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TAXONOMIC DESCRIPTION

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Photobacterium salinisoli sp. nov., isolated from a sulfonylurea herbicide-degrading consortium enriched with saline soil

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Abstract

A Gram-stain-negative, aerobic, motile, rod-shaped bacterium, designated strain LAM9072^T, was isolated from a sample of a sulfonylurea herbicide-degrading consortium enriched with saline soil. The optimal temperature and pH for the growth of strain LAM9072 T were 35 °C and 7.0, respectively. Strain LAM9072 T could grow in the presence of NaCl up to 9 % (w/v). Comparative analysis of the 16S rRNA gene sequences revealed that strain LAM9072^T was closely related to members of the family Vibrionaceae, with the highest similarities to Photobacterium halotolerans MACL01^T (97.7 %) and Photobacterium galatheae S2753^T (97.7%). Strain LAM9072^T formed a distinct phylogenetic subclade within the genus *Photobacterium* in the 16S rRNA gene phylogenetic trees. The results of multi-locus sequence analysis revealed a distinct lineage with P. halotolerans MACL01^T as its closest relative. The genomic G+C content was 50.2 mol%. The DNA-DNA hybridization values between strain LAM9072^T and P. halotolerans LMG 22194^T and P. galatheae LMG 28894^T were 41.6 and 22.2 %, respectively. The average nucleotide identity values were 90.9 and 78.8 %, respectively, by comparing the draft genome sequences of strain LAM9072^T and P. halotolerans LMG 22194^T and P. galatheae LMG 28894^T. The major fatty acids were summed feature 3 ($C_{16:1}\omega 6c$ and/or $C_{16:1}\omega 7c$), $C_{16:0}$ and summed feature 8 ($C_{18:1}\omega 7c$ and/or $C_{18:1}\omega 6c$). Ubiquinone 8 was detected as the predominant respiratory quinone. The main polar lipids were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, aminophospholipid and four unidentified lipids. Based on its phenotypic characteristics and the results of genotypic analyses, we propose that strain LAM9072^T represents a novel species, for which the name Photobacterium salinisoli sp. nov. is proposed. The type strain is LAM9072^T (=ACCC 19961^T=JCM 30852^T).

Sulfonylurea herbicides are widely used for weed control in the cultivation of many crops in China, such as maize, paddy rice and wheat. Some sulfonylurea herbicides, such as nicosulfuron, cinosulfuron and chlorimuron-ethyl, can persist in soil for a long time, causing significant damage to crops and affecting functional micro-organisms and enzymes in soil. Consequently, rapid detoxification of sulfonylurea herbicide residue in the environment is considered to be an urgent issue. The micro-organisms found in soil have been regarded as a key factor in the degradation of sulfonylurea herbicide residue in the environment [1]. During our research on the bacterial diversity in a sulfonylurea herbicide-degrading consortium, a strain, designated LAM9702^T, was isolated. Based on the combination of

the genotypic and phenotypic data of the strain, we propose a new species of the genus *Photobacterium*.

The genus *Photobacterium* belongs to the family *Vibrionaceae* and was proposed by Beijerinck *et al.* [2] with the description of *Photobacterium phosphoreum* as the type species. There are more than 38 recognized species described in the genus *Photobacterium* (www.bacterio.net/photobacterium.html). Species of the genus *Photobacterium* have been mostly isolated from marine and aquatic environments such as seawater [3–7], tidal flat [8–10] and marine animals [11–19]. In addition, the latest described species is *Photobacterium chitinilyticum*, which was isolated from seawater at the bottom of the East China Sea [20]. Members of this genus share the common characteristics of having

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Abbreviations: ANI, average nucleotide identity, DDH, DNA-DNA hybridization; MA, marine agar; MB, marine broth; ML, maximum-likelihood; MLSA, multi-locus sequence analysis; MP, maximum-parsimony; NJ, neighbour-joining.

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain LAM9072 T is KP054474. The GenBank accession number for the draft genome sequence of strain LAM9072 T is QZMS00000000.

One supplementary table and five supplementary figures are available with the online version of this article.