Phyllobacterium pellucidum

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Phyllobacterium pellucidum*	[pel.lu'ci.dum] **L. neut. adj.** *pellucidum*, transparent	The bacteria cells are 1.8–2.0 µm in length and 1.2–1.3 µm in width, Gram-negative, rod-shaped, and produce white-colored colonies when grown on R2A at 25 °C for 3 days. Growth occurs at 15–37 °C. Growth is observed at pH values of 5.0–8.0 and NaCl concentrations up to 2% (w/v). Catalase and oxidase are positive. In API 20NE test, the BT25T strain is positive for arginine dihydrolase, urease, and gelatin hydrolysis; weakly positive for assimilation of d-glucose, l-arabinose, d-mannose, d-mannitol, *N*-acetyl-d-glucosamine, and l-malate. In the API ZYM test, the BT25T strain is weakly positive for leucine arylamidase, acid phosphatase, and naphthol-AS-BI-phosphohydrolase, but negative for other enzyme activities. The major cellular fatty acids are summed feature 8 (C18:1 *ω*7*c*/C18:1 *ω*6*c*), cyclo-C19:0 *ω*8*c*, and C16:0. Menaquinone Q-10 is the predominant respiratory quinone. Phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidylglycerol, phosphatidylcholine, an unidentified phospholipid, and an unidentified aminolipid are present in polar lipid profile. The whole-genome sequence of the isolate contains 4,660,625 bp with a 59.1% G + C content. The BT25T strain (KCTC = 62765T, NBRC = 114381T) was isolated from a soil sample in South Korea (37°51′29.2″ N 127°08′38.0″ E). The NCBI GenBank/EMBL/DDBJ accession numbers for the BT25T 16S rRNA gene sequence is MN658537.	*Phyllobacterium*	NCBI Assembly: GCF_013327855.1 $_{Ts}$	seqco.de/i:49633