

***Frateuria soli* sp. nov. and *Frateuria edaphi* sp. nov., isolated from greenhouse soil**

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Supplementary Table S1. Genome features of *Frateuria soli* 5GH9-11^T, *Frateuria edaphi* 5GH9-34^T, *Frateuria flava* MAH-13^T and *Frateuria terrea* DSM 26515^T.

	<i>Frateuria soli</i> 5GH9-11 ^T	<i>Frateuria edaphi</i> 5GH9-34 ^T	<i>Frateuria flava</i> MAH-13 ^T	<i>Frateuria terrea</i> DSM 26515 ^T
Genome assembly number	CP088252	CP088251	GCA_017837635	GCA_900109025
Genome size	3,488,520	3,769,403	3,682,848	3,840,840
Assembly level	Complete	Complete	Scaffold	Scaffold
G+C content	68.7	67.8	68.0	67.9
Contig N50	3,488,520	3,769,403	145,048	551,212
Protein-coding genes	3,131	3,408	3,298	3,466
rRNAs (5S, 16S, 23S)	2, 2, 2	2, 2, 2	1, 1, 1	4, 2, 2
tRNAs	49	50	47	49
ncRNAs	4	4	4	4
Pseudo genes	26	15	16	36

Supplementary Table S2. Subsystem features of *Frateuria soli* 5GH9-11^T, *Frateuria edaphi* 5GH9-34^T, *Frateuria flava* MAH-13^T and *Frateuria terrea* DSM 26515^T classified by RAST server.

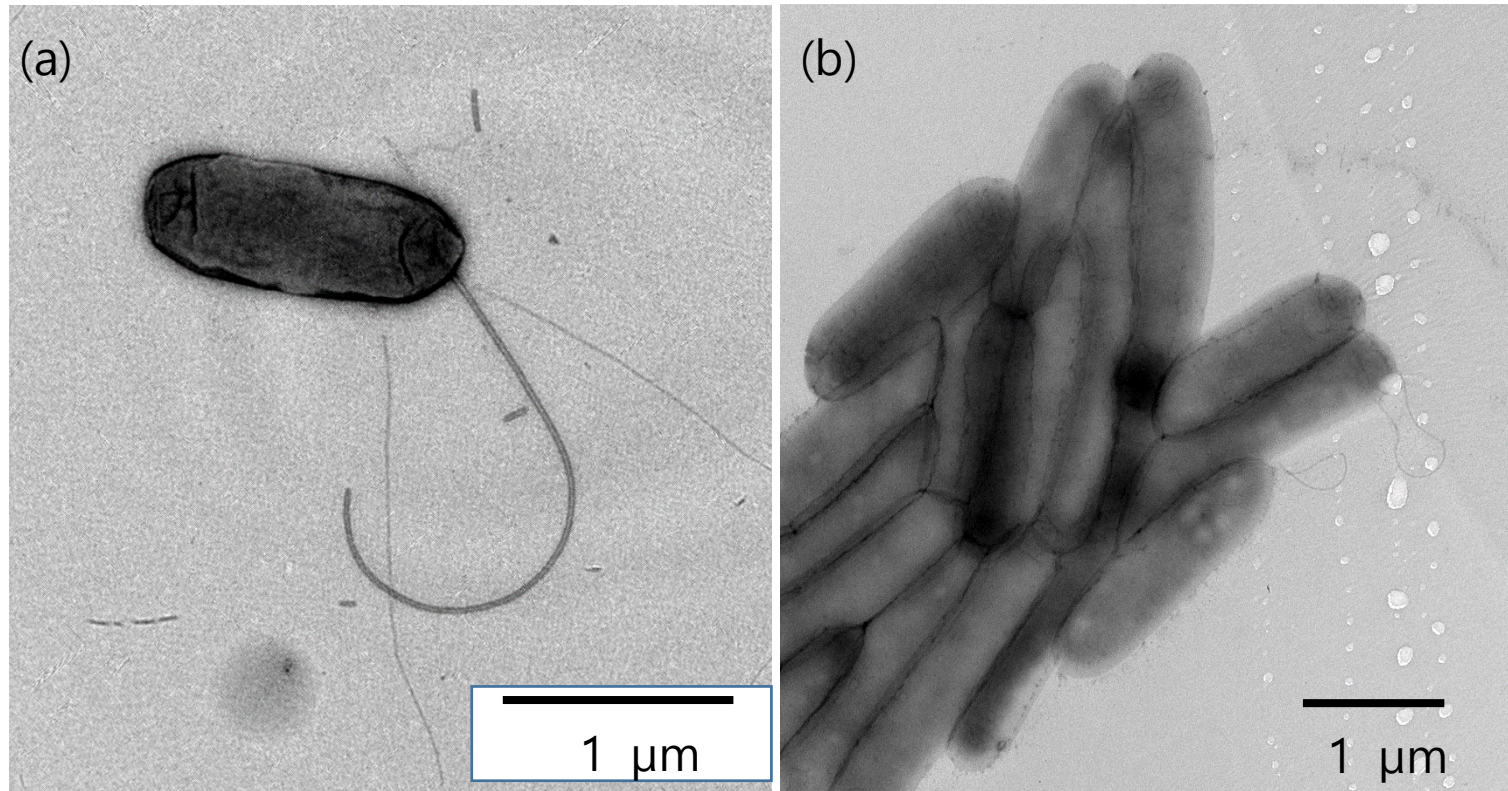
	<i>Frateuria soli</i> 5GH9-11 ^T	<i>Frateuria edaphi</i> 5GH9-34 ^T	<i>Frateuria flava</i> MAH-13 ^T	<i>Frateuria terrea</i> DSM 26515 ^T
Subsystem information				
Coding sequences	3,243	3508	3373	3578
Subsystem coverage	910 (29 %)	951 (28 %)	925 (28 %)	948 (27 %)
Subsystem category distribution				
Total	1275	1335	1310	1334
Amino acids and derivatives	177 (13.9 %)	185 (13.9 %)	182 (13.9 %)	208 (15.6 %)
Protein and nitrogen metabolism	221 (17.3 %)	207 (15.5 %)	204 (15.6 %)	199 (14.9 %)
Carbohydrate	147 (11.5 %)	156 (11.7 %)	145 (11.1 %)	157 (11.8 %)
Cofactors, vitamins, pigments, etc.	127 (10.0 %)	132 (9.9 %)	134 (10.2 %)	132 (9.9 %)
DNA and RNA metabolism	124 (9.7 %)	122 (9.1 %)	129 (9.8 %)	122 (9.1 %)
Membrane Transport	74 (5.8 %)	81 (6.1 %)	77 (5.9 %)	77 (5.8 %)
Motility and chemotaxis	22 (1.7 %)	23 (1.7 %)	23 (1.8 %)	22 (1.6 %)
Respiration	84 (6.6 %)	89 (6.7 %)	82 (6.3 %)	84 (6.3 %)
Stress response	53 (4.2 %)	71 (5.3 %)	52 (4.0 %)	71 (5.3 %)
Nucleosides and Nucleotides	59 (4.6 %)	55 (4.1 %)	56 (4.3 %)	57 (4.3 %)
Fatty acids, Lipids and isoprenoids	50 (3.9 %)	57 (4.3 %)	70 (5.3 %)	45 (3.4 %)
Cell wall and capsule	28 (2.2 %)	27 (2.0 %)	25 (1.9 %)	26 (1.9 %)
Others	109 (8.5 %)	130 (9.7 %)	131 (10.0 %)	134 (10.0 %)

Supplementary Table S3. Fatty acid composition of strains 5GH9-11^T, 5GH9-34^T and the closely related species.

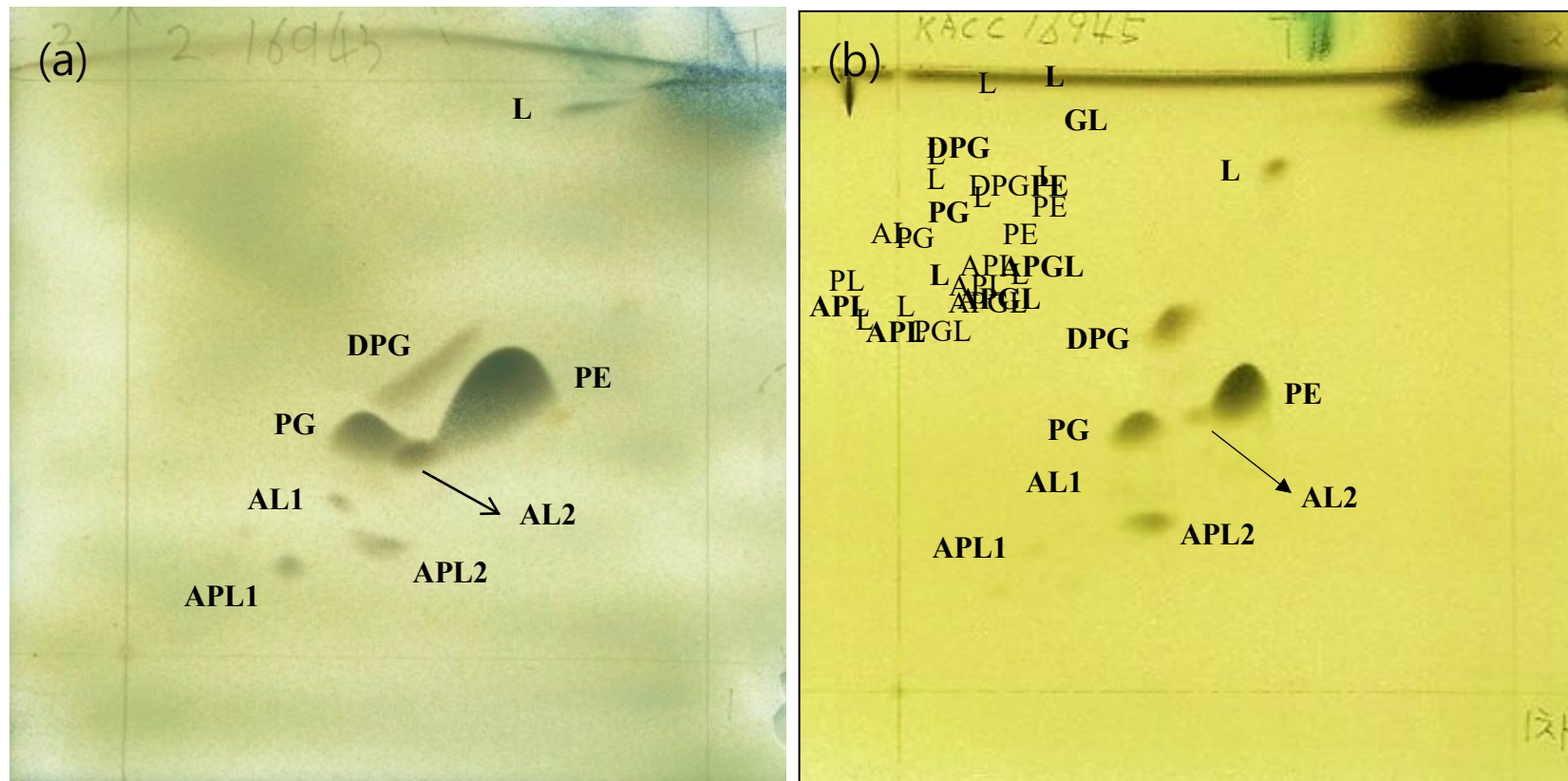
Strain: 1, *Frateuria soli* 5GH9-11^T; 2, *Frateuria edaphi* 5GH9-34^T; 3, *Frateuria autantia* KACC 11384^T; 4, *Frateuria defendens* KACC 22477^T; 5, *Frateuria flava* KACC 19743^T; 6, *Frateuria terrea* KACC 16757^T; 7, *Dyella ginsengisoli* KACC 12866^T; 8, *Dyella thiooxydans* KACC 12756^T; 9, *Rhodanobacter glycinis* KACC 19021^T. -, Not detected or <1.0 % of the total fatty acids. The fatty acids more than 10 % of the total fatty acids were bolded.

Fatty acids	1	2	3	4	5	6	7	8	9
iso-C _{11:0}	2.8	2.5	-	2.6	3.6	4.1	4.5	3.5	3.2
iso-C _{11:0} 3-OH	4.1	3.7	-	4.0	3.9	4.0	4.9	4.3	3.7
C _{12:0} 2-OH	-	-	2.1	-	-	-	-	-	-
C _{12:0} 3-OH	-	-	5.4	-	-	-	-	-	-
iso-C _{12:0} 3-OH	1.2	1.2	-	-	1.1	-	1.5	-	1.7
iso-C _{13:0} 3-OH	2.0	1.8	1.1	2.6	2.4	2.5	2.9	2.6	2.1
C _{14:0}	-	-	3.1	-	-	-	-	-	-
C _{14:1} ω5c	-	-	1.1	-	-	-	-	-	-
iso-C _{14:0}	1.1	1.5	-	-	1.1	-	1.4	1.0	2.2
anteiso-C _{15:0}	8.0	5.1	1.7	8.2	6.4	9.1	9.2	9.3	5.2
iso-C _{15:0}	18.0	14.6	49.1	23.6	16.0	10.5	6.2	15.4	11.7
C _{16:0}	3.6	5.9	5.2	2.4	6.2	7.7	2.0	1.6	1.6
iso-C _{16:0}	19.7	24.0	-	13.0	19.0	13.6	23.4	17.7	29.5
iso-C _{16:1} G	-	-	-	-	-	-	1.2	-	-
iso-C _{16:1} H	1.4	2.2	-	-	-	-	-	-	-
C _{17:0} cyclo	-	-	7.0	4.0	-	-	-	-	-
C _{17:1} ω6c	-	-	-	-	-	-	-	1.6	8.4
iso-C _{17:0}	3.3	3.8	4.6	12.1	6.8	11.3	7.7	9.8	7.7
anteiso-C _{17:0}	3.5	2.5	-	5.9	2.5	5.6	2.9	1.4	1.1
iso-C _{18:0}	1.3	1.9	-	1.1	1.3	1.4	1.6	1.0	2.7
Summed feature 3	6.9	6.7	12.0	3.9	5.9	5.1	4.1	4.3	3.5
Summed feature 9	19.2	18.2	2.3	11.5	19.4	20.4	23.4	22.8	12.6

[§] Summed features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 3 contains C_{16:1} ω6c and/or C_{16:1} ω7c; summed feature 9 contains iso-C_{17:1} ω9c and/or C_{16:0} 10-methyl.



Supplementary Fig. S1. Transmission electron micrographs of cell of strains 5GH9-11^T (a) and 5GH9-34^T (b). Bar, 1.0 μm. The strain was incubated on R2A medium at 28 °C for 48 h.



Supplementary Fig. S2. Polar lipids of strains 5GH9-11^T (a) and 5GH9-34^T (b). Two-dimensional TLC plates detected by spraying with molybdotophosphoric acid reagent. Abbreviations: DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; AL, unidentified aminolipid; APL, unidentified aminophospholipid; L, unidentified lipid.