A001

Halobacillus marina sp. nov. Isolated from the Beach Rhizosphere of *Blutaparon portulacoides* in Brazil

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Four gram-positive, halotolerant, and spore-forming strains were isolated from the rhizosphere of *Blutaparon portulacoides* in beaches in Brazil and were subjected to a polyphasic taxonomic study They grew in the presence of 0-20% NaCl. They have characteristics as degradation of casein and starch Phylogenetic analysis based on 16S rRNA gene sequences showed that they were associated with the genus *Halobacillus*. When the phenotypic tests were compared to those from the other species of *Halobacillus*, they did not match with any other known species On the basis of phenotypic and phylogenetic data, they should be placed in the genus *Halobacillus* as a novel species, for which the name of *Halobacillus marina* sp nov is proposed. The type strain of the new species is M9^T(= KCTC XXXXX^T).

[This work was supported by grant BDM0200413 from the Korean Ministry of Science and Technology]

A002

Simultaneous Detection and Differentiation of *Vairimorpha* spp. and *Nosema* spp. by Multi-plex PCR

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A multiplex polymerase chain reaction (PCR) was developed for the simultaneous detection and differentiation among *Vairimorpha* spp and *Nosema* spp and identification of *Vairimorpha necatrix* from Lepidoptera insect. Three sets of primers were selected from different genomic sequences to specifically amplify a 831 bp amplicon within the SSU rRNA gene, specific for both *Vairimorpha* spp and *Nosema* spp (MSSR primer), a 542 bp amplicon within the SSU rRNA gene, specific for *Vairimorpha* spp (VSSU primer), and a 476 bp amplicon within actin gene, specific for *Vairimorpha necatrix* (VNAG primer) Using the primers in conjunction (multiplex PCR) we were able to detect *Vairimorpha* spp and *Nosema* spp. and to differentiate between them The sensitivity of this PCR assay was approximately 10 spores per milliliter We proposed that the multiplex PCR was sensitive, specific and rapid tool that can serve as a useful differential diagnostic tool for detecting *Vairimorpha* spp and *Nosema* spp in Lepidoptera insect

A003

Marinobacterium halophilum sp. nov., a Marine Bacterium Isolated from the Yellow Sea

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A gram-negative, aerobic, and halophilic bacterium, which was designated as strain mano11^T, was isolated from a tidal flat area of Dae-Chun, Chung-Nam, Korea. Analysis of the 16S rRNA gene sequence revealed that this strain belongs to a cluster within the α-*Proteobacteria*. The similarity values of the 16S rRNA gene sequences between the strain mano11^T and the most closely related species, *Marinobacterium georgiense* DSM 11526^T, was 98 5 %. The level of DNA-DNA relatedness between the mano11^T strain and the *Marinobacterium georgiense* type strain was 6 2-11 2 % The result of DNA-DNA hybridization and the polyphasic data verified the classification of the mano11^T strain as a novel taxon in the *Marinobacterium* genus Therefore, the name *Marinobacterium halophilum* sp. nov. has been proposed for this tidal flat area isolate. The type species of the new species is strain mano11^T (=KCTC 12240^T).

[This work was supported by grant BDM0200413 from the Korean Ministry of Science and Technology]

A004

Biodiversity in Phototrophic Consortia Sampled from Baltic Sea

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Phototrophic consortia were obtained by enrichment of sea water and fresh water samples, which originated from a Baltic Sea area of north Germany and pools near the sea shore, respectively Enrichment was performed with AT medium containing various combinations of carbon sources, electron donors, and electron acceptors. Enriched cultures were screened and each isolate underwent common phylogenetic analyses The 16S rDNA-sequence profile revealed that diverse anoxygenic phototrophs existed in the consortia. They mainly belonged to *a-Proteobacteria* Thereafter, intensive phylogenetic studies have been done with the isolates and 5 strains are now considered as new taxa candidates

[Supported by grants from the 21C Frontier Microbial Genomics and Applications Center Program, the Ministry of Science and Technology (Grant MG02-0101-001-2-2-0) and by grants from the Brain Korea 21 Project Fund, the Ministry of Education]