

## RICE ASCORBATE PEROXIDASE GENE FAMILY ENCODES FUNCTIONALLY DIVERSE ISOFORMS LOCALIZED IN DIFFERENT SUBCELLULAR COMPARTMENTS

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Ascorbate peroxidases (APx) play a key role in the elimination of toxic amounts of intracellular H<sub>2</sub>O<sub>2</sub>. In higher plants, APx are encoded by a multigene family and the different isoforms are classified according to their subcellular localization. Soluble isoforms are found in the cytosol and chloroplast stroma, while membrane-bound isoforms are found in the peroxisomes and chloroplast thylakoids. APx subcellular location is determined by the presence of targeting peptides and transmembrane domains in the amino- and carboxy-terminal regions of the proteins. Eight APx genes were identified in the rice (*Oryza sativa* L.) genome through *in silico* analysis: 2 cytosolic isoforms, 2 putative peroxisomal isoforms and 4 putative chloroplastic ones. We are studying the subcellular localization of rice APx isoforms using GFP-fusion proteins in BY-2 tobacco cells and transgenic rice plants. Our first results showed that in accord with the initial prediction, OSAPX3 was localized in the peroxisomes. Conversely, the OSAPX6-GFP fusion protein was found in mitochondria of the BY-2 cells, in contrast to the chloroplastic location predicted by sequence analysis. The analysis of the phylogenetics and structural organization of APx genes indicate that the different APx isoforms arose by a complex evolutionary process involving several gene duplications and suggest a close relationship among proteins located in the same subcellular compartment.