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Responses of antioxidant enzymes and their corresponding genes in rice leaf under salt stress

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Objectives

Although a number of studies have manifested the salt stress-induced responses of antioxidant enzymes in rice, there has been only limited information on the regulation of antioxidant enzymes at the transcriptional level. In this study, salt stress-induced responses of major antioxidant enzymes in rice were examined in terms of their activities and gene transcriptional profiles.

Material and Methods

Rice (*Oryza sativa* L. cv. Nipponbare) was grown hydroponically with Yoshida's nutrient solution in a growth chamber. The eighteen-day-old seedlings were treated with 130 mM NaCl. After 3, 4 and 6 days of treatment, the fully expanded 3rd leaves were harvested for analysis. The activity of antioxidant enzymes (Superoxide dismutase; SOD, Ascorbate peroxidase; APX, Glutathione reductase; GR, Catalase; CAT) was measured spectrophotometrically. For RT-PCR analysis of the mRNA expression of genes corresponding to antioxidant enzymes, specific primers were designed form the 3'-UTR regions of each of the genes used in this study by comparison and alignment with all available related genes in the NCBI and KOME databases.

Results and Discussion

- ☐ It can be suggested that Mn-SOD may be the major isoform responsible for superoxide radical scavenging in rice leaf under salt stress.
- ☐ The down-regulation of thylakoid-bound APX could be an important factor in the increase in chloroplastic H_2O_2, which may be involved in the up-regulation of stromal APX.
- ☐ It was assumed that the expression of *CatA* and *CatC* in rice leaves which were down-regulated by salt stress resulted in inhibition of CAT activity, and this led to insufficient removal of H_2O_2. Hence, manipulation of the *Cat* gene in rice could be an effective strategy to enhance the tolerance against salt stress.

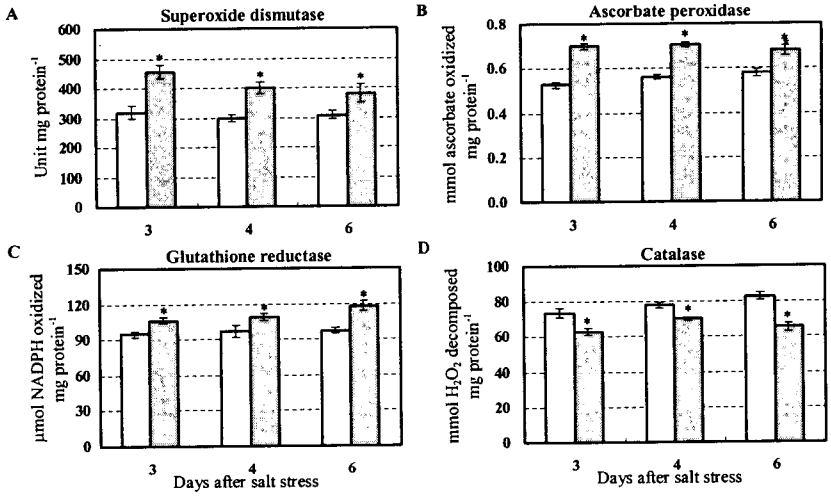

Figure 1. Effect of salt stress on antioxidant enzyme activities.

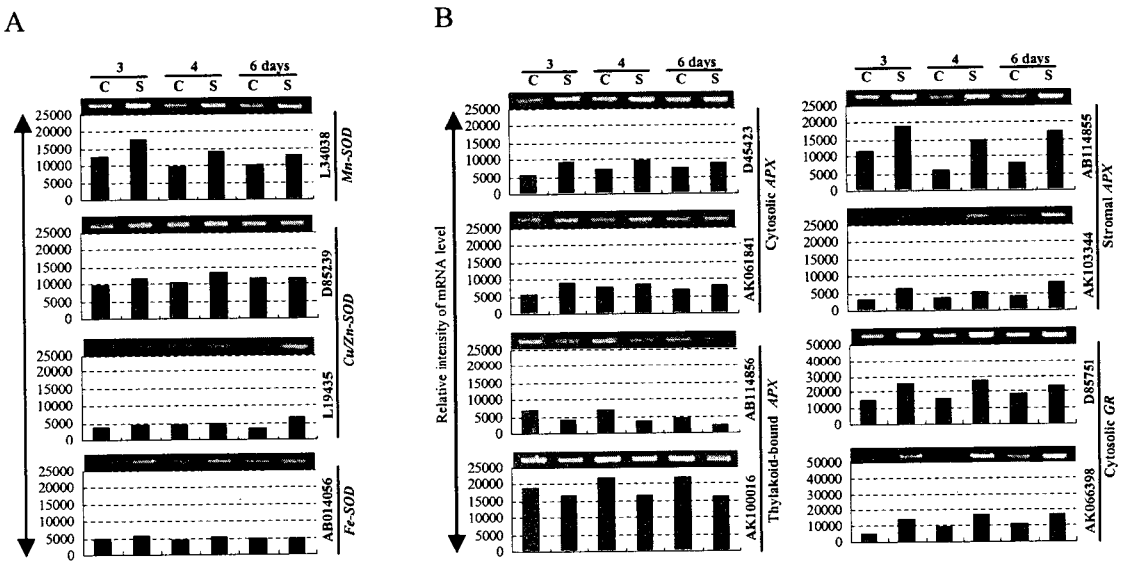

Figure 2. RT-PCR analysis of the mRNA expression of genes corresponding to the SOD (A), APX and GR (B) and Cat (C) genes. Histograms below each gel image represent relative intensity of mRNA level. AK numbers represent full length cDNA clones obtained from the KOME and NCBI database.