Sulfate is the predominant sulfur source for plants. After uptake from the soil via specific transport proteins into plant roots, sulfate is activated by the enzyme ATP-sulfurylase to APS. ATP-sulfurylase activity in plants is detectable in green tissues and roots (Ellis, 1969; Lunn et al., 1990). Isoforms of the enzyme are localized in plastids and in the cytosol (Lunn et al., 1990; Renosto et al., 1993). In mutants of *Euglena gracilis* lacking plastids an ATP-sulfurylase could be purified from mitochondria (Li et al., 1991). There is considerable evidence that activated sulfate in the form of APS is the sulfate donor for the APS-sulfotransferase reaction leading to the reductive part of sulfur assimilation (Schmidt and Jäger, 1992). Further activation of APS is achieved by the enzyme APS kinase to 3'-phosphoadenosine-5'-phosphosulfate, the substrate for sulfate transfer reactions.

We are interested in the molecular physiology of sulfate uptake and activation by higher plants, and therefore, we have isolated two ATP-sulfurylase cDNAs from *Solanum tuberosum* by functional complementation of a yeast mutant that is deficient in ATP-sulfurylase activity (met3; Klonus et al., 1994). Following the same approach we have cloned three different full-length cDNAs from *Arabidopsis thaliana* encoding ATP-sulfurylases. Coincident with our work, two deduced amino acid sequence of a third clone (ATMET3-1) encoding an ATP-sulfurylase (Table I).

The ATMET3-1 cDNA consists of 1706 nucleotides with an open reading frame of 1431 bp. The predicted polypeptide encoded by ATMET3-1 is 475 amino acids in length and has a calculated molecular mass of 53,638 D. The first 63 amino acids contain no acidic amino acids (Asp, Glu) and elevated levels of hydroxylated residues (Ser, Thr). These are typical features of a chloroplast transit peptide (Heinje et al., 1989). The ATMET3-1 polypeptide is very similar on the amino acid level to the other reported *A. thaliana* cDNAs: 72.7% to APS1 and 73.5% to APS3 (Leustek et al., 1994). When ATMET3-1 is compared to the deduced potato polypeptides STMET3-1 (Stmet3-2), there are 74.5% (73.7%) identical amino acids (Klonus et al., 1994). Only the deduced mature sequences without leader peptides are considered for these calculations. The ATMET3-1 sequence compared to the MET3 yeast sequence is 31% identical on the amino acid level, whereas no similarities can be found to bacterial ATP-sulfurylases. These data emphasize the existence of two unrelated families of ATP-sulfurylase in bacteria and eukaryotic organisms.

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1 D.K. was funded by the Schering Forschungsgesellschaft.

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ACKNOWLEDGMENTS

We thank Dr. Michele Minet (Centre de Génétique Moléculaire, Gif sur Yvette, France) for providing the A. thaliana cDNA yeast expression library.

Received August 19, 1994; accepted August 29, 1994.
Copyright Clearance Center: 0032-0889/95/107/0653/02.
The GenBank/EMBL accession number for the sequence reported in this article is X79210.

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