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**Phylogenetic Relationships among Extant Classes of Echinoderms Inferred from Mitochondrial 12S rDNA Sequences**  
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Using sequence data derived from 12S rDNA, we have investigated the phylogenetic relationships among five extant classes of echinoderms such as crinoids, asteroids, ophiuroids, echinoids, and holothuroids. About 300 bp of 12S rDNA were determined for one species in each class and phylogenetic trees were constructed by the maximum likelihood (ML), maximum parsimony (MP), and neighbor joining (NJ) methods, with a hemichordate as an outgroup. All the trees constructed by these methods have the same tree topology except relationships among Ophiroidea, Echinoidea, Holothuroidea in ML tree. The results suggested that the phylum Echinodermata is divided into two groups such as Asterozoa and Crinozoa-Ophirozoa-Echinozoa-Holothurozoa. As a result, identical relationships among three phylogenetic trees of ML, MP and NJ have been established. Particularly, in case of ML phylogenetic tree, a close relationship has been shown with echinoids and holothuroids which have never been proved with MP and NJ phylogenetic trees. It can be concluded that holothuroids is highly advanced form with echinoderms and also has a close relationship with echinoids in ML phylogenetic tree. The relationships of holothuroids and echinoids coincide with results based on previous 18S rDNA sequences and fossil records.

A701

**Molecular Phylogenetic Characterization of X-Bacteria in *Amoeba proteus* as a *Legionella* Species**  
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The X-bacteria which initiated organismic association with D strain of *Amoeba proteus* in 1966 as parasites have been changed to obligate endosymbionts on which the host nucleus depends. The identity of the X-bacteria has not been determined due to the difficulty in cultivating the bacteria in vitro. As the life cycle of X-bacteria is similar with that of *Legionella* species in soil amoebae, we applied polymerase chain reaction (PCR)-method with specific primers aimed at *Legionella* species for the detection and cloning of 16S rRNA gene. In addition we cloned RNA polymerase  $\beta$ -subunit gene (*rpoB*) of the X-bacteria in genomic library tagging. A phylogenetic analysis of 16S rRNA gene placed the bacterium within a unique monophyletic group containing all other members of the genus *Legionella*. The phylogeny from *rpoB* and *mip* gene further confirmed the taxonomic context of X-bacteria as a *Legionella* species. In all three phylogeny, X-bacterium was placed apart from *Legionella*-like amoebal pathogens (LLAPs) present in soil amoeba. Thus, the endosymbiotic X-bacterium in *A. proteus* was named as *Legionella apoteus*.

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**RAPD Fingerprints of *Atractylodes* Plants for Discrimination**  
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RAPD (random amplified polymorphic DNA) fingerprints have recently been used to estimate identification and genetic relationships in plants. In this study RAPD analysis was performed to discriminate among *Atractylodes* plants. *A. membranaceus* used in Korea for herbal medicine, and *A. mongholicus* import medicine from China. Three primers out of the 15 tested, were selected on the basis of the polymorphism produced. Although obtained with a limited number of DNA primers, allow us to discriminate between *A. membranaceus* and *A. mongholicus*, even among those that cannot be distinguished on the basis of morphological traits.