

## 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 marma* sp. nov. is proposed. The type strain of the new species is M9<sup>T</sup> (= KCTC XXXXX<sup>T</sup>).

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## 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*<sup>T</sup>, 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  $\alpha$ -*Proteobacteria*. The similarity values of the 16S rRNA gene sequences between the strain *mano11*<sup>T</sup> and the most closely related species, *Marinobacterium georgiense* DSM 11526<sup>T</sup>, was 98.5%. The level of DNA-DNA relatedness between the *mano11*<sup>T</sup> strain and the *Marinobacterium georgiense* type strain was 62-112%. The result of DNA-DNA hybridization and the polyphasic data verified the classification of the *mano11*<sup>T</sup> 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*<sup>T</sup> (=KCTC 12240<sup>T</sup>).

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## 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  $\alpha$ -*Proteobacteria*. Thereafter, intensive phylogenetic studies have been done with the isolates and 5 strains are now considered as new taxa candidates.

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