morphological and molecular studies for clarifying the interfamilial relationships with Korean representatives of Chordariales; *Acrothrix pacifica, Chordaria flagelliformis, Tinocladia crassa, Halothrix ambigua* and *Ishige sinicola*, belonging to the families mentioned above. The chordarialean algae are generally characterized morphologically by having structure with central cells, intermediate layer, long indeterminate and short determinate assimilatory filaments in macrothallus, or filamentous tufts, microscopic gametangia in life history, and subapical growth by meristematic cell situated below the terminal cell. In comparision of nuclear small-subunit rDNA Sequences together with retrieved sequences from GenBank, the Korean representatives of the families of Chordariales did not form a monophyletic group. This result agrees with the reports on the phylogenetic relationships of brown algae dealing with only a few Chordariales species (Tan 1993, Siemer *et al.* 1998).

A214

A Phylogenetic Relationship of *Porphyra suborbiculata* Kjellman and *P. okamurae* Ueda Based on Nuclear SSU rDNA and ITS 1 Sequences

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Porphyra (Bangiales, Rhodophyta) species, edible marine algae, currently include approximately 130 species in the world. Fourteen species and two forms have been reported in Korea. Among these taxa, *P. okamurae* that grows on the eastern coast is characterized by having round, ovate or obovate shaped blade, while *P. suborbiculata* has a funnel-shaped one. Therefore, they were described as independent species each other (Ueda, 1932). However, *P. okamurae* resembles *P. suborbiculata* in reproduction; division formulas of spermatangia and carposporangia,and a microscopic spinulate process, except for differences of the range of distribu tion and appearance. Allozyme analysis also shows no difference between the two species. For these reasons, Hwang (1994) treated these taxa as two subspecies of one identical species, *P. suborbiculata*. In this research, their taxonomic status was reexamined by studying the morphology, reproduction, biogeography, nuclear small subunit rDNA (SSU rDNA) and internal transcribed spacer 1 (ITS 1) sequences. Although they were apparently distinguished by the biogeographic distribution, nuclear SSU rDNA data indicated an identical sequence, except for the difference of number of introns, which varied in other Porphyras as well (Kunimoto, 1999). The ITS 1 sequences from 10 populations ranged 271-276 bp in length. The final data matrix alignment consisted of 277 characters and the pairwise sequence divergence ranged 0-1.12%. Our molecular data indicated that *P. okamurae* and *P. suborbiculata* were conspecific, and could not be separated as independent subspecies.

A215

Interrelationship among the Genera of Dictyotaceae (Dictyotales, Phaeophyta) Based on SSU and RuBisCo Spacer Region Sequence

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A phylogeny of marine Dictyotaceae was inferred by several methods from nucleotide sequences of nuclear gene encoding small subunit rRNA and plastid gene RuBisCo from 15 species in 8 genera. Sequence

divergence of SSU is relatively large, especially in Zonariae. In phylogenetic analysis including other phaeophytes, *Zonaria* was on the paraphyletic clade. The species of Dictyotae are more related to each other's than species of Zonariae to each other. 750 bp were aligned in RuBisCo spacer region including partial *rbcL* and *rbcS* for 13 species. The sequence divergence was relatively large in the *rbcL* portion but very small in the *rbcS* portion among genera. These sequence divergence pattern showed that the generic concept on *Dilophus*, *Dictyota* and *Pachydictyon* in the Dictyotaceae based on morphology need to be reviewed. And the taxonomic position of *Zonaria* should be reappraised based on other molecular and morphological characteristics

A301

Phylogenetic Relationships of *Xylobolus* and Allied Genera Based on ITS1-5.8S-ITS2 Sequences

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To elucidate phylogenetic relationships of *Xylobolus* and allied genera, nuclear ribosomal ITS1-5.8S-ITS2 regions from 23 strains were analyzed. Our results show that members of *Xylobolus* form a polyphyletic group and are merged into the genus *Acanthophysium*. The *Stereum* subgenus *Acanthostereum* proved to be genetically not related with other *Stereum* and thus considered having different lineages; *Stereum illudens* was grouped into *Xylobolus* and *Stereum peculiare* was grouped into *Acanthophysium*. Due to ITS sequences and taxonomic considerations on morphological characters, we propose to transfer *S. peculiare* into *Acanthophysium*.

A302

Characterization of Strains with the *Lactobacillus casei* Group and the *Lactobacillus acidophilus* Group by Automated Ribotyping

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A total of 91 type and reference strains of the *L. casei* group and the *L. acidophilus* group were characterized by the automated ribotyping device Riboprinter^{R} microbial characterization system. The *L. casei* group was divided into 5 (C1~C5) genotypes at a similarity level of 50% by ribotyping as follows: *L. paracasei* strains (C1and C3), *L. rhamnosus* strains (C2), *L. casei* strains (C1 and C5) and a *L. zeae* strain (C4). Among them, *L. casei* ATCC 334 was clustered to the same genotype group as most of *L. paracasei* strains. The result corresponded to the data published previously (Dellaglio *et al.*, 1991; Dicks *et al.*, 1996). *L. casei* JCM 1134T generated a ribotype pattern that was different from the type strain of *L. zeae*. This result agreed with previous data (Tynkkynen *et al.*, 1999). The *L. acidophilus* group was divided into 14 (A1~A11, B1~B3) genotypes at a similarity level of 50% by ribotyping. *L. acidophilus* strains (A6 and A9), *L. amylovorus* strains (A3, A5, A7 and A11), *L. crispatus* strains (A1, A2, A8 and A10) and *L. gallinarum* strains (A4) generated ribotype patterns that were distinct from the patterns produced by *L. gasseri* strains (B1 and B3) and *L. johnsonii* strains (B1, B2 and B3). These results were consistent with the data published previously (Johnson *et al.*, 1980; Lauer *et al.*, 1980). Several strains were not grouped with strains of the same species. The ribotype data suggests that these strains should be reclassified as different species. This reclassification is further supported by

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 isoalted 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 monophylectic 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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