

***Pseudomonas tumuqiensis* sp. nov., isolated from greenhouse soil**

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Table S1. The GenBank accession number for the genome and three housekeeping gene (*gyrB*, *rpoB* and *rpoD*) sequences of strain LAMW06^T was JAAOJA000000000 and the other related strains of genus *Pseudomonas* used for phylogenetic analysis in this study.

Strain	<i>gyrB</i>	<i>rpoB</i>	<i>rpoD</i>
<i>Pseudomonas cuatrocienegasensis</i> 1N ^T	HE800475	HE800509	HE800492
<i>Pseudomonas borbori</i> R-20821 ^T	FN554175	FN554730	FN554456
<i>Pseudomonas neuropathica</i> P155 ^T	LR797695	LR797717	LR797658
<i>Pseudomonas taeanensis</i> MS-3 ^T	HE800486	HE800518	HE800502
<i>Pseudomonas palleroniana</i> LMG 23076 ^T	FN554213	FN554747	FN554497
<i>Pseudomonas piscium</i> P50 ^T	LR797684	LR797706	LR797625
<i>Pseudomonas simiae</i> OLi ^T	FN554227	FN554757	FN554513
<i>Pseudomonas taetrolens</i> IAM 1653 ^T	AB039412	AJ717423	AB039523
<i>Pseudomonas peli</i> LMG 23201 ^T	FN554217	FN554750	FN554501
<i>Pseudomonas marincola</i> JCM 14761 ^T	FN554201	FN554739	FN554483
<i>Pseudomonas lalucatii</i> R1b-54 ^T	LR880910	LR880914	LR880906
<i>Pseudomonas oleovorans</i> IFO 13583 ^T	AB039396	AJ717461	AB039601
<i>Pseudomonas mendocina</i> ATCC 25411 ^T	AJ633103	AJ279967	AJ633567
<i>Pseudomonas fulva</i> IAM 1529 ^T	AB039395	AJ717419	AB039586

Table S2. Comparison of LAMW06^T and the other related strains of genus *Pseudomonas* genomes by the Genome-to-Genome Distance Calculator (GGDC) and average nucleotide identity (ANI) analysis, and overall characteristics of genomes.

Strain	Accession no.	dDDH (%)	ANI (%)
<i>Pseudomonas cuatrocienezasensis</i> 1N ^T	FOFP00000000	24.6	81.5
<i>Pseudomonas borbori</i> R-20821 ^T	FOWX00000000	43.0	90.9
<i>Pseudomonas neuropathica</i> P155 ^T	JACOPX000000000	21.4	76.8
<i>Pseudomonas taeanensis</i> MS-3 ^T	AWSQ00000000	25.9	82.4
<i>Pseudomonas palleroniana</i> LMG 23076 ^T	PYWX00000000	21.4	77.0
<i>Pseudomonas piscium</i> P50 ^T	JACMYF000000000	21.4	76.3
<i>Pseudomonas simiae</i> OLi ^T	MDFH00000000	21.6	77.2
<i>Pseudomonas taetrolens</i> IAM 1653 ^T	JYLA00000000	21.2	75.9
<i>Pseudomonas peli</i> LMG 23201 ^T	FMTL00000000	24.6	81.1
<i>Pseudomonas marincola</i> JCM 14761 ^T	FPBC00000000	21.7	77.2
<i>Pseudomonas lalucatii</i> R1b-54 ^T	JADPMV000000000	27.3	83.9
<i>Pseudomonas oleovorans</i> IFO 13583 ^T	UGUV00000000	23.8	80.1
<i>Pseudomonas mendocina</i> ATCC 25411 ^T	BBQC00000000	23.2	79.7
<i>Pseudomonas fulva</i> IAM 1529 ^T	BBIQ00000000	21.5	76.4

Fig. S1. Transmission electron micrograph of cell of strain LAMW06^T showing the single polar flagellum. Bar, 0.5 μm . The strain was incubated on TSA at 30 °C for 3 days.

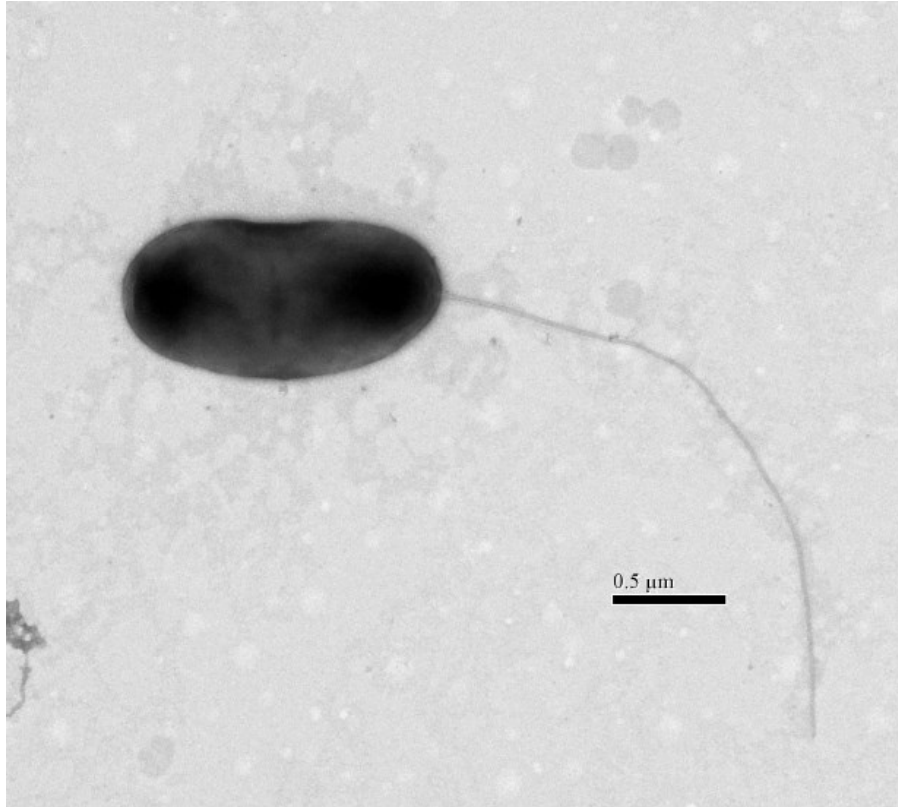


Fig. S2. Maximum-likelihood phylogenetic tree of strain LAMW06^T and its relatives based on the comparison of the 16S rRNA gene sequences. The sequence of *Azotobacter chroococcum* IAM 12666^T was used as outgroup. Genbank accession numbers were given in parentheses. Bootstrap values (those above 50 %) are shown as percentages of 1000 replicates. Bar, 0.005 substitutions per nucleotide position.

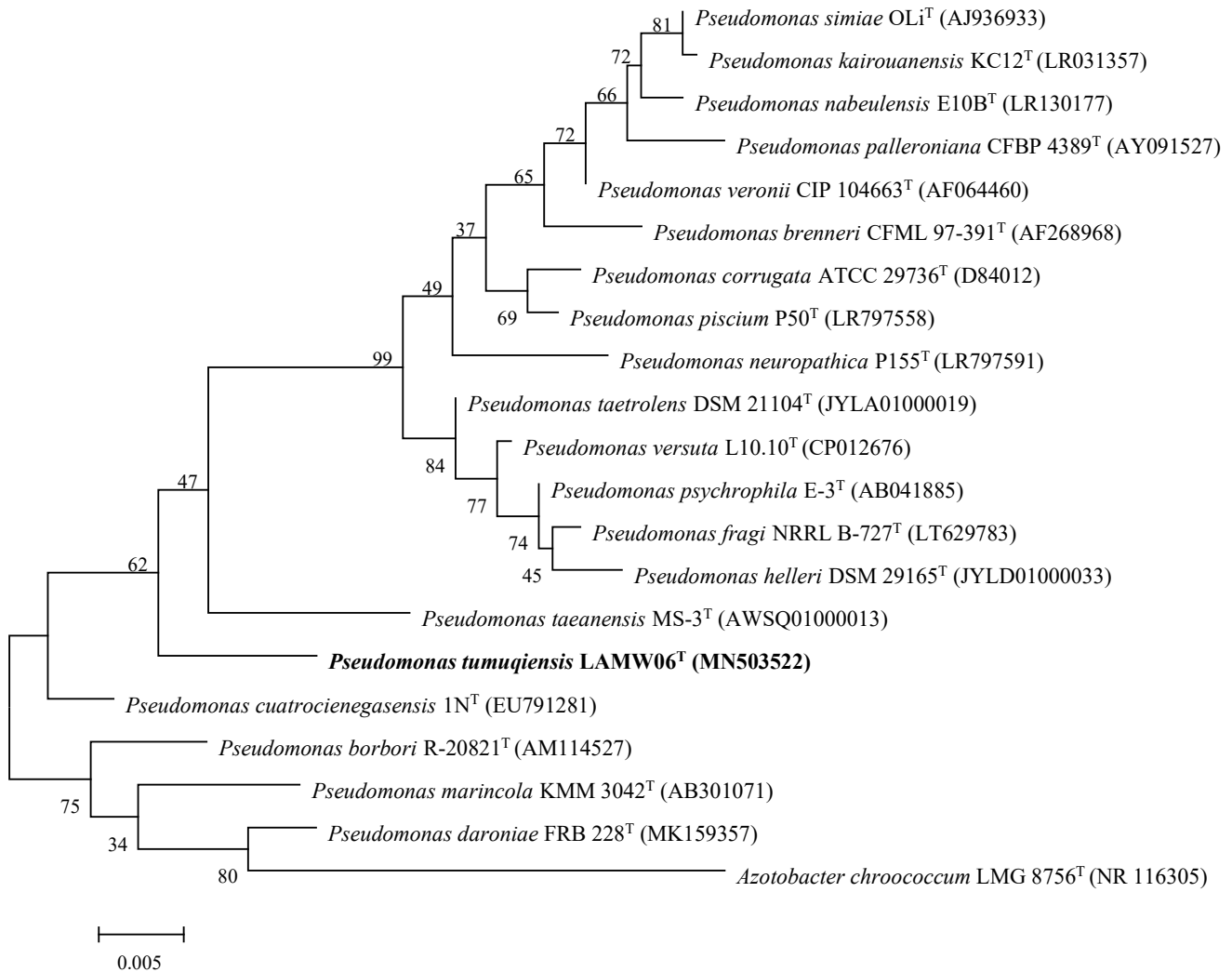


Fig. S3. Maximum-parsimony phylogenetic tree of strain LAMW06^T and its relatives based on the comparison of the 16S rRNA gene sequences. The sequence of *Azotobacter chroococcum* IAM 12666^T was used as outgroup. Genbank accession numbers were given in parentheses. Bootstrap values (those above 50 %) are shown as percentages of 1000 replicates. Bar, 5 substitutions per nucleotide position.

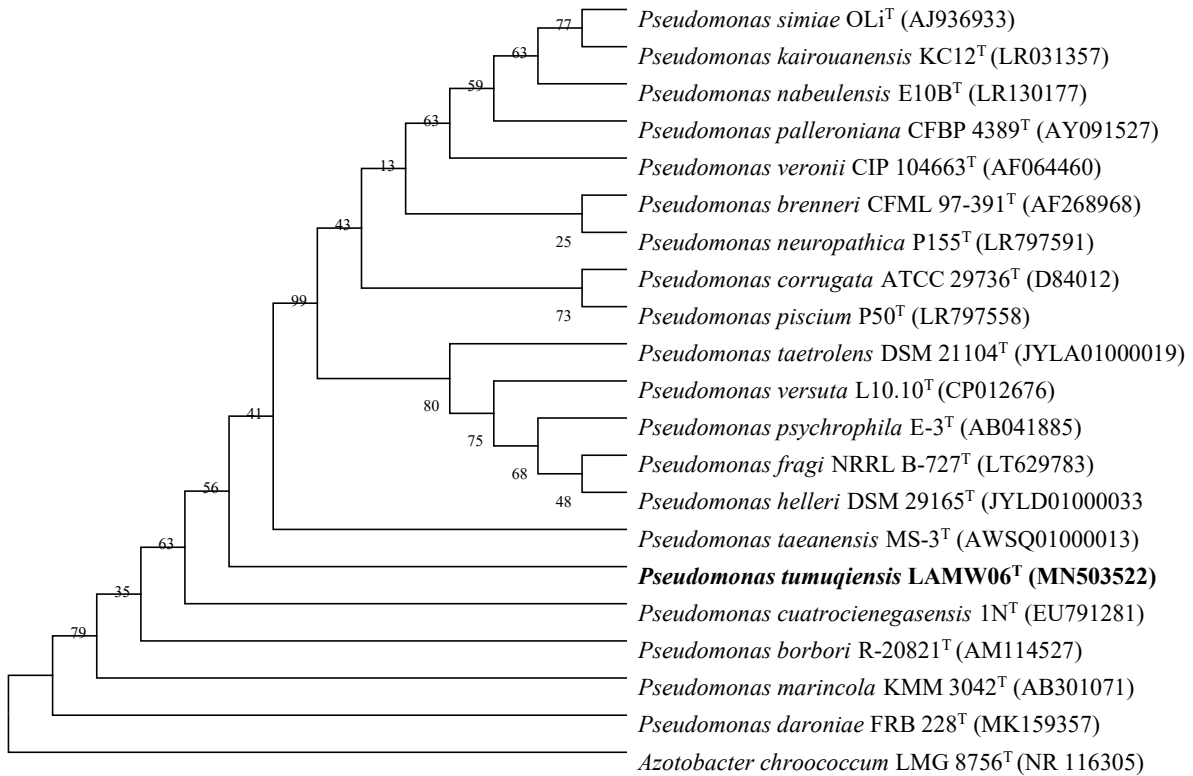
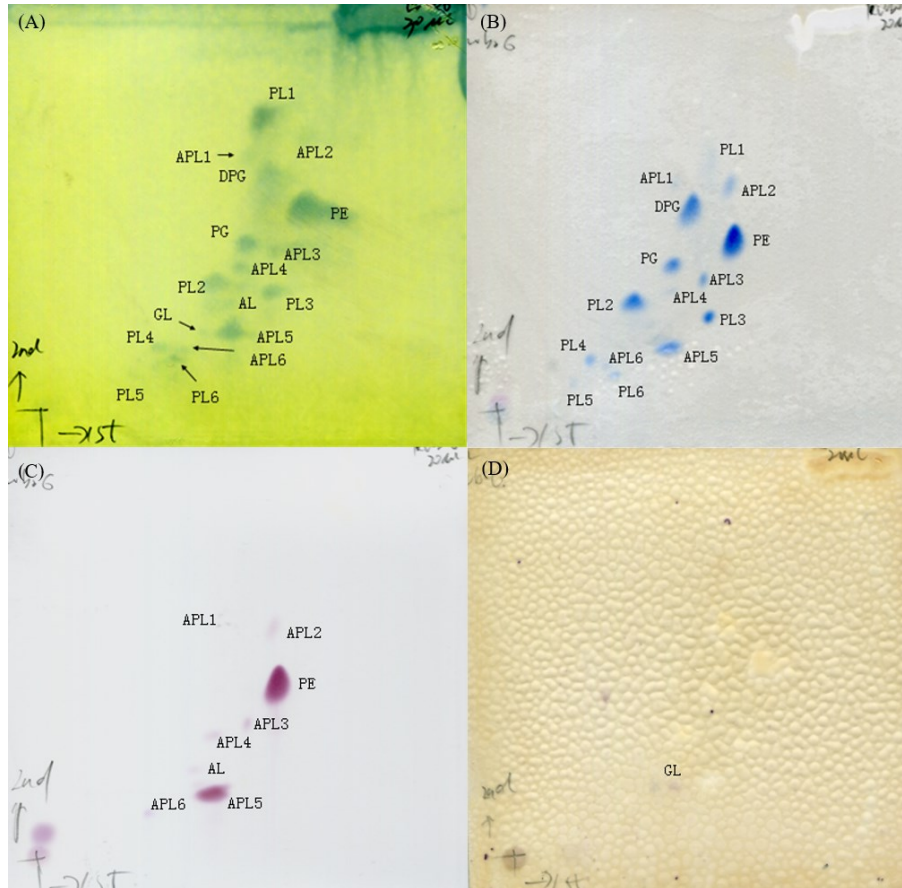


Fig. S4. The polar lipids of strain LAMW06^T. DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PE, phosphatidylethanolamine; AL, aminolipid; APL (1-6), aminophospholipids; PL (1-6), phospholipids; GL, glycolipid. (A), molybdophosphoric acid was used to reveal total polar lipids; (B), ammonium molybdate reagent for phospholipids; (C), ninhydrin reagent for aminolipids; (D), a-naphthol reagent for glycolipids.



Gene sequences (*gyrB*, *rpoB*, *rpoD*) from *Pseudomonas tumuqiensis* LAMKW06^T
(accession number JAAOJA000000000)

> *gyrB* of LAMW06^T

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