

Phylogeny of three *Exiguobacterium* isolates from Arctic permafrost

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Even though DNA- DNA hybridization is the recommended standard for the delineation of a bacterial species, it is not effective in the estimation of genetic distances between distantly and very closely related species. As a complement to DNA-DNA hybridization, sequence analysis of 16S rDNA is frequently used. However, the degree of resolution obtained with this gene is generally not sufficiently discriminatory for closely related species. Instead, housekeeping genes that evolve faster than 16S rDNA genes provide higher resolution, such as *gyrB* (gyrase B), *rpoB* (RNA polymerase beta subunit), *recA* (homologous recombination), *hsp70* (Class I-heat shock protein) and *citC* (isocitrate dehydrogenase).

In the present study, these five housekeeping genes were sequenced along with the 16S rDNA genes from *Exiguobacterium* strains, namely 255-15 (2-3 million years), 7-3 (20-30 thousands years) and 190-11 (200-600 thousands years) isolated from the Siberian permafrost and four reference strains (*E. acetylicum*, *E. aurantiacum*, *E. antarcticum* and *E. undae*). These data were compared to DNA-DNA hybridization results.

The tree topologies of *rpoB*, *recA*, *hsp 70*, *gyrB* and *citC* were very similar to each other. The high bootstraps values of the branches in these trees were able to better classify the new isolates from the Siberian permafrost in relation to the reference strains, which was not possible with only the 16S rDNA gene sequence. These data were consistent with the

data obtained in DNA-DNA hybridizations and showed that 255-15 and 7-3 strains are members of the same new species and strains 190-11 is member of the *undae* species.