

## A025

**Isolation and Characterization of Novel Anaerobic Chemolithoautotrophic Thiosulfate-oxidizing Bacteria.**

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Novel anaerobic thiosulfate oxidizing bacteria were isolated from an anaerobic denitrifying conditions. For isolation, the use of thiosulfate, which is abundant in nature, as the electron donor was an effective measure to establish an enrichment culture of these strains. Based on the morphological, physiological, and 16S rDNA sequence analysis, two strains ATO1 and ATO2 were identified and affiliated with members of the genus *Pseudomonas*. Both strains were able to oxidize thiosulfate under anaerobic conditions. Two strains could not grow on aerobic conditions in any case. Organic carbons could not serve as carbon and energy sources. The results demonstrated that these strains were important sulfur-related populations involved in the sulfur cycle occurring in the anaerobic conditions.

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Key words: thiosulfate, oxidation, denitrification

## A027

**Isolation and Characterization of New Species in the Genus *Ureibacillus***Seon Young Lee<sup>1,2\*</sup>, Byung Yong Kim<sup>1</sup>, Soon Wo Kwon<sup>1</sup>, Seung Joo Go<sup>1</sup>, and Yong Keun Park<sup>2</sup>

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Classification of eighteen bacterial strains that were isolated from diverse environment was investigated by a polyphasic approach (Two strains from cotton composts for the cultivation of mushroom, seven strains from composts for crop cultivation, four strains from ginseng cultivated fields and five strains from green house soil.)

All isolates were aerobic and endospore-forming rod shaped bacteria.

The sequencing comparative analysis for the 16S rRNA genes of these strains clearly showed the phylogenetic affiliation to the genus *Ureibacillus*.

Among them, ten isolates showed low similarities to *Ureibacillus thermosphaericus* and *Ureibacillus terrenus*. In the chemotaxonomic analyses of all isolates the main cellular fatty acid was iso-C<sub>16:0</sub> and the dominant isoprenoid quinones was MK-7.

Based on the polyphasic data, these ten isolates (6T19, 6T29, GH2-3, GH4-4, HC81, HC110, HC145, HC148, HT36-1, HT44-1) can be proposed to novel species in the genus *Ureibacillus*.

## A026

**A New *Pseudoxanthomonas* Species, *Pseudoxanthomonas suwonensis* sp. nov.**In-Bae Cha<sup>1,2\*</sup>, Hang-Yeon Weon<sup>3</sup>, Byung-Yong Kim<sup>1</sup>, Jong-Shik Kim<sup>4</sup>, Seon-Young Lee<sup>1,5</sup>, Seung-Joo Go<sup>1</sup>, Seung-Beom Hong<sup>1</sup>, Wan-Taek Im<sup>6</sup>, and Soon-Wo Kwon<sup>1</sup>

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On the basis of phenotypic and genotypic data, one novel species belonging to the genus *Pseudoxanthomonas* was described. Three strains, 4M1<sup>T</sup>, 4M9 and 4M12, were isolated from the cotton waste composts. These strains are Gram-negative, aerobic, and nonspore-forming rods. 16S rRNA gene sequence comparisons demonstrated that these isolates were clustered phylogenetically within the genus *Pseudoxanthomonas* and 4M1<sup>T</sup> revealed the sequence similarity levels of 96.9 - 99.0% to six validly published *Pseudoxanthomonas* species. According to DNA-DNA hybridization test, DNA-DNA homology value between 4M1<sup>T</sup> and six known *Pseudoxanthomonas* species was on the range of 52.6 - 63.2%. The DNA G+C content of strain 4M1<sup>T</sup> was 63.5 mol%. For the more detailed characterization of these strains, the physiological, chemotaxonomic and genotypic properties were evaluated. From the results of this study, the name *Pseudoxanthomonas suwonensis* sp. nov. (4M1<sup>T</sup>=KACC 11320<sup>T</sup>=DSM) is proposed.

## A028

***Bacillus alkalogaya* sp. nov., a Novel Alkaliphilic Bacterium from Soil**Ji-Yeon Kim<sup>1\*</sup>, Sung-Ho Hur<sup>2</sup>, and Jeong-Hwa Hong<sup>3</sup>

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An alkaliphilic bacterium was isolated from soil in Gimhae, Korea. The isolate grew optimally at pH 10.0 (the pH growth range was 9.0-10.5) and at temperature 30°C (the temperature growth range was 15-40°C). It was Gram-positive, strictly aerobic, motile, rod-shaped bacterium that produced ellipsoidal endospore. The isolate grew in 0.5-7% (w/v) NaCl but not at NaCl concentrations higher than 8% (w/v). Phylogenetic analysis based on 16S rDNA sequencing indicated that this bacterium belongs to the genus *Bacillus*, with 97% sequence similarity to *Bacillus krubwicheiae*. On the basis of morphological and physiological characteristics, and 16S rDNA sequence analysis, it is concluded that the isolate should be classified as representing a novel species, for which the name *Bacillus alkalogaya* is proposed.