

Genome-Wide Assessment of Putative Superoxide Dismutases in Unicellular and Filamentous Cyanobacteria

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Abstract : Cyanobacteria are photoautotrophic prokaryotes able to grow in diverse ecological habitats, originated 2.5 - 3.5 billion years ago and brought oxygenic photosynthesis. Since then superoxide dismutases (SODs) acquired great significance due to their ability to catalyze detoxification of byproducts of oxygenic photosynthesis, i.e. superoxide radicals. Sequence information from several cyanobacterial genomes offers a unique opportunity to conduct a comprehensive comparative analysis of the superoxide dismutases family. In the present study, we extracted information regarding SODs from species of sequenced cyanobacteria and investigated their diversity, conservation, domain structure, and evolution. 144 putative SOD homologues were identified. SODs are present in all cyanobacterial species reflecting their significant role in survival. However, their distribution varies, fewer in unicellular marine strains whereas abundant in filamentous nitrogen-fixing cyanobacteria. Motifs and invariant amino acids typical in eukaryotic SODs were conserved well in these proteins. These SODs were classified into three major families according to their domain structures. Interestingly, they lack additional domains as found in proteins of other family. Phylogenetic relationships correspond well with phylogenies based on 16S rRNA and clustering occurs on the basis of structural characteristics such as domain organization. Similar conserved motifs and amino acids indicate that cyanobacterial SODs make use of a similar catalytic mechanism as eukaryotic SODs. Gene gain-and-loss is insignificant during SOD evolution as evidenced by absence of additional domain. This study has not only examined an overall background of sequence-structure-function interactions for the SOD gene family but also revealed variation among SOD distribution based on ecophysiological and morphological characters.

Keywords : comparative genomics, cyanobacteria, phylogeny, superoxide dismutases

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