E234 Ozone attacks a D1-protein of Photosystem II complexes

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Ozone diffuses into cell via stomata of leaves and it destroys the cell wall and plasmamembranes. It inhibits the ionic metabolism in cell and it then changes the state of inner side of chloroplast. The results appear with the decrease of the oxygen-evolving activity. We studied why oxygen-evolving mechanisms are disturbed by ozone. *Chlamydomonas reinhardtii* CC400 is selected for this experiment since it is a unit cell organism with no cell wall. Ozone treatment for 30 minutes decreases in Fv (variable fluorescence yield) values to 70%. Fo also decreased to about 30% by the same treatment. It shows that photosynthetic apparatus partially inactivates, and the system itself is damaged in part. It also shows the decrease of Oxygen-evolving activity up to 47% by the above treatment, though 13% of Chlorophyll contents decrease occurs at same time. Thermoluminescence(TL) signals from S2QA recombination also decreases gradually as the treatment goes. Above results are concomitant with that of fluorescence when ozone attacks a photosystem II complexes. Therefore, the decrease of TL shows the complete blockage of electron transport from water to QB. Immunoblots analysis of the ozone treated PSII complexes shows the increase of the D1 protein degradation. However, we don't see any changes in the D2 protein and the external 33kDa protein. We conclude that the inhibition of oxygen evolution results from the degradation of D1 protein composing heterodimer center of PSII complexes by the ozone treatment.

E235 Expression of Cytosolic Ascorbate Peroxidase in Strawberry with Polyploid Genome

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To understand the molecular basis of the expression of cytosolic ascorbate peroxidase (ApxSC) in strawberry with polyploid genome, we isolated several cDNAs and genomic DNAs. The isolated twenty-eight cDNA clones encoding ApxSC could be grouped into seven clones (APX7, 11, 18, 20, 22, 26, and 27) on the basis of partial sequences. Sequences of seven groups were very similar, but not identical. Nuclotide sequences of three genomic clones were analyzed and showed the different sequences. These observations were constitent with those of cDNAs that showed three different residues in the deduced amino acid sequences. Three genomic clones of X5, X6, and X7 corresponded to APX26, APX20, and APX11. It implies that the expression of multiple ApxSC alleles in strawberry are codominant, which was supported by genomic blot and primer extension analysis.

Changes of peroxide concentration during its ripening in strawberry fruit was similar with the ApxSC expression patten in later stage (mature green to full red), which showed a peak. These suggest that the expression of ApxSC may be related to the peroxide production during fruit ripening of strawberry.