



## Corynebacteria from relict permafrost

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Strain F4-5 was isolated from samples the alluvial sand sediments of relict permafrost collected at Mammoth Mountain, Central Yakutia, Siberia, Russia. Mammoth Mountain is an outcrop of relict permafrost, extending for 12 km along the left bank of the Aldan River, 300 km from its confluence with the Lena River. It is a part of the upland and consists of a series of alluvial deposits (up to 80 m thick) of different ages. The lower part of the sediments, from which the samples were taken for microbiological analysis, consists predominantly of sandy sediments with abundant inclusions of Neogene fossil flora. The sand sediments were formed in the Middle Miocene 11–16 million years ago. The formation of permafrost started apparently in the Late Pliocene, 3.5 million years ago, when the average July temperature dropped to  $+12 \div +16^\circ\text{C}$ , and the average January temperature was  $-12 \div -32^\circ\text{C}$ . Relict permafrost rocks have not been thawed in more recent geological time. The samples of frozen rocks for microbiological analysis were taken from depths of 1–1.5 m below the active layer, which prevented the previously thawed rocks from entering this zone. The sampling technique eliminates the possibility of infiltration of surface contamination.

Subsamples (0.3g) were inoculated into of ISP 1 medium (2 ml) (Difco). Enrichment culture of strain F4-5 was incubated at  $28^\circ\text{C}$ . For strain isolation, samples were transferred onto plates with ISP3 medium (Difco). On solid medium ( $28^\circ\text{C}$ ), the strain produces whitish/cream-colored or light yellow, smooth, convex, mat or slightly glossy colonies (5–7 mm in diameter) with uneven edges. The cells of strain F4-5 are straight or slightly curved rods 2.0–6.0  $\mu\text{m}$  long and 0.3–0.5  $\mu\text{m}$  in diameter, non-spore-forming, non-motile, and sometimes granulated. The main feature of these cells is that they occur as "V" shapes. It is known that the morphology of these cells is similar to that of corynebacteria. The results of the 16S rRNA gene sequence analysis demonstrated that strain F4-5 has 99% sequence similarity with *Corynebacterium callunae* NCIMB 10338T.