

A009

Analysis of Soil Fungal Diversity of Pine Forest in Korea Based on PCR-DGGE

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Numerous and various microbial communities in soil play a fundamental role in degradation process, subsequent acquisition and translocation of nutrient to their plant host. To characterize of pine tree inhabiting soil fungi, we used the denaturing gradient gel electrophoresis (DGGE). DGGE analysis of soil samples showed 10 detectable bands. After partial 18S rDNA amplification using FR1/FF390 primer, products of PCR, 390bp, were loaded on denaturing gradient gel, excised, reamplified, cloned with λ T&A vector and sequenced. The sequence analysis were compared with known sequence in BLAST-N (NCBI, WI).

A011

Phylogenetic Studies of *Piptoporus* Based on Nuclear Ribosomal DNA Sequences

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For the phylogenetic studies of *Piptoporus* and related genera, nuclear ribosomal RNA genes of ITS and partial 28S regions from nine species of *Piptoporus* and ten related species were sequenced. *Piptoporus* was phylogenetically heterogeneous and its members consisted of six distinct groups. *Piptoporus betulinus* made a group with the members of *Fomitopsis* (*F. pinicola*, *F. palustris*, *F. feei*, *Piptoporus cretaceus*, *P. portentosus*, *P. officinalis* and *P. latinus*). *Piptoporus solomensis* grouped with *Antrodia serialis* and *A. variiformis* at the basal position of *Fomitopsis* clade composed of *F. africana*, *F. dochmia* and *F. spraguei*. *Buglossoporus pulvinus* was clustered with *F. africana* of *Fomitopsis* clade. *Piptoporus australiensis* formed one group with *Spongipellis spumeus* and *A. sichensis*. *Piptoporus pseudobetulinus* and *P. betulinus* are similar in microscopic morphologies but their phylogenetic positions were different. Present phylogenetic findings indicated that *Piptoporus* was composed of apparently artificial taxa and certain species need to be newly transferred into several different genera like *Antrodia*, *Fomitopsis*, *Polyporus* and *Datronia*.

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A010

A New Strain of *Hypocrea* that Produces Harzianum A

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Based on morphological characteristics and ITS rDNA sequence data, a new fungus was identified as a strain of *Hypocrea* that produces a trichothecene metabolite, and its cytotoxicity was evaluated against tumor cell lines. The metabolite was isolated from wheat bran culture by 50% acetone extraction, silica gel chromatography, Sephadex LH-20 chromatography and HPLC. The chemical structures were discovered by ESI- or HRFAB-MS and ¹H and ¹³C-NMR analyses, and the metabolite was determined as harzianum A with a chemical formula of C₂₃H₂₈O₆. Harzianum A showed cytotoxicity to HT1080 and HeLa cell lines with IC₅₀ values of 0.65 and 5.07 μ g ml⁻¹ respectively, and moderate to strong cytotoxicity to human cancer cell lines. This is the first report on the production of cytotoxic harzianum A by a new *Hypocrea* strain.

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A012

Phylogenetic Studies of *Perenniporia* Based on Ribosomal and RPB2 DNA Sequences

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Perenniporia s. l. is a large heterogeneous group that overlaps with several related genera in taxonomic concepts and makes the classification of polypores problematic. For the phylogenetic studies, ITS1 rDNA, partial 28S rDNA, and 6-7 regions of RPB2 DNA from 48 taxa of *Perenniporia* and related genera were sequenced and resulting phylogenetic trees were compared. The species of *Perenniporia* s. l. proved to be polyphyletic and were divided into six subgroups, *Abundisporus* (*A. fuscopurpureus*, *A. sclerosetosus*, *Loweoporus pubertatis*, *L. violaceus*), *Loweoporus* (*L. lividus*, *L. roseoalbus*, *L. tephroporus*), *Perenniporia* s. s. (*Perenniporia medullaripans*, *P. narymca*, *P. subacida*), *Perenniporiella* (*Perenniporiella micropora*, *P. neofulva*), *Truncospora* (*Perenniporia aurantiaca*, *P. ochroleuca*, *P. ohnensis*), and *Vanderbylia* (*Perenniporia delavayi*, *P. fraxinea*, *P. latissima*). And another subgroup *Ganoderma* (*G. applanatum*, *G. meredithiae*, *G. lucidum*, *G. resinaceum*, *Perenniporia robinophila*) with truncate thick-walled spores was also included in *Perenniporia* s. l.

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