Nucleotide sequence of the 5.8S ribosomal RNA gene of *Lentinula edodes*

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The gene encoding the 5.8S rRNA is a part of the rDNA cluster and flanked by two internal transcribed spacer (ITS) regions. During our characterization of four *Lentinula edodes* (Shitake mushroom) strains based on ITS sequence differences, we amplified part of the rDNA cluster using the primers ITS2, ITS3, ITS4 and ITS5 by polymerase chain reaction (1). In addition to the determination of the DNA sequence of the ITS regions, we also determined the DNA sequence of the 3' end of the 18S rDNA, the 5' end of the 25S rDNA, and the entire 5.8S rDNA. The arrangement of the rRNA genes and ITS regions of this mushroom follows that of other eukaryotes. We present here the DNA sequence of the 5.8S rDNA and its flanking sequences (Figure 1). An analysis of the possible stem-loop structures led to a putative secondary structure of the 5.8S rDNA (Figure 2). This secondary structure is very similar to that originally predicted for *Xenopus laevis* (2). We found that the 5.8S rDNA of *Lentinula edodes* is very closely related to those of *Saccharomyces cerevisiae* (3) (92% homology), *Schizosaccharomyces pombe* (4) (87% homology), and *Neurospora crassa* (5) (89% homology). The base differences between the 5.8S rDNA sequence of *L. edodes* and each of those of the other three fungi occur mainly in the last stem-loop that is closest to the 3' end of the 5.8S rRNA (Figure 1).

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REFERENCES