

Characterization of *Micrococcus porci* sp. nov., isolated from pig feces

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An aerobic bacterium, designated as strain KD337-16_T, was isolated from the fecal samples of a black pig. It exhibited spherical, non-motile and non-spore-forming, Gram-positive cells. KD337-16_T was identified as a member of the genus *Micrococcus* through 16S rRNA gene sequencing, and its closest relatives were found to be *Micrococcus endophyticus* YIM 56238_T (99.6% similarity), *Micrococcus luteus* NCTC 2665_T (99.1%), *Micrococcus yunnanensis* YIM 65004_T (99.1%), *Micrococcus aloeverae* AE-6_T (99.1%), *Micrococcus antarcticus* T2_T (99.0%), and *Micrococcus flavus* LW4_T (98.8%). Phylogenomic trees were constructed, and strain KD337-16_T was found to form its own cluster as an independent lineage of *M. flavus* LW4_T. Between KD337-16_T and its close relatives, the average nucleotide identity, average amino acid identity, and digital DNA–DNA hybridization were below the respective species delineation thresholds at 82.1%–86.6%, 78.1%–86.1%, and 24.4%–34.9%. The predominant isoprenoid quinone was MK-8(H₂), and the major fatty acids were anteiso-C_{15:0} and iso-C_{15:0}. Taken together, the results indicate that strain KD337-16_T is a novel species of the genus *Micrococcus*, for which the name *Micrococcus porci* sp. nov. is proposed. The type strain is KD337-16_T (= BCRC 81318_T = NBRC 115578_T).

Key words: gut microbiota, *Micrococcus porci*, new taxa, polyphasic analysis