

3-4-5. Genomic Structure and Molecular Characterization of the Superoxide Dismutase Gene of *Paecilomyces tenuipes*

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We describe here the complete nucleotide sequence and the exon-intron structure of the superoxide dismutase (SOD) gene of *Paecilomyces tenuipes*. The SOD gene of *P. tenuipes* spans 966 bp and consisted of three introns and four exons coding for 154 amino acid residues. The SOD cDNA was also cloned from *P. tenuipes*. The deduced amino acid sequence of the SOD of *P. tenuipes* showed 95.7% identity with *Cordyceps militaris* Cu,Zn SOD (SOD1), *Aspergillus fumigatus* SOD1 (88.3% identity), *Claviceps purpurea* SOD1 (88.3% identity), and 67.9%~83.3% with other fungi SOD1s. Phylogenetic analysis further confirmed that the deduced amino acid sequences of the *P. tenuipes* SOD1 gene belonged to the fungi group. The SOD1 of *P. tenuipes* did not form any helical regions in the predicted three-dimensional structure, suggesting that *P. tenuipes* SOD1 seems to be α -barrel structure. Genomic Southern blot analysis of genomic DNA suggested the presence of the *P. tenuipes* SOD1 gene as a single copy. Furthermore, the SOD1 enzyme assay showed that SOD1 activity in the late stage of *P. tenuipes* growth was 120.7 IU/mg sample and 598.4 IU/mg protein.