

Supplementary Materials

***Roseateles agri* sp. nov., a new species isolated from fresh soil in Uiwang, South Korea**

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Contents category: New Taxa; Subsection:

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Figure S1. Transmission electron microscopy of strain R3-3^T grown on R2A medium plates for 2 days at 28°C. Bar 1 μm

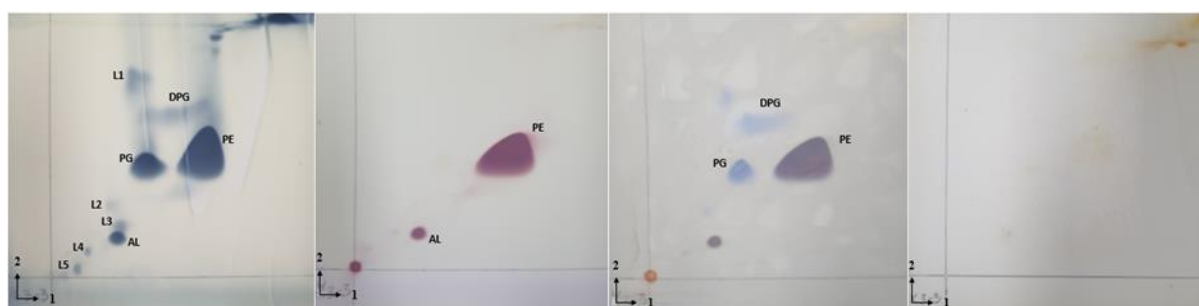


Figure S2. Polar lipid profile of strain R3-3^T. PE - phosphatidylethanolamine; PG - phosphatidylglycerol; DPG - diphosphatidylglycerol; AL– unidentified aminolipid, L - unidentified polarlipid.

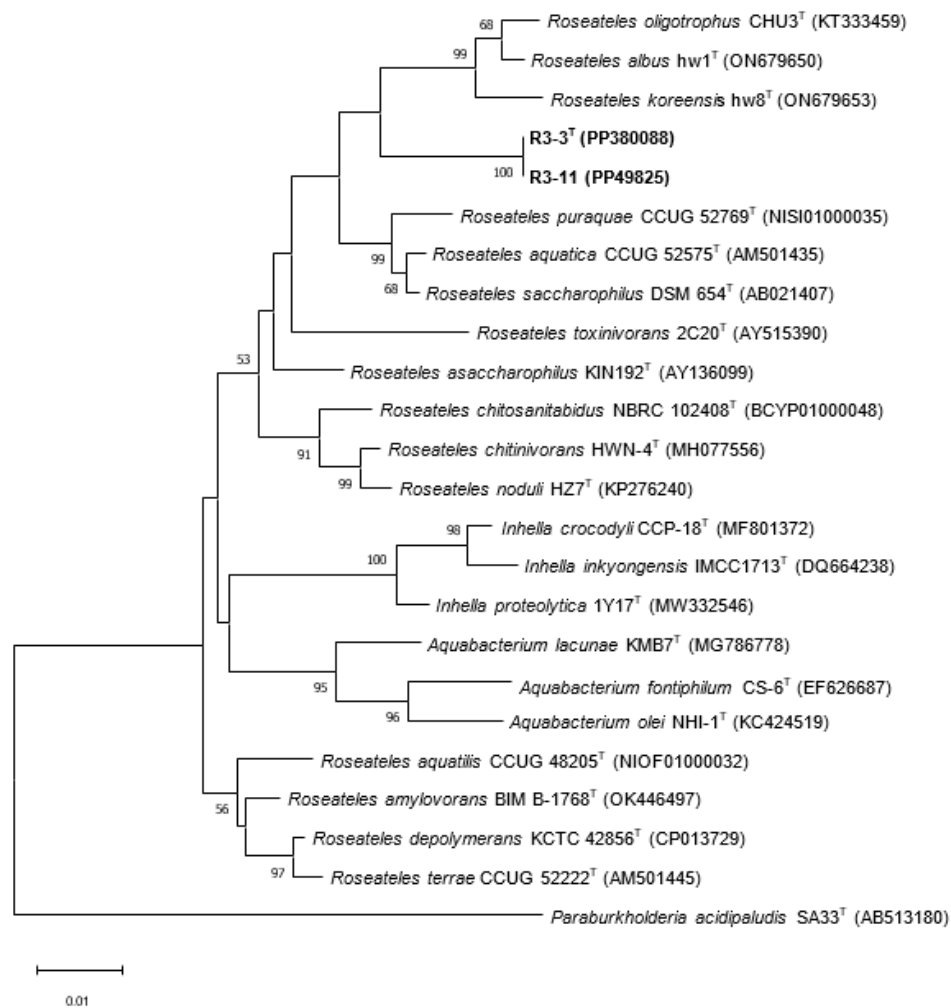


Figure S3. The phylogenetic tree was reconstructed with the neighbor-joining method based on 16S rRNA gene sequences of strains R3-3^T, R3-11, and some related strains based on 16S sequencing. *Paraburkholderia acidipaludis* SAA33^T was used as an outgroup. Numbers at branch nodes represent confidence levels (values > 50% are shown) from 1000 replicate bootstrap samplings. GenBank accession numbers are shown in parentheses. Bar, 0.01 substitutions per nucleotide position.

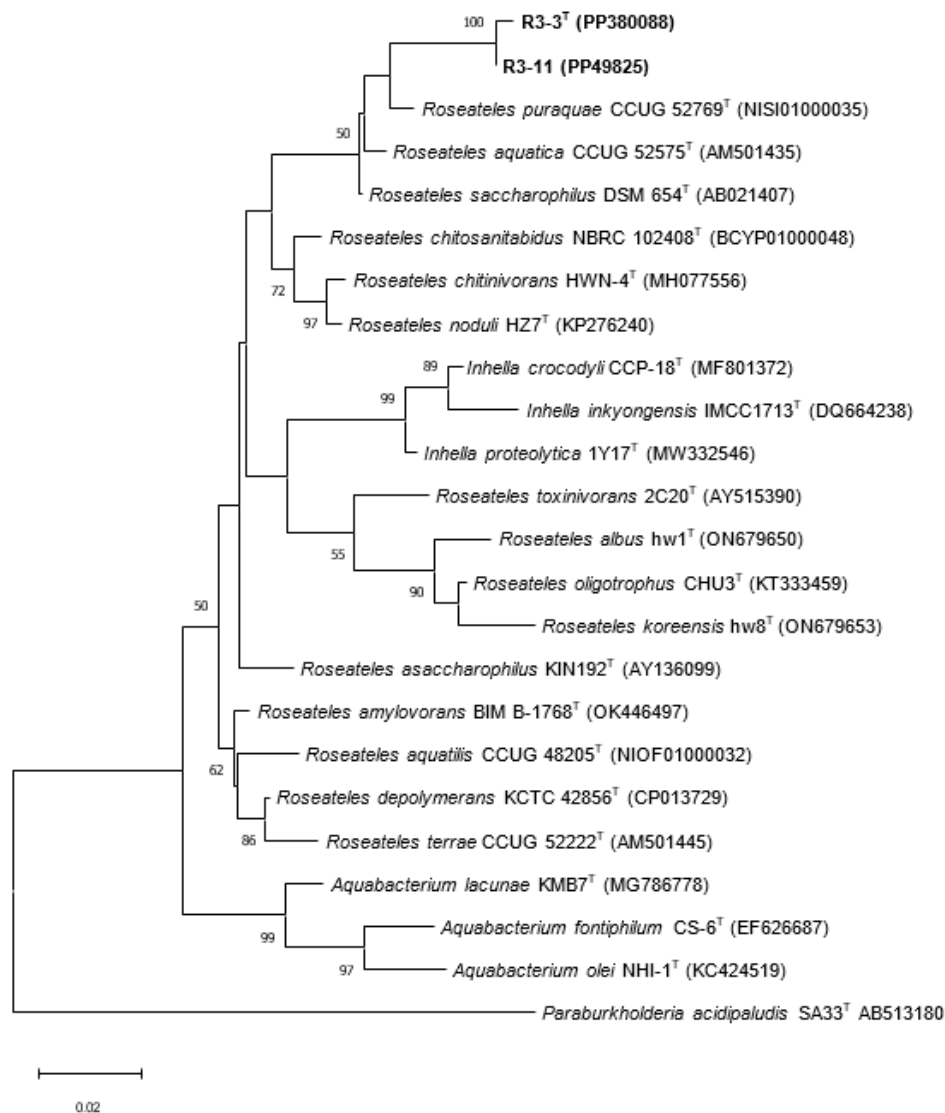


Figure S4. Phylogenetic tree reconstructed with the maximum likelihood method based on 16S rRNA gene sequences of strains R3-3^T, R3-11, and some related strains based on 16S sequencing. *Paraburkholderia acidipaludis* SAA33^T. Numbers at branch nodes represent confidence levels (values >50% are shown) from 1000 replicate bootstrap samplings. GenBank accession numbers are given in parentheses. Bar, 0.02 substitution per nucleotide position. Evolutionary analyses were conducted in MEGA 11.

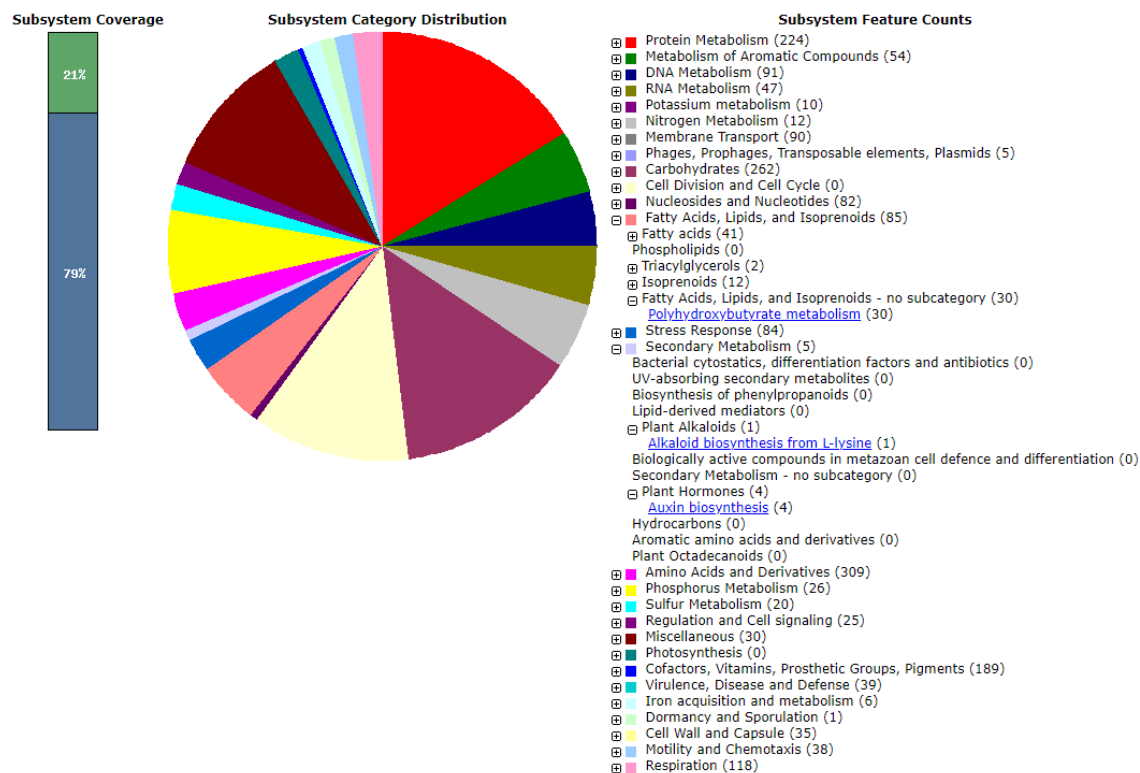


Figure S5. Subsystem feature of strain R3-3^T revealed by RAST (Rapid Annotation using Subsystem Technology) server version 2.0.

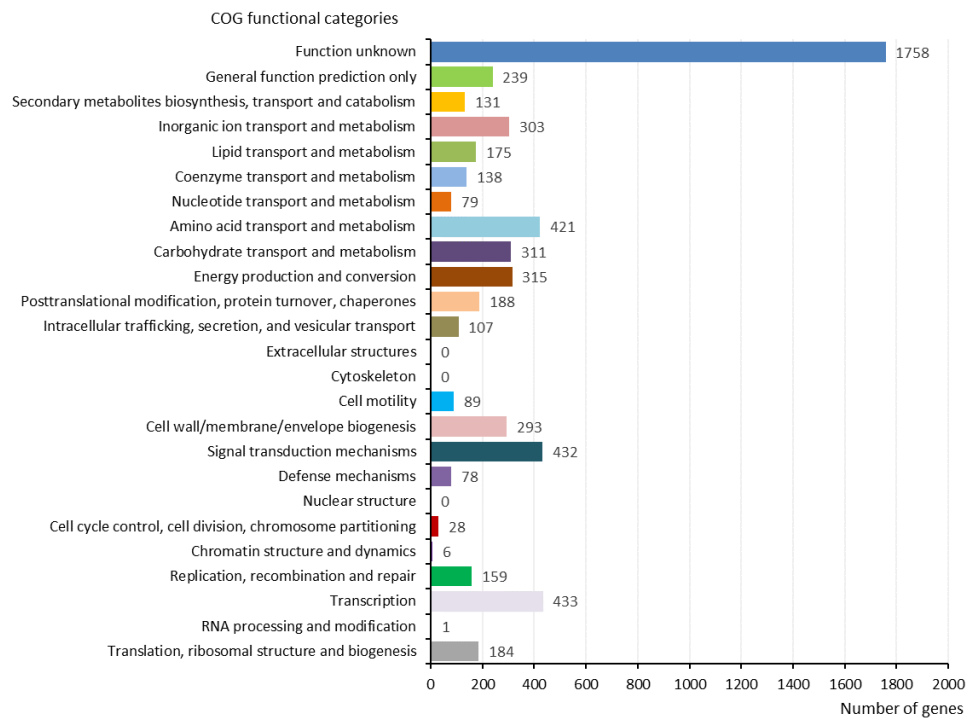


Figure S6. COG functional classification of proteins in strains R3-3^T genome.

Table S1. Results from API ZYM, API 20NE test. 1, R3-3^T; 2, R3-11; 3, *Roseateles toxinovorans* (data are from the present study, except G+C content of reference strains, which were retrieved from the literature in parentheses) [6]; 4, *Roseateles koreensis* [8]; 5, *Roseateles albus* [8]; 6, *Roseateles oligotrophus* [7]. +, positive; -, negative; +/-, weak positive or ambiguous; nd, no data.

Characteristics	1	2	3	4	5	6
Enzymatic reaction (API ZYM)						
Alkaline phosphate	+	+	+	+	+	+
Esterase (C4)	+	+	+	+	+	w
Esterase lipase (C8)	+	+	+	w	+	w
Lipase (C14)	-	-	-	-	-	-
Leucine arylamidase	+	+	+	-	+	+
Valine arylamidase	w	w	w	-	-	+
Cystine arylamidase	-	-	w	-	-	+
Trypsin	-	-	-	-	-	+
Alpha chymotrypsin	+	+	+	-	-	+
Acid phosphatase	+	+	w	w	-	+
Naphthol-AS-BI- phosphate	+	+	w	w	w	w
Alpha galactosidase	-	-	-	-	-	-
Beta galactosidase	+	+	-	-	-	-
Beta glucuronidase	-	-	-	-	-	-
Alpha glucosidase	+	+	-	-	-	-
Beta glucosidase	w	+	-	-	-	+
N-acetyl beta glucosaminidase	-	-	-	-	-	w
Alpha monosidase	w	+	-	-	-	-
Alpha fucosidase	-	-	-	-	-	-
API 20NE						-
Nitrate reduction	-	-	+	+	+	+
Indole production	-	-	-	-	-	-
Glucose fermentation	-	-	-	-	-	-
Arginine dihydrolase	-	-	+	-	-	-
Urease	w	w	-	-	-	-
Aesculin hydrolysis	-	-	-	-	-	+
Gelatin hydrolysis	-	-	-	+	+	-
β - Galactosidase	+	+	+	-	-	+
Assimilation of						
D-Glucose	-	-	-	+	-	-
L-Arabinose	+	-	-	-	-	+
D-Mannose	-	-	-	-	-	-
D-Mannitol	+	+	-	-	-	-
N-Acetyl-glucosamine	-	-	-	-	-	-
D-Maltose	+	+	+	-	-	-
Potassium gluconate	-	-	+	-	-	-
Capric acid	-	-	-	-	-	-
Adipic acid	-	-	-	-	-	-
Malate	-	-	w	-	-	-
Trisodium citrate	-	-	-	-	-	-

Characteristics	1	2	3	4	5	6
Phenylacetic acid	-	-	+	nd	nd	nd

Table S2. Detailed cellular fatty acid profiles (% of totals) of strain 1. R3-3^T AND 2. R3-11. Fatty acids that represent < 0.1% of the total in all strains are not shown; -, < 0.1% or not detected.

Fatty acid	R3-3 ^T	R3-11
Saturated		
C _{10:0}	0.21	0.20
C _{12:0}	2.00	2.23
C _{14:0}	2.89	3.10
C _{16:0}	29.34	26.85
C _{17:0}	0.23	0.19
C _{18:0}	0.45	0.37
Unsaturated		
C _{14:1} ω5c	0.32	0.37
C _{15:1} ω6c	0.19	0.15
Branched-chain		
iso C _{10:0}	0.34	0.30
iso C _{16:0}	0.15	-
anteiso C _{15:0}	0.18	0.10
anteiso C _{17:0}	0.10	-
cyclo C _{17:0}	7.27	3.78
Hydroxy		
C _{10:0} 3OH	3.27	2.91
C _{12:0} 2OH	1.03	0.82
C _{14:0} 2OH	1.03	0.72
iso C _{11:0} 3OH	-	0.11
Summed features*		
Summed Feature 3	37.09	43.05
Summed Feature 8	13.91	14.56

Table S3. The average nucleotide identity and digital DNA–DNA hybridization value values between strains R3-3^T and related taxa.

Strain		NCBI accession number	dDDH values were predicated by the Genome to Genome distance calculator															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	R3-3 ^T	AXCLA010000001.1	-	21.80	21.70	22.20	21.30	21.70	22.10	21.90	20.70	22.10	22.70	21.30	21.10	21.10	21.10	21.00
2	<i>R. aquaticus</i> CCUG 52575 ^T	SGUG01000098.1	78.30	-	21.5	22.20	39.10	22.10	22.10	22.00	22.40	21.90	27.80	21.60	21.40	19.80	19.80	20.20
3	<i>R. asaccharophilus</i> DSM 25082 ^T	SNXE01000001.1	77.82	77.39	-	22.40	21.50	22.20	22.30	22.20	22.80	22.50	21.20	22.50	22.00	22.00	20.10	22.80
4	<i>R. chitosanitabidus</i> NBRC 102408 ^T	BCYP01000001.1	77.59	77.10	77.46	-	22.30	28.70	28.80	28.40	21.10	25.10	21.70	24.10	23.60	20.30	20.50	20.50
5	<i>R. saccharophilus</i> DSM 654 ^T	SMBU01000001.1	77.50	89.80	77.42	77.37	-	21.80	22.10	22.00	20.40	21.90	26.50	21.50	21.50	19.70	19.80	20.90
6	<i>R. chitinivorans</i> HWN-4 ^T	PEOG01000001.1	77.49	77.07	77.34	84.41	76.99	-	28.60	31.10	21.00	25.20	21.40	23.80	23.60	20.20	20.40	20.40
7	<i>R. aquatilis</i> CCUG 48205 ^T	NIOF01000011.1	77.29	77.29	77.33	84.55	76.96	84.34	-	28.40	20.90	25.60	21.30	24.20	24.00	20.20	20.60	20.50
8	<i>R. noduli</i> HZ7 ^T	NIOE01000013.1	77.03	77.04	76.80	84.23	76.93	86.07	84.08	-	20.90	24.80	21.20	23.30	23.20	20.10	20.40	20.30
9	<i>R. toxinivorans</i> DSM 16998 ^T	SNXS01000001.1	76.56	76.30	76.88	75.95	75.95	75.93	75.95	75.58	-	21.30	20.20	20.80	20.50	19.90	19.90	20.30
10	<i>R. amylovorans</i> BIM B-1768 ^T	CP104562.2	76.46	76.32	77.07	80.94	76.05	81.23	81.58	80.68	75.79	-	21.40	24.70	24.50	21.20	21.20	21.20
11	<i>R. puraquae</i> CCUG 52769 ^T	NISI01000012.1	76.44	84.09	76.70	76.36	83.30	76.13	76.10	75.68	75.16	75.54	-	21.50	21.00	19.70	19.50	20.30
12	<i>R. depolymerans</i> KCTC 42856 ^T	CP013729.1	76.24	76.27	76.91	79.89	76.00	79.90	79.97	79.25	75.75	80.24	75.88	-	30.30	20.50	20.50	20.70
13	<i>R. terrae</i> CECT 7247 ^T	JACHXO010000001.1	75.64	75.41	76.61	79.23	75.54	79.52	79.68	79.05	75.08	79.84	75.40	85.04	-	20.10	20.40	20.80
14	<i>R. albus</i> hw1 ^T	JAQQXT010000001.1	75.61	74.74	75.30	74.45	74.65	74.59	74.54	74.10	75.02	74.46	73.95	74.13	74.07	-	27.50	20.20
15	<i>R. oligotrophus</i> CHU3 42519 ^T	JAJIRN010000001.1	75.61	74.81	75.28	74.72	74.69	74.70	74.72	74.42	75.26	74.42	73.95	74.16	73.98	84.12	-	20.30
16	<i>R. korensis</i> hw8 ^T	JAQQXS010000001.1	75.14	74.46	75.48	74.29	74.45	74.39	74.38	74.37	74.58	74.28	74.22	74.38	74.33	75.45	75.68	-
			ANI was computed from the protein-coding gene of the genomes															