



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

A. IMTIAJ<sup>1</sup>, T. S. LEE<sup>2</sup> AND S. OHGA<sup>1\*</sup>

<sup>1</sup> Division of Forest Environmental Sciences, Department of Agro-environmental Sciences, Kyushu University, Fukuoka 811-2415, Japan.

<sup>2</sup> Department of Biology, University of Incheon, Incheon 402-749, Korea.

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.

---

\* Corresponding author: Phone: +81-929483118. Fax: +81-929483116. E-mail: ohga@forest.kyushu-u.ac.jp