*Micologia Aplicada International*, 23(1), 2011, pp. 1-10

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# SEQUENCE VARIATION OF *PLEUROTUS* SPECIES COLLECTED FROM EASTERN ASIA

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Accepted for publication December 21, 2010

## ABSTRACT

**The systematic and genetic relationship among different species of *Pleurotus* mushrooms is still unclear. Because of that, 20 strains of *Pleurotus* spp. collected from differing regions, such as Korea (*P. djamor*, *P. eryngii*, *P. ostreatus*, *P. pulmonarius*), China (*P. cornucopiae*, *P. eryngii*, *P. ferulae*, *P. nebrodensis*, *P. ostreatus*), and Taiwan (*P. cornucopiae*, *P. cystidiosus*, *P. ostreatus*) were used to study their genetic make-up. In this study, we used DNA sequences of the ITS (Internal Transcribed Spacer) region to analyze the genetic diversity of *Pleurotus* strains. A few differences were found in the sequences implying that all strains belonged to *Pleurotus* regardless of the geographical origin and species. This is also supported by phylogenetic analysis, which revealed that *Pleurotus* strains collected from different environments have a little genetic variation in case of differing species. Some strains belonging to the same species showed 100% similarities, even those collected from different regions, suggesting that strains studied might be distributed from a common ancestor.**

**Key words: DNA sequences, ITS region, phylogeny, *Pleurotus* spp.**

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