

Exon/Intron Structure of Cu,Zn Superoxide Dismutase (SOD1) Genes from *Cordyceps militaris*, *Paecilomyces tenuipes* and *P. sinensis*

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We describe here the complete nucleotide sequence and the exon-intron structure of the Cu,Zn superoxide dismutase (SOD1) gene of *Cordyceps militaris*, *Paecilomyces tenuipes* and *P. sinensis*. The SOD1 gene of *C. militaris* and *P. tenuipes* spans 922 bp and 966 bp, respectively, and consisted of both four exons coding for 154 amino acid residues and three interspersed introns, and each exon length is identical. On the other hand, the SOD1 gene of *P. sinensis*, which contains 946 bp is consisted of five exons coding for 154 amino acid residues and four interspersed introns. Interestingly, the total length of exons 2 (180 bp) and 3 (152 bp) of *P. sinensis* SOD1 is same to that of exon 2 (332 bp) of *C. militaris* SOD1 and *P. tenuipes* SOD1. The deduced amino acid sequence of the *C. militaris* SOD1 showed 95% identity to *P. tenuipes* SOD1 and 78% to *P. sinensis* SOD1. The typical metal binding ligands of six histidines and one aspartic acid common to fungi SOD1 were all well conserved in the SOD1 of the three species. Phylogenetic analysis placed the *C. militaris* SOD1 and *P. tenuipes* SOD1 in a relatively strong cluster (86% bootstrap value), and *P. sinensis* SOD1 were unresolved within the ascomycetes group of fungal clade.