Promicromonospora flava* sp. nov., isolated from sediment of the Baltic Sea. *Int Syst Evol Microbiol* **59**, 1599–1602.