

***Laetantesicola maris* gen. nov., sp. nov. isolated from the Sea of Japan shallow sediments.**

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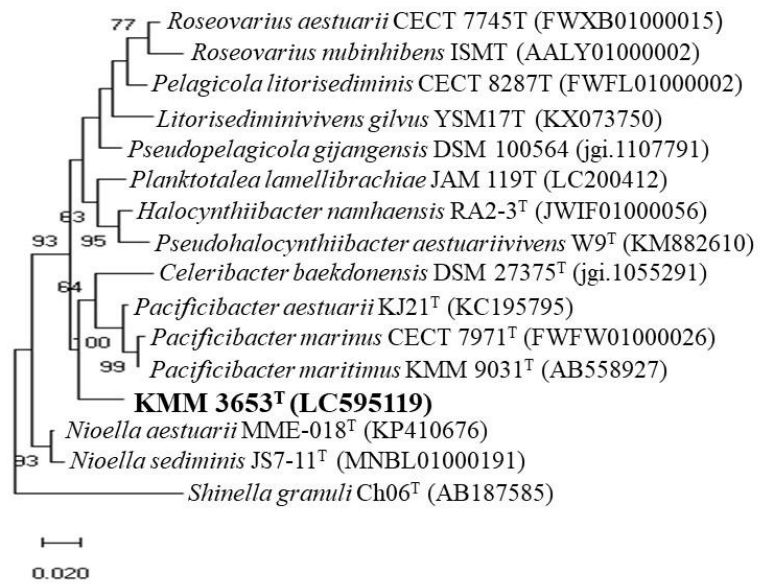
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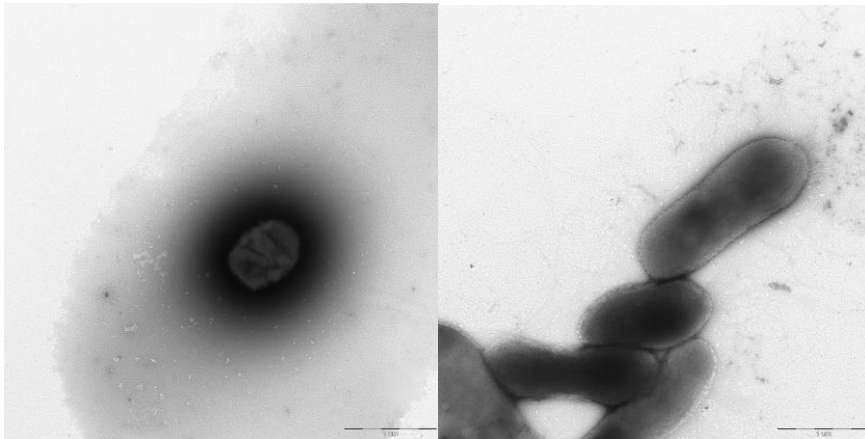
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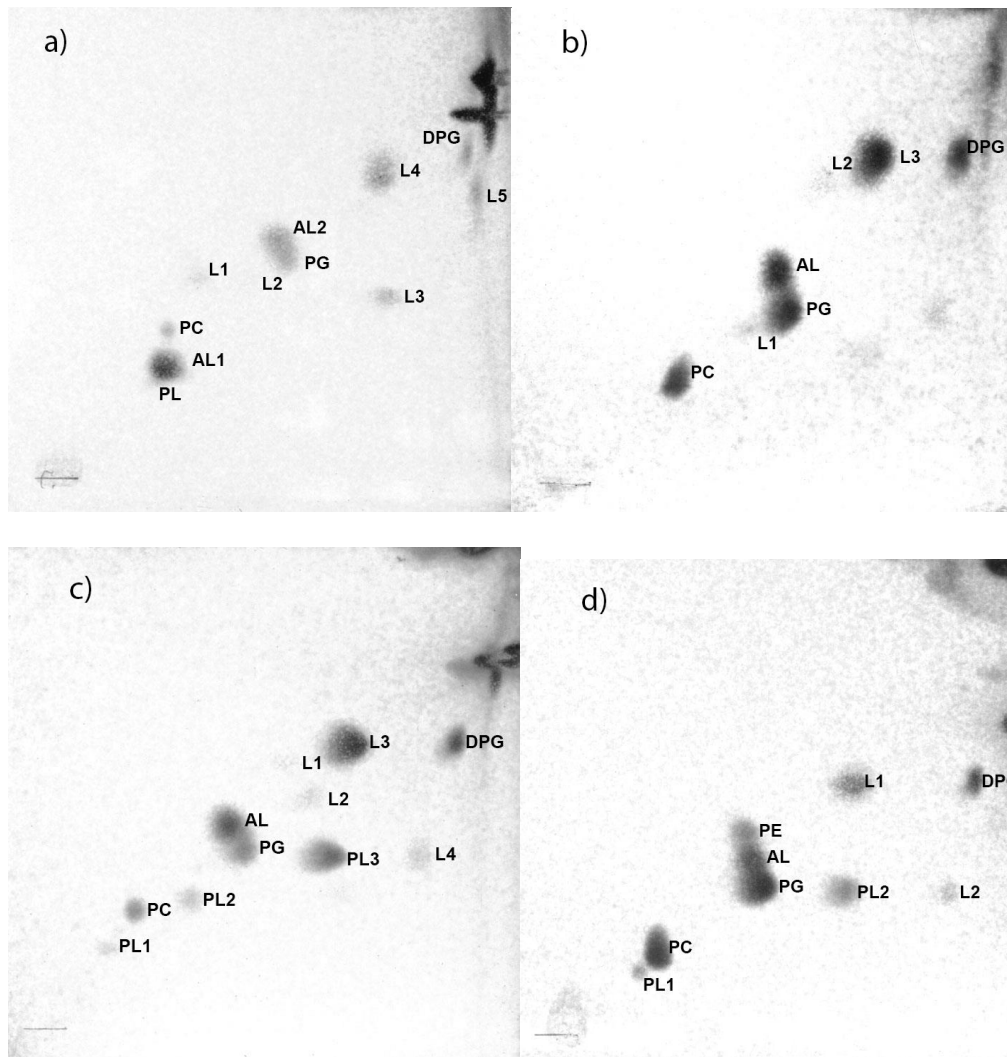
Supplementary Figure S1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences available from the GenBank/EMBL/DDBJ databases (accession numbers are given in parentheses) showing a relationship of the novel strain KMM 3653^T and related taxa. Bootstrap values based on 1000 replications are given as percentages at the branching points and numbers indicate percentages greater than 60%. Bar, 0.020 substitutions per nucleotide position.



Supplementary Figure S2. Transmission electron micrographs of bacterial cells of KMM 3653^T. Bar, 1 μ m.



Supplementary Figure S3. Two-dimensional thin-layer chromatograms of polar lipids: **a)** KMM 3653^T; **b)** *Pacificibacter maritimus* KMM 9031^T; **c)** *Pacificibacter aestuarii* JCM 31805^T; **d)** *Vanniella litorea* KCTC 32083^T; **e)** *Nioella nitratireducens* KCTC 32417^T; **f)** *Nioella aestuarii* JCM 30752^T. Abbreviations: PC, phosphatidylcholine; PG, phosphatidylglycerol; PE, phosphatidylethanolamine; DPG, diphosphatidylglycerol; PL, unidentified phospholipids; AL, unidentified aminolipids; L, unidentified lipids.



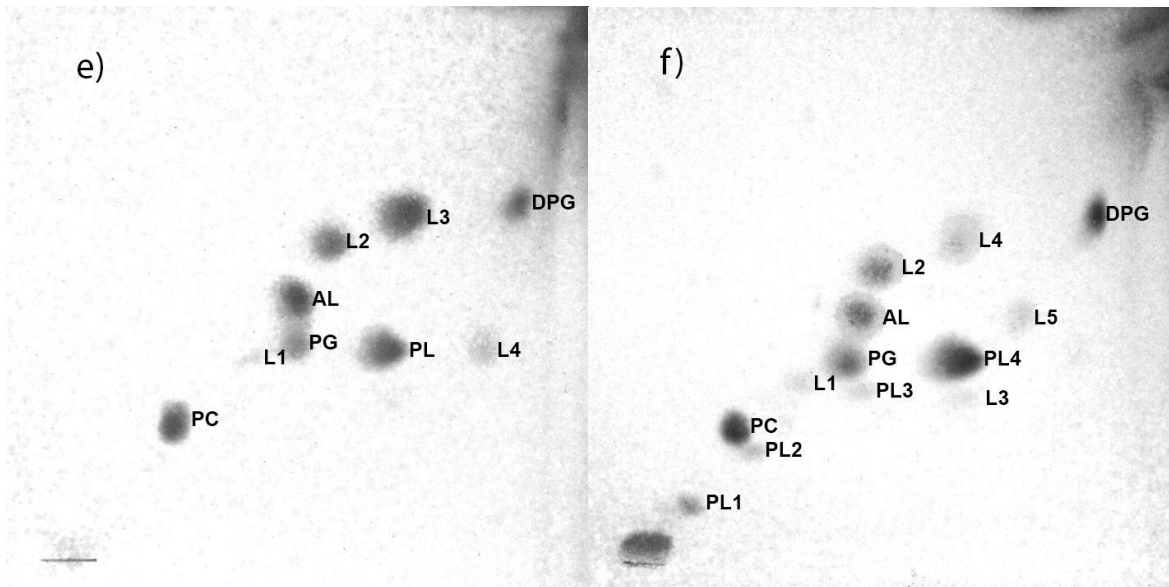


Table S1. Genome characteristics of strain KMM 3653^T.

| Feature | KMM 3653 ^T |
|-------------------------|-----------------------|
| Genome size, bp | 4,000,144 |
| G+C Content, % | 61.8 |
| Total number of contigs | 9 |
| N50, bp | 1,228,671 |
| L50 | 2 |
| Coverage | 25.0x |
| CDS (by NCBI) | 3,801 |
| rRNAs(5S/16S/23S) | 2/2/2 |
| tRNAs | 41 |
| Pseudogenes | 16 |

Table S2. Negative API 20NE, API 20E, ID32 GN test results obtained for strain KMM 3653^T.

| <u>API 20NE</u> | <u>API 20E</u> |
|------------------------------------|--------------------------------|
| Nitrate reduction | |
| Indole production | ONPG (β -galactosidase) |
| Glucose fermentation | Arginine dihydrolase |
| Arginine dihydrolase | Lysine decarboxylase |
| Urease | Ornithine decarboxylase |
| Gelatin hydrolysis | Citrate utilization |
| Assimilation of: | H ₂ S production |
| D-glucose | Tryptophane deaminase |
| L-arabinose | Indole production |
| D-mannose | Acetoin production |
| D-mannitol | Gelatin hydrolysis |
| N-acetylglucosamine | Oxidation/fermentation of: |
| Maltose | D-glucose |
| D-gluconate | D-mannitol |
| L-malate | Inositol |
| Caprate | D-sorbitol |
| Adipate | L-arabinose |
| Citrate | D-melibiose |
| Phenylacetate | |
| <u>ID 32 GN</u> | |
| Assimilation of: | |
| L-rhamnose | |
| N-acetylglucosamine | D-mannitol |
| D-ribose | D-glucose |
| Inositol | Salicin |
| D-sucrose | D-melibiose |
| D-maltose | L-fucose |
| itaconic acid | D-sorbitol |
| suberic acid | L-arabinose |
| sodium malonate | Capric acid |
| sodium acetate | Valeric acid |
| lactic acid | Trisodium citrate |
| L-alanine | L-histidine |
| potassium 5-ketogluconate | L-proline |
| Glycogen | Potassium 2-ketogluconate |
| 3-hydroxybenzoic acid | 4-hydroxybenzoic acid |
| L-serine | 3-hydroxybutyric acid |
| <u>ZYM</u> | |
| lipase (C14) | |
| valine arylamidase | |
| cystine arylamidase | |
| trypsin | |
| α -chymotrypsin | |
| acid phosphatase | |
| β -galactosidase | |
| β -glucosidase | |
| N-acetyl- β -glucosaminidase | |
| α -galactosidase | |
| β -glucuronidase | |

α -glucosidase

α -mannosidase

α -fucosidase
