**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 Pseudopephe, Umbilicaria, and Usnea. The lichen species were collected from "Leningradskaya," and "Russkaya" Stations, Lindsey Island, Mt. Moses, Maish Nunatak and King George Island. From the phylogenetic tree of Pseudopephe, 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 idea of easy geographical distribution of lichen species in Antarctic continent.

**Keywords**: Evolution, lichen, Antarctic

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**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 anaerobic 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 biocatalytically reduce Mn(IV) to Mn(II). In this research, we employed a non-compartmented electrochemical bioreactor to biocatalytically 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

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**A006**

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

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A Gram-negative, motile, aerobic bacterium, designated DCY36T, 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 DCY36T contained ubiquinone Q-8. The major fatty acids were C16:0 (29.6%), C17:0 (22.3%), Summed feature 7 (C18:1ω7c / C18:1ω9t / C18:1ω11t, 14.5%) and Summed feature 4 (C16:1ω7c / C15:0 iso 2OH, 11.7%). Comparative 16S rRNA gene sequence analysis showed that strain DCY36T belongs to genus Castellaniella in the family Alcaligenaceae of the Betaproteobacteria. Similarities between the 16S rRNA gene sequences of strain DCY36T and three validly represented representatives of the genus, Castellaniella caeni Ho-1T, Castellaniella defrangi DSM 12141T and Castellaniella densitifarcens DSM 11034T were 98.4, 97.5 and 98.1%, respectively. Strain DCY36T 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 DCY36T (KCTC 22398T) 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

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**A008**

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

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Strain Ch07T, a Gram-negative, non-spor-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 Ch07T belongs to the beta subclass of the Proteobacteria, and the highest sequence similarity was found with *Pseudomonas aeruginosa* DSM 45122T (96.6%), *Pigementiphaga kallae* DSM 13608T (96.6%), *Achromobacter insolitus* DSM 6003T (96.5%) and *Achromobacter densitifarcens* DSM 30026T (96.4%). Chemotaxonomic data revealed that strain Ch07T possesses ubiquinone Q-8 and the major fatty acids included hexadecanoic acid (C16:0, 33.2%), cyclo-heptadecanoic acid (C17:0 cyc, 18.2%), Summed feature 4 (C16:1ω7c / C15:0 iso 2OH) and Summed feature 7 (C16:1ω7c / C14:0 ω9t / ω12). The results of physiological and biochemical tests clearly demonstrated that strain Ch07T represents a distinct species. Based on these data, Ch07T (= KCTC 12668T = LMG 24012T) 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