Identification of Retrotransposons in an Edible Mushroom *Pleurotus eryngii*

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Mushrooms are fungal groups that form characteristic spore-bearing fruiting bodies. Some of the fruiting bodies have been cultivated and consumed as healthy food. *Pleurotus eryngii*, the king oyster mushroom, is one of the most cultivated mushrooms with high commercial value. It shares more than 30% of the edible mushroom market in Korea. Its cultivation from the mycelia to full-grown fruiting bodies requires massive input of resources and human efforts for 3 months. Maintenance of the healthy mushroom spawn is the key step in the sustainable production of the mushroom. However, it has been reported that mushroom industries suffer from various spawn-related diseases including virus and bacterial infections. Moreover, some recent cases have been reported that the spawn often loses its ability to form healthy fruiting bodies due to the spawn degeneration. While we had worked on the molecular classification of the cultivars of *P. eryngii* by the employment of retrotranposon satellite amplified polymorphism analysis (REMAP), we found that the degenerated spawn contained elevated concentration of retrotranposons and the concentration appeared to be correlated with the frequency of subculture [1].

Retrotransposons (RTNs) are ubiquitous genomic elements in most eukaryotic organisms. They amplify themselves in the host genome through the transcription by host RNA polymerase and the subsequent reverse transcription by retrotransposon-encoded reverse transcriptase to generate multiple copies of their cDNA. RTNs comprise more than 40% human genome. In the mushrooms, a gypsy-type retroelement marY1 was the first identified RTN in the mushroom *Tricholoma matsutake* [2] and later in other basidiomycetes species [3-5]. The intact unit of the marY1 may be contained in the genomic DNA several to more than one thousand copies, which are equivalent to 0.05% to 5.5% of approximate 34 Mb genomic sequences of each different *Tricholoma* species [6]. The roles of RTNs have been implicated in the regulation of gene expression, evolution, and chromosome stability. Therefore it is conceivable that the mushroom spawn degeneration may relate with the activity of RTNs.

In order to investigate the diversity and the concentration of the RTNs in the genome of *P. eryngii*, we designed degenerate PCR primer sets which target 500bp conserved region of RTN reverse transcriptase gene. Sequence analyses of the PCR products revealed that the mushroom genome contains at least 26 distinct RTN reverse transcriptase genes. 66% of the RTNs were gypsy type while 16% were non-LTR RTNs. Full length DNA sequence of a RTN was determined by employing DNA walking methodology. Genes in the RTN

arranged as a typical gypsy type RTN, in the order of gag, protease, reverse transferase, RNase H, and integrase. We are conducting detailed analysis on the relationship of these RTNs with the mushroom spawn degeneration.

References

[1] QV Le, HK Won, TS Lee, CY Lee, HS Lee, and HS Ro *Mycobiology*, 35, 161, 2008.

[2] H Murata and A Yamada *Appl Environ Microbiol* 66, 3642, 2001.

[3] H Murata and Y Miyazaki *Biosci Biotechnol Biochem* **65**, 993, 2001.

[4] H Murata et al. *Biosci Biotechnol Biochem* **65**, 2297, 2001.

[5] H Murata et al. *Mycorrhiza* **15**, 179, 2005.

[6] H Murata and K Babasaki *Mycorrhiza* **15**, 381, 2005.