



***In silico* comparative analysis and expression profile of antioxidant proteins in plants**

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ABSTRACT. The antioxidant system in plants is a very important defensive mechanism to overcome stress conditions. We examined the expression profile of antioxidant enzymes superoxide dismutase (SOD), catalase (CAT) and ascorbate peroxidase (APX) using a bioinformatics approach. We explored secondary structure prediction and made detailed studies of signature pattern of antioxidant proteins in four plant species (*Triticum aestivum*, *Arabidopsis thaliana*, *Oryza sativa*, and *Brassica juncea*). Fingerprinting analysis was done with ScanProsite, which includes a large collection of biologically meaningful signatures. Multiple sequence alignment of antioxidant proteins of the different plant species revealed a conserved secondary structure region, indicating homology at the sequence and structural levels. The secondary structure prediction showed that these proteins have maximum tendency for α helical structure. The sequence level similarities were also analyzed with a phylogenetic tree using neighbor-joining method. In the antioxidant enzymes SOD, CAT and APX, three major families of signature were predominant and common; these were PKC_PHOSPHO_SITE, CK2_PHOSPHO_SITE and N-myristoylation

site, which are functionally related to various plant signaling pathways. This study provides new strategies for screening of biomodulators involved in plant stress metabolism that will be useful for designing degenerate primers or probes specific for antioxidant. These enzymes could be the first line of defence in the cellular antioxidant defence pathway, activated due to exposure to abiotic stresses.

Key words: Antioxidant proteins; Comparative analysis; Signature pattern; Evolutionary trend