

A005

Evolution and Geographical Distribution of Lichens in Antarctic

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Distribution of lichens in Antarctic regions was investigated by phylogenetic analysis of lichen species of the genera *Pseudephebe*, *Umbilicaria*, and *Usnea*. The lichen species were collected from "Leningradsкая", and "Russkaya" Stations, Lindsey Island, Mt. Moses, Maish Nunatak and King George Island. From the phylogenetic tree of *Pseudephebe*, *Umbilicaria*, and *Usnea* based on combined sequences of ITS and 28S rDNA, geographical isolation of lichen species in Pacific coast of continental Antarctic was not evident. Instead, samples from long distance were clustered together and contained rDNA sequences of high similarity, implying that lichen species can be easily transferred and widely distributed in Pacific coast of continental Antarctic. Particularly, *Usnea* species with close phylogenetic relationships showed variation in intron possession pattern, implying that introns are easily lost or obtained. However, sequences of introns were generally well conserved in the same phylogenetic lineages. Sharing of same type of intron by lichens from different geographical origin supported the hypothesis of easy geographical distribution of lichen species in Antarctic continent.

Keywords: Evolution, lichen, Antarctic

A006

Castellaniella ginsengisoli sp. nov., Isolated from Soil of a Ginseng Field

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A Gram-negative, motile, aerobic bacterium, designated DCY36^T, was isolated from soil of a ginseng field in South Korea and was characterized taxonomically using a polyphasic approach. The G+C content of the genomic DNA was 63.7 mol%. Strain DCY36^T contained ubiquinone Q-8. The major fatty acids were C_{16:0} (29.6%), C_{17:0} (22.3%), Summed feature 7 (C_{18:1} ω7c / C_{18:1} ω9t / C_{18:1} ω12t, 14.5%) and Summed feature 4 (C_{16:1} ω7c / C_{15:0} iso 2OH, 11.7%). Comparative 16S rRNA gene sequence analysis showed that strain DCY36^T belongs to genus *Castellaniella* in the family *Alcaligenaceae* of the *Betaproteobacteria*. Similarities between the 16S rRNA gene sequences of strain DCY36^T and three validated representatives of the genus, *Castellaniella caeni* Ho-11^T, *Castellaniella defragrans* DSM 12141^T and *Castellaniella denitrificans* DSM 11046^T were 98.4, 97.5 and 98.1%, respectively. Strain DCY36^T exhibited relatively low levels of DNA-DNA relatedness values with respect to these three species. On the basis of its phenotypic, genotypic properties and phylogenetic distinctiveness, strain DCY36^T (= KCTC 22398^T) should be classified in the genus *Castellaniella* as the type strain of a novel species, for which the name *Castellaniella ginsengisoli* sp. nov. has been proposed.

Keywords: *Castellaniella* sp., 16S rRNA

A007

Bioelectrochemical Reduction of Mn(IV) to Mn(II) by *Lactococcus lactis* Isolated from Soil

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Mn(IV) is not reduced by electrochemical reduction potential, and higher energy is required for chemical reduction. *Lactococcus lactis* metabolically reduced Mn(IV) to Mn(II) in the medium containing glucose under anoxic condition. In this condition, glucose and Mn(IV) function as an electron donor and electron acceptor, respectively. However, the part of the reducing power generated in coupling with metabolic glucose oxidation can be consumed to reduce Mn(IV) because most of the free energy has to be consumed for biosynthesis. Accordingly, extra-reducing power may be helpful to biochemically reduce Mn(IV) to Mn(II). In this research, we employed a non-compartmented electrochemical bioreactor to biochemically reduce Mn(IV). A modified electrode with neutral red was used to transfer electrochemical reduction potential to bacterial cell. Much more Mn(IV) was reduced to Mn(II) in the electrochemical bioreactor than the conventional bioreactor.

Keywords: *Lactococcus lactis*, Mn(V) reduction, electrochemical bioreactor, Nm-modified electrode

A008

Paracastellaniella terrae gen. nov., sp. nov. Isolated from the Granule in a Wastewater-Treatment Bioreactor

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Strain Ch07^T, a Gram-negative, non-spore-forming, short rod-shaped, non-motile bacterium was isolated from the granule in a wastewater-treatment bioreactor in South Korea and characterized in order to determine its taxonomic position. 16S rRNA gene sequence analysis revealed that strain Ch07^T belongs to the beta subclass of the *Proteobacteria*, and the highest sequence similarity was found with *Pusillimonas noertemannii* BN9^T (96.6%), *Pigmentiphaga kullae* DSM 13608^T (96.6%), *Achromobacter insolitus* LMG 6003^T (96.5%) and *Achromobacter denitrificans* DSM 30026^T (96.4%). Chemotaxonomic data revealed that strain Ch07^T possesses ubiquinone Q-8 and the major fatty acids included hexadecanoic acid (C_{16:0}, 33.24%), cyclo-heptadecanoic acid (C_{17:0} cyclo, 18.20%), Summed Feature 4 (C_{16:1} ω7c / C_{15:0} iso 2OH) and Summed Feature 7 (C_{18:1} ω7c / ω9t / ω12t). The results of physiological and biochemical tests clearly demonstrated that strain Ch07^T represents a distinct species. Based on these data, Ch07^T (= KCTC 12668^T = LMG 24012^T) should be classified as the type strain of a novel genus, *Paracastellaniella* for which the name *Paracastellaniella terrae* gen. nov., sp. nov. has been proposed.

Keywords: *Paracastellaniella terrae*, 16S rRNA, Chemotaxonomic, Beta *Proteobacteria*