

Genomic Structure of the Cu/Zn-Superoxide Dismutase Gene in *Cordyceps militaris*

**Nam Sook Park, Kwang Sik Lee, Hung Dae Sohn,
Byung Rae Jin and Sang Mong Lee¹**

College of Natural Resources and Life Science, Dong-A University,
Busan, Korea,

¹Department of Sericultural and Entomological Biology,
Miryang National University, Miryang, Korea

Superoxide dismutase (SOD), one of the essential element of the antioxidant defense system, mainly removes O_2^- and also prevents O_2^- mediated reduction of iron and subsequent OH^- generation, which is highly toxic to the organism. This enzyme is classified into three forms based on its active site metal requirements namely Cu/Zn-SOD, Mn-SOD, and Fe-SOD. In general, Cu/Zn-SOD is present in the cytosol of eukaryotes, Mn-SOD is present in the mitochondria of both prokaryotes and eukaryotes, and Fe-SOD is found in both eubacteria and archaeobacteria. We describe here the nucleotide sequencing and genomic structure of the Cu/Zn-SOD gene in *Cordyceps militaris*. The Cu/Zn-SOD gene of *Cordyceps militaris* spans 922 bp and consisted of three introns and four exons coding for 154 amino acid residues with a molecular mass of approximately 16 kDa. The deduced protein sequence of the Cu/Zn-SOD gene of *C. militaris* was aligned to that of other known Cu/Zn-SOD from various organisms. Phylogenetic analysis resulted in a monophyletic group in the deduced protein sequences of the fungi Cu/Zn-SOD. The deduced protein sequence identity among fungi ranged from 89.4% - 67.1%.