

the result obtained (Pot *et al.*, 1999). Several strains generated unique ribotype patterns and were not grouped with strains of the same species. Further work with these strains is required in order to the correct classification.

**A303**

**Molecular Phylogeny of *Lactobacillus* spp. by a Random Amplified Polymorphic DNA-PCR Method**

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The genetic relationships of six *Lactobacillus* strains and five laboratory isolates from fermented milk were determined by a random amplified polymorphic DNA (RAPD)-PCR method. With 42 random primers, the results were analyzed by using the NTSYS-PC software for phenetic analysis. It revealed that all tested bacteria were divided into three distinct clusters. The clusters implied three subgenuses existed for the genus *Lactobacillus*, which were previously proposed by Rogosa and Sharpe. From the results, it was also possible to determine that the isolated *Lactobacillus* strains from fermented milk were grouped into *L. acidophilus* or *L. bulgaricus*. Interestingly, the three tested *L. casei* strains were divided into different clusters implying different subgenuses, i.e., *Thermobacterium* (*L. casei* YIT 9018) and *Streptobacterium* (*L. casei* CHR. Hansen and *L. casei* ATCC 4646). According to the distance matrix generated by an UPGMA program, the isolated bacteria LT01 and LT02 were determined as a subspecies of *L. bulgaricus*. The HK01, HK02 and HK03 were very closely related to either *L. acidophilus* or *L. casei* YIT 9018. Hence, RAPD-PCR appears to be a very practical method to determine the genetic

relationships of the *Lactobacillus* species and to characterize the unknown *Lactobacillus* strains at the subspecies level.

**A304**

**시화호에서 분리한 신규 호염성 세균  
*Silicibacter shihwensis* sp. nov. 의  
계통분류학적 특성**

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A moderate halophilic bacterium, designated JC1077, was isolated from the Lake Shihwa, an artificially saline lake built in 1994 in Korea. The isolate was Gram-negative, facultative aerobic, rod-shaped and motile by means of subpolar flagellum. Phylogenetic analysis based on 16S rDNA sequences indicated that JC1077 strain belonged to the alpha subclass of the proteobacteria and formed a significant monophyletic clade with *Silicibacter lacuscaerulensis*. Sequence similarity between the two strains was 97.4%. The major cellular fatty acid was C18:1 w7c, and the overall fatty acid composition significantly differed from that of *S. lacuscaerulensis*. In addition to genetic and chemical differences, several phenotypic characters can be used to differentiate the isolate from *S. lacuscaerulensis*. On the basis of polyphasic evidence, the name, *Silicibacter shihwensis* sp. nov., is proposed to include strain JC1077.

**A305**

**한국산 *Cordyceps hepialidicola*의  
분류학적 특성**

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국내에서 채집된 *Cordyceps hepialidicola*의

형태학적 특성과 분자생물학적 방법을 통한 분류를 시도하였다. 상기 동충하초는 박쥐나방의 애벌레를 기주로 하여 발생하였으며, 애벌레의 머리끝에서 1-3개의 자실체를 형성하였다. 자실체의 크기는 3-10 cm X 0.12-0.2 cm, 자낭각은 32 X 55 mm, 자낭은 1.5 X 43.3 mm의 크기였으며, 자낭포자는 1-2 X 7-8 mm의 크기로 직사각형 형태였다. ITS 영역을 PCR 기법으로 증폭하여 530 bp 크기의 product를 얻었으며 염기서열을 분석한 결과, *C. militaris*와는 91 %, *C. nutans*와는 88 %의 identity를 보였다.

**A306**

***Sporobolomyces koreensis* sp. nov.,  
a Novel Yeast Species Isolated from  
*Lilium* sp. in Korea**

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A novel ballistosporic basidiomycetous yeast, *Sporobolomyces koreensis* (type strain SG99-37), was described that was isolated from flowers of *Lilium* sp. in the province Kyungsangbukdo. Comparative analysis of the D1/D2 domain of 26S rDNA of all available sequences for basidiomycetous yeasts showed that the strain did not match with any other species in the database. The closest relative was *Sporidiobolus pararoseus* Fell & Tallman, but the two species differed in 6 out of 591 nucleotide positions (98.98% similarity). The strain was assigned to the anamorphic genus *Sporobolomyces* because sexual reproduction was not found. The strain could not ferment any carbon sources tested. It had Q10 as a major ubiquinone system and showed positive results for a urease and a Diazonium Blue B tests. Content of G+C was 58.5%. It differed from *Sporidiobolus pararoseus* in the following characteristics: ability to assimilate raffinose,

L-arabinose, glycerol, succinate, and citrate as a carbon sources and ethylamine, L-lysine, and cadaverine as a nitrogen sources, sensitivity to 0.01% cycloheximide, and ability to grow in high osmotic pressure (16% NaCl/5% glucose).

**A307**

**A New Yeast Species Isolated from  
Beer Sludge**

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The taxonomic position of a yeast strain H12, formerly identified as *Saccharomyces cerevisiae* H12, was reexamined. Sequence analysis of D1/D2 LSU rDNA as well as physiological and chemotaxonomical studies on strain H12 placed it under the genus *Candida*, including *Clavispora lusitaniae* (*Candida lusitaniae*) and *Clavispora opuntiae*. However, there were several differences in some physiological characteristics and 26S partial sequence (more than 5% similarity difference level), which are making the strain recognizable from other *Candida* species. The results of the present study indicated that strain H12 should be placed under the genus *Candida* as a new species. The type strain of the new species is strain H12 (= KCTC 7268<sup>T</sup>).

**A308**

***Paenibacillus taejonensis* sp. nov., a  
New Alkali-tolerant Bacterium from  
Soil**

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