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Pinisolibacter aquiterrae sp. nov., a novel aromatic hydrocarbon-degrading bacterium isolated from benzene-, and xylene-degrading enrichment cultures, and emended decription of the genus *Pinisolibacter*

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Abstract:

Two Gram-reaction-negative strains, designated as B13^T and MA2-2, were isolated from two different aromatic hydrocarbon-degrading enrichment cultures and characterized using a polyphasic approach to determine their taxonomic position. The two strains had identical 16S rRNA gene sequences and were most closely related to *Pinisolibacter ravus* E9^T (97.36 %) and *Siculibacillus lacustris* SA-279^T (96.33 %). Cells were facultatively aerobic rods and motile with a single polar flagellum. The strains were able to degrade ethylbenzene as sole source of carbon and energy. The assembled genome of strain B13^T had a total length of 4.91 Mb and the DNA G+C content was 68.8 mol%. The predominant fatty acids (>5 % of the total) of strains B13^T and MA2-2 were $C_{18:1}$ *ω7c*/$C_{18:1}$ *ω6c*, $C_{16:1}$ *ω7c*/C16 : 1 *ω6c* and $C_{16:0}$. The major ubiquinone of strain B13^T was Q10, while the major polar lipids were phosphatidyl-*N*-methylethanolamine, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and a phospholipid. Based on phenotypic characteristics and phylogenetic data, it is concluded that strains B13^T and MA2-2 are members of the genus *Pinisolibacter* and represent a novel species for which the name *Pinisolibacter aquiterrae* sp. nov. is proposed. The type strain of the species is strain B13^T (=LMG 32346^T=NCAIM B.02665^T).

Keywords: *Pinisolibacter aquiterrae*, new taxa, *Hyphomicrobiales*, BTEX degradation