

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^T).

A308

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

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