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## Abstract Book

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**Abstract** The identified compounds were less in *Fuligo septica*. Some fatty acids and D-mannose were identified from fruiting body, and yellow pigments Fuligorubin A and Fuligoic acid were from plasmodium. Currently, the antibacterial activity of *Fuligo septica* had not been reported. Most myxomycetes had better inhibition on gram-positive bacteria, and no inhibition on gram-negative bacteria. In this study, the antibacterial experiments on methanol extracts and water (37 °C, 80 °C) extracts of *Fuligo septica* plasmodium and sclerotium were conducted by filter paper dispersion method. Strains were *Escherichia coli*, *Salmonella typhimurium*, *Pseudomonas pyocyaneum*, *Staphylococcus aureus* and *Bacillus subtilis*. The results showed that the methanol extracts of *Fuligo septica* had a better inhibition on *Escherichia coli* and *Bacillus subtilis*, the inhibition rates of plasmodium were 68.00% and 59.45%, and sclerotium were 38.89% and 53.45%. They had a less effect on *Salmonella typhimurium* (30.23% and 25.16%) and *Staphylococcus aureus* (22.05% and 18.87%), little effect on *Pseudomonas pyocyaneum*, while the water extracts didn't work on bacteria. In this study, the activity of enzymes in *Fuligo septica* were destroyed using methanol in extraction. It meant that the inhibition might work by chemical composition, rather than phagocytic enzymes. Early reported that crude extracts of *Physarum melleum* exhibited antimicrobial properties against *Bacillus subtilis*. It was thought that the compounds found in the crude extract that showed antimicrobial activity were unstable yellow pigments in the plasmodium. So it inferred that the methanol extracts of *Fuligo septica* may contain this ingredient.

#### A-24

##### Phylogenetic analysis of *Trichoderma* strains from paddy fields based on *tef1a* sequences

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**Abstract** Fungi belonging to genus *Trichoderma* are well known for their effectiveness in the biological control of different plant pathogenic fungi, inducing systemic resistance in crops and for promoting plant growth. Phylogeny of the 81 *Trichoderma* isolates (with emphasis on some biocontrol strains) which were belonged to six species and obtained from paddy fields in Northern Iran, was studied by sequence analyses of the translation elongation factor 1 (*tef1a*) gene. Sequences were aligned with Clustal X and GeneDoc programs. Data were analyzed by Neighbor-Joining, Maximum Parsimony and Minimum Evolution methods using PAUP 4.0b10 and MEGA programs. Phylogenetic trees of the 41 *Trichoderma* isolates inferred by all methods and programs were similar. Result showed that 14 *tef1a* genotypes can be recognized for *T. harzianum* (the most frequent species in rice fields) isolates which grouped into five

clades. Therefore, this species complex was presented the highest interspecific variability when compared with other species in this study. In contrast, only two genotypes were recognized for *T. virens*, the second most dominant species. Furthermore, sequence analyses revealed three and two haplotypes for *T. atroviride* and *T. hamatum*, respectively. Results indicated that biological control strains represented various genotypes and along with other native isolates placed in different clades. Consequently, a specific *tef1 $\alpha$*  genotype which related to antagonism was not distinguished. In addition, there was no correlation of the *tef1 $\alpha$*  haplotype with the geographic location and thus different species and genotypes were isolated from the same sampling site.

#### A-25

##### Fungal diversity in the soil of Gangwon province, South Korea

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**Abstract** The study was conducted to find the fungal diversity in the soil of Gangwon province, Korea. Sixty soil samples were collected from various places and fungi were isolated through serial dilution technique. Isolated fungi were purified and differentiated according to their morphological and microscopic characteristics. The identification of fungi was carried out by sequence analysis of internal transcribed spacer (ITS) region of the 18S ribosomal DNA (18S rDNA). A total of 75 fungal isolates were recovered and they belonged to 29 genera comprising *Acremonium*, *Actinomucor*, *Aspergillus*, *Chaetomium*, *Cladosporium*, *Cochliobolus*, *Cunninghamella*, *Dothideomycetes*, *Emericellopsis*, *Emericellopsis*, *Fusarium*, *Geomyces*, *Humicola*, *Leptosphaeria*, *Leptosphaerulina*, *Mortierella*, *Mucor*, *Neosartorya*, *Oidiodendron*, *Paecilomyces*, *Penicillium*, *Pleosporales*, *Podospora*, *Purpureocillium*, *Sordariomycetes*, *Stachybotrys*, *Talaromyces* and *Scytalidium*. Among them, *Aspergillus* spp., *Fusarium* spp., *Penicillium* spp. and *Talaromyces* spp. were the most dominant taxa in this study.

#### A-26

##### Establishment of efficient transformation system via *Agrobacterium tumefaciens* in *Tremella fuciformis*

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**Abstract** *T. fuciformis*, or white jelly mushroom, is a typical dimorphic fungus with great nutritional and medicinal value. In this study, partial cDNA sequence of  $\alpha$ -tubulin gene was amplified from *T. fuciformis* by degenerate primer PCR. The DNA and cDNA full length sequences of  $\alpha$ -tubulin gene of *T. fuciformis* were cloned by SEFA-PCR and RACE, respectively. The DNA sequence of  $\alpha$ -tubulin gene consisted of 1962 bp, containing 9 introns. The cDNA sequence of  $\alpha$ -tubulin gene consisted of 1347 bp, coding 448