Supplementary Material

Analysis of genomic and characterization features of *Luteolibacter soli* sp. nov., isolated from soil

Jing An¹, Xiaoqi Xuan¹, Yanan Wang¹, Linwei Wu^{2,3}, Jizhong Zhou^{3,4,5,6*} and Dashuai Mu^{1,3,7,8*}

¹ Marine College, Shandong University, Weihai, Shandong, China.

² Institute of Ecology, Key Laboratory for Earth Surface Processes of the Ministry of Education, College of Urban and Environmental Sciences, Peking University, Beijing, China.

³ Department of Microbiology and Plant Biology, University of Oklahoma, Norman, OK, USA.

⁴Institute for Environmental Genomics, University of Oklahoma, Norman, OK, USA

⁵ Department of Microbiology and Plant Biology, University of Oklahoma, Norman, OK, USA.

⁶ State Key Joint Laboratory of Environment Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing, China.

⁷ School of Civil Engineering and Environmental Sciences, University of Oklahoma, Norman, OK, USA.

⁸ School Key Laboratory of Microbial Technology, Shandong University, Qingdao, Shandong, China.

⁹ Weihai Research Institute of Industrial Technology of Shandong University, Weihai, China.

*Correspondence:

Da-Shuai Mu, Email: <u>dashuai.mu@sdu.edu.cn</u> Ji-Zhong Zhou, Email: <u>jzhou@ou.edu</u> **Figure S1.** Scanning electron micrograph of strain $Y139^T$ after growing on R2A plates at 30°C for 2 days, Bar: 4 µm.



Figure S2. Two-dimensional TLC plate images of polar lipids of strain Y139^T (A); *L.arcticus* CCTCC AB 2014275^T (B); *L.flavescens* MCCC 1K03193^T (C); *L.pohnpeiensis* CCTCC AB 2011006^T (D).

Abbreviation: PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidyldimethylethanolamine; DPG, diphosphatidylglycerol; GL, (unidentified) glycolipid; L, unidentified lipids.



Figure S3. The secondary metabolite biosynthetic gene clusters of all strains in the genus *Luteolibacter*. Solid circles and hollow circles represent the presence or absence of the metabolite, respectively.



Figure S4. Genome analysis of the genus *Luteolibacter* (9 genomes). (A) Venn diagram displaying the numbers of core gene families and unique genes for each *Luteolibacter* strain. (B) Percentage of core, accessory, and unique genes in each genome.



Figure S5: The distribution of core genes, accessory genes and unique genes to different metabolic pathways in the genus *Luteolibacter*.







Strain	Genome	Number	Complet	G+C	Genes	Protein-	Pseudogene	RNA	GenBank
	size	of	eness	content		coding		gene	
	(Mb)	scaffolds	(%)	(%)		gene			
<i>L. ambystomatis</i> 32A ^T	5.3	1	99.1	62.0	4178	4112	7	59	GCA_0181379 65.1
<i>L. arcticus</i> CCTCC AB 2014275 ^T .	7.5	43	98.5	63.0	5848	5756	31	61	GCA_0259502 35.1
L. flavescens MCCC 1K03193 ^T	5.9	73	98.0	64.0	4911	4836	21	54	GCA_0259500 85.1
<i>L. luteus</i> G-1-1- 1 ^T	6.4	1	98.9	61.0	5268	5176	32	60	GCA_0129134 85.1
<i>L. marinus</i> NBU1238 ^T	6.2	355	96.4	65.0	5053	4889	103	61	GCA_0149047 55.1
<i>L. pohnpeiensis</i> CCTCC AB 2011006 ^T	4.7	254	97.5	53.5	4251	4180	16	54	GCA_0165954 35.1
<i>L. rhizosphaerae</i> GHJ8 ^T	6.2	33	99.0	62.5	5267	5194	18	55	GCA_0259500 95.1
L. yonseiensis JCM 18052 ^T	5.7	13	98.6	60.5	4581	4499	9	73	GCA_0165954 65.1
L. soli Y139 ^T	7.1	31	98.9	62.5	5715	5651	5	59	GCA_0380667 15.1

Table S1. Genomic dataset of Y139^T and other strains of genus *Luteolibacter* analyzed in the pan-genome analysis.