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Mycoplasma Diversity in Arctic Permafrost

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Abstract

© 2016, Springer Science+Business Media New York. Viable bacterial cells and its genetic material can be stably maintained in Arctic permafrost for a long geological time. Because of the seasonal melting of permafrost strata, it cannot be excluded an access to the surface of ancient highly invasive species with increased pathogenicity. Mycoplasmas are very successful pathogens in humans, mammals, birds, insects, and plants, with high genome plasticity and ability to avoid immune response of host organism. The metagenomic approach allowed us to predict mycoplasma diversity in the Arctic permafrost. The number of mycoplasma DNA fragments in soil deposits of comparable age (~30,000 years) and origin (the late Pleistocene Ice Complexes) is not so abundant compared with other microorganisms, but it is enough for a chance in the presence of living mycoplasmal cells in permafrost. DNA fragments of human, animal, insect, and plant pathogens were identified. The “ubiquitous” mycoplasma *Acholeplasma laidlawii* is the undisputed leader in the number of identified sequences in all three metagenomes. It may indicate a higher adaptive capacity and more powerful metabolic potential of *A. laidlawii* among Mollicutes.

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Keywords

Acholeplasma laidlawii, Metagenome, Mycoplasma, Pathogens, Permafrost