

**F321**      **Terminal proteins and terminal region recognition factor of mitochondrial linear plasmids from *Pleurotus ostreatus***

Eun Kyoung Kim\* and Jung-Hye Roe

Department of Microbiology, Seoul National University

Linear mitochondrial plasmid DNAs, mlp1 and 2 were detected from *Pleurotus ostreatus*. mlp1 and 2 were linear double-stranded DNAs and the terminal proteins were covalently linked to 5' ends of plasmids. Plasmid mlp1 also contained terminal inverted repeat (TIR) sequence that is 381 bp long at both DNA ends. The terminal proteins of 70 and 73 kDa were purified from mitochondrial plasmids by digestion with Exo III nuclease. To identify an activity that recognized the terminal region of mlp1, gel retardation assay was performed with mitochondrial extract. Deletion analysis experiments demonstrated that the activity recognized 1-248 bp, but did not recognize 1-123 bp within the TIR. The amino acid sequences of the mORF1 indicated that its product was a highly basic protein. When the gel retardation assays with *E. coli* extract expressing the mORF1 and purified mORF1 protein were performed, the same results were acquired. This suggests that the product of mORF1 may recognize the terminal regions containing TIR of mlp1 as terminal region recognition factor.

**F322**      **Sequences Analysis of the Internal Transcribed Spacer (ITS) regions of ribosomal DNA in *Fusarium* spp.**

Lee, Young-Mi<sup>1</sup>\*, Young-Keel Choi<sup>2</sup> and Byung-Re Min<sup>1</sup>

1. Department of Biology, Sangmyung University

2. Department of Biology, Hanyang University

The internal transcribed regions sequences have been reported to provide reliable information concerning intra- and interspecific variation and phylogeny of fungi species. The relatedness of ten species of *Fusarium*, belonging to section *Discolor*, *Martiella*, *Roseum* and *Liseola*, was compared by sequences analysis based on direct sequencing of PCR-amplified the internal transcribed spacer region. The ITS2 region of rDNA was amplified with primer pITS3 and pITS4. Length of PCR products was approximately 150 bp and the DNA sequences of region aligned with published sequences from other fungi to identify gene-spacer junctions. The 3'end of 5.8S and 5'end of 28S nuclear rDNA were very conserved. Comparison to the published sequences of other species of *Fusarium* (EMBL data library, accession number X65477 through X65482) revealed that the DNA sequences of ITS2 region did not show homology with previously reported DNA sequences. Differences among species in the ITS2 region were occurred mainly between position 30 and 40. Only a few nucleotide substitutions were observed within each species. Considerably more differences in the ITS2 sequence were observed in *F. culmorum*. Sequences data obtained from this study will used to confirm more detailed phylogenetic relationship by electrophoretic karyotypes using Pulsed-Field Gel Electrophoresis (PFGE) in *Fusarium* species.