Diadenosine 5',5'''-P¹,P⁴-tetraphosphate (Ap₄A) Hydrolase from Tomato (*Lycopersicon esculentum* cv. Lukullus) – Purification, Biochemical Properties and Behaviour during Stress

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Peptide Sequence, Phosphonate Analogues of Ap₄A, Nucleotide Binding Site, Stress

Dinucleoside 5',5"'-P¹,P⁴-tetraphosphate hydrolase (EC 3.6.1.17) has been purified to homogeneity from tomato (*Lycopersicon esculentum*) cells grown in suspension. The purification procedure comprised ammonium sulphate fractionation following five standard chromatography steps and a final chromatography on Ap₄A-Sepharose.

The homogeneous hydrolase has a molecular mass of 20 kDa and an isoelectric point of 4.5. The enzyme hydrolyses diadenosine tetraphosphate (Ap₄A) asymmetrically to AMP and ATP. Among other naturally occurring dinucleoside oligophosphates, Ap₅A and Ap₆A are substrates whereas Ap₃A is not. Of various phosphonate analogues tested, the Ap₅A analogue, AppCH₂pCH₂ppA, was not cleaved and the Ap₃A analogue, ApCH₂CH₂ppA, was a very poor substrate. Enzyme activity is stimulated by 5 mm Mg²⁺ and inhibited by fluoride anion; $I_{50} = 6.25 \,\mu\text{m}$. The K_m value for Ap₄A is $0.8 \,\mu\text{m}$. The enzyme exhibits a broad pH optimum from pH 6.5 to 9.0. In order to analyze the protein at the molecular level an internal peptide sequence from the homogeneous enzyme was identified. Within the sequence of 17 amino acids a kinase II motif as a general part of a conserved sequence of nucleotide binding sites was found.

Against the internal peptide sequence a polyclonal antiserum was raised. By investigating the intracellular level of Ap_4A hydrolase under different kinds of environmental stress, no changes occurred in response to heat shock. But, heavy metal stress and phosphate deprivation lead to a decrease in Ap_4A hydrolase.

Introduction

Diadenosine 5',5"'-P¹,P⁴-tetraphosphate (Ap₄A) and other dinucleoside oligophosphates (DNOPs) occur in both prokaryotes and eukaryotes. Their

Abbreviations: p₄A, adenosine 5'-tetraphosphate; Ap₃A, diadenosine 5',5"'-P¹,P³-triphosphate; Ap₄A, diadenosine 5',5"'-P¹,P⁴-tetraphosphate; Ap₅A, diadenosine 5',5"'-P¹,P⁵-pentaphosphate; Ap₆A, diadenosine 5',5"'-P¹,P⁶-hexaphosphate; DNOP, dinucleoside oligophosphate; DppCH₂ppD, didiaminopurine 5',5"'-P¹,P⁴-(P²,P³-methylene)tetraphosphate; HSP, heat shock protein; IEF, isoelectric focusing; IEP, isoelectric point; PAGE, polyacrylamide gel electrophoresis; PEI, polyethyleneimine; Np_nN', pyrimidine or purine- dinucleoside 5',5"'-P¹,Pⁿn-phosphates; SDS, sodium dodecyl sulphate; TLC, thin layer chromatography.

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synthesis, demonstrated first *in vitro* by Zamecnik *et al.* (1966), can be catalyzed by some aminoacyltRNA synthetases originating from various organisms as archaebacteria, eubacteria, fungi, plants or mammals (for review see McLennan, 1992). More recently, the synthesis of Ap₄A and related compounds has been demonstrated *in vitro* for firefly luciferase (Guranowski *et al.*, 1990).

Whereas the synthesis of Ap₄A seems to be an unspecific process, there are known to be at least three different classes of specific degrading enzymes. In bacteria (Guranowski *et al.*, 1983) and in the slime mould *Physarum polycephalum* (Barnes and Culver, 1982), Ap₄A is cleaved by a symmetrically acting hydrolase. In mammals (Lobatón *et al.*, 1975) and plants (Jakubowski and Guranowski, 1983), it is hydrolyzed asymmetrically to ATP and AMP. In the yeast *Saccharomyces cerevisiae* (Guranowski and Blanquet, 1985) and some protozoa,

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Euglena gracilis and Acanthamoeba castellanii (Guranowski et al., 1995), Ap₄A is cleaved by phosphorolysis to ADP plus ATP.

Several biological functions are suggested for DNOPs. First, because the concentration of Ap₄A and other DNOPs increases dramatically in response to environmental stress, it has been suggested that they act as modulator of the cellular stress response (Johnstone and Farr, 1991). Secondly, binding sites for Ap₄A at DNA polymerase a (Baxi et al., 1994; Grummt et al., 1979) and the observation that Ap₄A may initiate replication eyes (Grummt, 1978) suggested a role in replication of DNA. This accords with the observation that proliferative activity of mammalian tissues (Rapaport and Zamecnik, 1976) and initiation of DNA replication during the S-phase of cell cycle (Weinmann-Dorsch et al., 1984) coincide with an enhanced level of Ap₄A. Although this assumed function of Ap₄A was supported by several experiments, a final proof for the involvement of Ap₄A in DNA replication is still lacking, and parts of these results could not be confirmed by others (for review see Remy, 1992). Thirdly, Ap₄A and related DNOPs have been shown to modulate activities of various enzymes of purine metabolism (Fernandez et al., 1984) and of ADP-ribosylation (Surowy and Berger, 1982). Alternatively, they act in some instances as transition state analogues e.g. for adenylate kinase (Purich and Fromm, 1972). In addition, Ap₅A and Ap₆A were found to regulate the vascular tonus (Schlüter et al., 1994). Finally, an Ap4A receptor has been demonstrated on the cell surface of mouse heart cells (Walker et al., 1993) which has a preference for binding Ap₄A relative to Ap5A and Ap6A (Hilderman et al., 1994).

The supposition that Ap₄A may play an important role in vascular plants is strengthened by the existence of a highly specific Ap₄A hydrolase (Jakubowski and Guranowski, 1983). This Ap₄A hydrolase from yellow lupin seedlings is practically the only enzyme of plant origin characterized so far. Our experience with plant cells grown in suspension as a convenient experimental model (Wasternack *et al.*, 1985) has encouraged us to check if such cells contain Ap₄A hydrolase. In preliminary trials we found that tomato cells are quite a good source of that enzyme. Here we present some of its properties

and give first sequence information on an plant Ap_4A hydrolase. After purification, studies on natural and artificial substrates were presented to categorize the type of this enzyme. To substantiate these data we determined a peptide sequence from the homogeneous protein, prepared a monospecific antibody against the peptide sequence and investigated the influence of stress on the intracellular level of Ap_4A hydrolase.

Materials and Methods

Chemicals and radiochemicals

The unlabelled nucleotides were from Boehringer (Mannheim, Germany). Ap₃A, Ap₄A, Ap₅A, Ap₆A and Gp₄G were from Sigma (Deisenhofen, Germany). Phosphonate analogues of Ap₃A, Ap₄A and Ap₅A including the analogue bis-2,6-diaminopurine β-D-ribofuranoside P¹,P⁴tetraphosphate (Dp₄D) were synthesized as previously described (Blackburn et al., 1992; Blackburn and Guo, 1991) and kindly provided by Drs. M.-J. Guo and G.M. Blackburn (University of Sheffield, U.K.). The chromatographic media as DEAE-Sephacel, Sephadex G-75 (superfine), and the FPLC-column MonoQ HR 5/5, were from Pharmacia (Freiburg, Germany). Epoxyactivated Sepharose and hydroxyapatite were from Sigma. TLC plastic sheets precoated with PEI-cellulose and a fluorescent indicator were from Merck (Darmstadt, Germany). Protein molecular weight markers were from Boehringer. Di[2,8-3H]-Ap₄A (6.2 Ci/ mmol) was kindly provided by Dr. F. Grummt (University of Würzburg, Germany).

Plant material

Tomato (*Lycopersicon esculentum* cv. Lukullus) cells were grown in suspension as described by Tewes *et al.* (1984). Inoculum of 2 x 10⁷ mid-log phase cells per 15 ml were supplemented with 100 ml fresh nutrient medium containing 30 g/l sucrose, cultivated on a rotary shaker (150 rpm) at 29 °C without light, and collected at day 3 (mid-log phase, cell density of 0.7 - 1.0). The stock culture of the tomato cell suspension culture is deposited in the Department of Biochemistry at the University of Halle/Saale, Germany.

For heavy metal stress $CdCl_2$ was added to a final concentration of $100 \, \mu m$ on the second day of culture. For heat shock 3 days old tomato cell cultures were treated subsequently as follows: variant I: 1 h 37 °C; 2 h 38,5 °C; 1 h 40 °C; variant II: 15 min 40 °C; 2,5 h 25 °C; 2 h 40 °C. Phosphate deprivation was achieved by lack of KH_2PO_4 in the culture medium.

Enzyme assays

Activities of tomato Ap₄A hydrolase were determined at 37 °C using a standard incubation that contained in a final volume of 25 µl (during enzyme purification) or 50 µl (during quantitative measurements) 50 mm 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid, pH 8.0, 5 mm MgCl₂, 100 μm dithiothreitol, 500 μm Ap₄A (or other DNOPs) and rate-limiting amounts of enzyme fraction. For quantitative measurements, incubation mixture contained radioactive substrate. The reaction was terminated, usually after 15, 30, 60 and 90 min by transferring 3 µl aliquots onto TLC sheets. During enzyme purification, the substrate Ap₄A and the products AMP, ADP and ATP were separated by TLC. Plates were precoated with silicagel and fluorescent indicator. The TLC was developed in dioxane/H₂O/ammonia (v/v/v; 6:5:1) and the products were visualized under UV light. For quantitative measurements of Ap₄A cleavage, substrate and products were separated on PEI-cellulose plates and quantified as described by Jakubowski and Guranowski (1983). Quantification of the products of cleavage of DNOP analogues was analyzed by HPLC (Jasco, Groß Zimmern, Germany; UV detector model UV-975, pump model PU-980) as specified below.

Protein analysis and immunoblotting

Protein concentrations were determined according to Bradford (1976) during enzyme purification and according to Esen (1978) for SDS-PAGE- and IEF-PAGE-analysis. SDS-PAGE was performed according to Laemmli (1970) in a 15 % separation gel followed by Coomassie-staining or silver-staining (Blum *et al.*, 1987). IEF under non-equilibrium conditions was performed in presence of 8 M urea in a pH gradient 3–10 according to Robertson *et al.* (1987). For Western blot analysis, the proteins were transferred onto nitrocellulose filters and

stained with Fast Green (Serva, Heidelberg, Germany) in order to control transfer quality.

For antibody formation, a synthetic peptide (cys-pro-glu-gly-gly-val-asp-asp-asn-gly-asp-pro) derived from the partial peptide sequence of tomato Ap₄A hydrolase (see Results) was used. The peptide was coupled to the high molecular carrier proteins bovine serum albumin and keyhole limpet hemocyanine (Calbiochem, Frankfurt, Germany) with the coupling reagent m-maleimidobenzoyl-N-hydroxysulfosuccinimide ester (Pierce, Rockford, USA) as described previously (Harlow and Lane, 1988).

Two New Zealand rabbits were immunized subcutaneously on the first, 7th and 22nd day with each 1 mg peptide coupled to bovine serum albumin and to keyhole limpet hemocyanine, supplemented with 0.2 mg adjuvants peptide and 0.5 ml Freund incomplete adjuvant (Sigma, Deisenhofen, Germany). Two weeks after third immunization rabbits were bleeded.

To detect Ap_4A hydrolase on Western blots the incubations followed a standard protocol (Harlow and Lane, 1988). The antiserum was used in a dilution of 1:1000 and the specific bound antibodies were visualized with a secondary antibody against rabbit IgG conjugated with alkaline phosphatase (Boehringer). The antiserum raised against HSP 17 was used in a dilution of 1: 1000 (Neumann *et al.*, 1987).

Preparation of the Ap₄A-Sepharose column

To prepare Ap₄A-Sepharose, 330 mg freezedried epoxy-activated Sepharose was swollen in 10 ml bidistilled H₂O, washed three times with 10 ml H₂O and suspended in 2 ml 0.4 м potassium bicarbonate, pH 11.0, containing 64 mg Ap₄A. After overnight incubation at 37 °C, the column was formed with this gel. Non-covalent bound Ap₄A was washed by alternate use of 0.1 m ammonium bicarbonate, pH 8.6, and 0.1 m sodium acetate, pH 4.5. Unoccupied free epoxy groups were blocked by incubation with 1 M ethanolamine. Before using the column the Ap₄A-Sepharose gel was washed with binding buffer (20 mm 2-[N-morpholinolethanesulfonic acid, pH 6.0, 5 mm MgCl₂, 5 mm β-mercaptoethanol, 10 % (v/v) glycerol; A. G. McLennan, Liverpool, U.K., pers. communication).

Purification of Ap₄A hydrolase

Lyophilized tomato cells were suspended in buffer C (20 mm potassium phosphate, pH 6.8, 5 mm MgCl₂, 5 mm β-mercaptoethanol, 10 % glycerol) placed on ice and disrupted by sonification. The homogenate was centrifuged for 30 min at $15,000 \times g$. The supernatant, referred to as a crude extract, was subjected to ammonium sulphate fractionation. Ap₄A hydrolase was precipitated in the range of 30-50 % saturation, resolubilized with buffer D (as buffer C but 50 mm potassium phosphate, pH 6.8), dialyzed against this buffer and centrifuged for 15 min at 10,000×g. The clear supernatant was loaded onto a Sephadex G-75 (superfine) column, equilibrated with buffer D, and was eluted with buffer D. The pooled active fractions of Ap₄A hydrolase which appeared at V_e/ $V_0 = 1.9$ were free of phosphodiesterase activity. They were applied onto a DEAE Sephacel column (equilibrated with buffer D). After a wash, elution was performed with a linear gradient of 0-500 mm KCl in buffer D. Fractions containing Ap₄A hydrolase appeared at 200 mm KCl and were pooled and dialyzed against buffer D. Up to this step, the procedure was performed three times to get a sufficient amount of the protein. Next, the active fractions were loaded onto a second DEAE Sephacel column and eluted as described for the first one. The active fractions were pooled and dialyzed overnight against buffer E (as buffer C but containing 10 mm potassium phosphate, pH 6.8) and then applied onto a hydroxyapatite column, equilibrated with buffer E. The break-through fractions containing Ap₄A hydrolase activity were free of adenylate kinase activity.

Further purification was performed by FPLC (Pharmacia) on a MonoQ HR 5/5 column equilibrated with buffer D. After loading of pooled Ap₄A hydrolase-containing fractions, the column was washed with buffer B and eluted with a linear gradient of 0–350 mm KCl in buffer D. Ap₄A hydrolase activity appeared at 140 mm KCl as a sharp peak. After dialyzing the Ap₄A-hydrolase against buffer E, aliquots of the pooled MonoQ-fractions were loaded onto a Ap₄A-Sepharose column. The column was washed first with buffer E and then with the buffer E containing 50 mm KCl. Desorption of Ap₄A hydrolase was performed with the buffer E containing, in addi-

tion to 50 mM KCl, $100 \mu\text{M}$ Ap₄A. Due to the fact that the coupled Ap₄A was degraded by Ap₄A hydrolase, the Ap₄A-Sepharose column could be used only once.

Analysis of partial amino acid sequences

The purified Ap₄A hydrolase was cleaved with CNBr. The peptides were separated on SDS-PAGE according to Schägger and von Jagow (1987) and blotted onto PVDF membrane. The dominant fragment was submitted to a pulse liquid phase sequencing system (Applied Biosystems, Weiterstadt, Germany). Phenylthiohydantoin amino acids were identified by the on-line-HPLC-systems 120 A (Applied Biosystems; Weiterstadt) by their specific retention times.

Results and Discussion

Purification of Ap₄A hydrolase

In the present paper we describe the occurrence of a specific Ap₄A hydrolase in tomato cells grown in suspension and a procedure which yields homo-

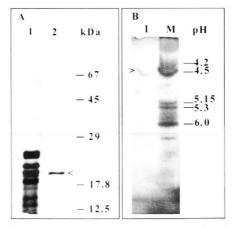


Fig. 1. SDS-PAGE (A), and IEF-PAGE (B) of tomato Ap₄A hydrolase. In (A) purification of hydrolase to homogeneity by affinity chromatography on Ap₄A-Sepharose is documented. Only one band (arrow in lane 2) appeared in the elute fraction, whereas the break-through fraction (lane 1) still contained other proteins. Molecular weight markers are given on the right margin. In (B) IEP was determined by IEF-PAGE under non-equilibrium conditions in the presence of 8 м urea and a pH gradient from 3 to 10. For lane 1 0.1 μg homogeneous Ap₄A hydrolase was used and compared with markers (M) whose IEPs are given on the right margin. Ap₄A hydrolase is indicated by an arrow.

Purification steps	Total protein [mg]	Specific activity ^a [nmol/mg protein×min]	Purification (-fold)		
Crude extract	1,400	104 ^b	1		
Dialysed ammonium sulphate (30–50%) precipitate	216	298 ^b	2.9		
Sephadex G-75 (superfine)	22.4	2,410	23.2		
DEAE-Sephacel I	1.56	11,384	109.5		
DEAE-Sephacel II	1.07	19,833	190.7		
Hydroxyapatite	0.214	42,584	407.4		

Table I. Purification of Ap₄A hydrolase of tomato cells grown in suspension.

468,750

0.002

geneous enzyme. The purification procedure of Ap₄A hydrolase from tomato cells is summarized in Table I. After FPLC purification step at a MonoQ column, a 4,500-fold purification was achieved. For getting homogeneous protein a purification step at a Ap₄A-Sepharose column was added. Since Ap4A was used as the eluent in this affinity chromatography step, quantitative determination of Ap₄A hydrolase activity could not exactly be performed at this stage without further loss of homogeneous protein. However, homogeneity of the protein has been demonstrated by SDS-PAGE (Fig. 1A, lane 2). Additionally, after two-dimensional electrophoresis using denaturing IEF (pH 4.5 to 7.5) followed by SDS-PAGE, only a single spot was observed (data not shown). The achieved Ap₄A hydrolase of different steps of purification was stable at -20 °C for several month.

Properties of Ap₄A hydrolase

FPLC (MonoQ)

Homogeneous Ap_4A hydrolase of tomato, obtained after affinity chromatography on Ap_4A -Sepharose was subjected to one-dimensional SDS-PAGE and approximate molecular mass of 20 kDa was determined (Fig. 1A, lane 2). Due to the binding of Ap_4A hydrolase at pH 6.8 on DEAE-Sephacel, an acidic IEP was indicated. Using IEF-PAGE an IEP of 4.5 was determined (Fig. 1B). With Ap_4A as a substrate, the hydrolase exhibited an apparent K_m value of 0.8 μ m.

By recording initial velocities of Ap₄A hydrolase activity at various concentrations of Mg²⁺,

 $\rm Mn^{2+}$ or $\rm Co^{2+}$, maximal activity was found with $\rm Mg^{2+}$ above 5 mm, whereas with 5 mm $\rm Mn^{2+}$ only half of full enzyme activity was found. With $\rm Co^{2+}$, a weak stimulation of $\rm Ap_4A$ hydrolase activity (about 35% of that found with $\rm Mg^{2+}$) was observed at 1 mm. Without divalent cations no $\rm Ap_4A$ hydrolase activity was detectable.

4.507.0

To determine pH dependence standard incubation mixture was used with varying pH range between 5.7 and 11. The pH optimum for Ap_4A hydrolase was broad between pH 6.5 to 9.0 with a maximum at 6.8.

Among the naturally occurring DNOPs, Ap_4A , Ap_5A , Ap_6A and Gp_4G were found to be substrates of the tomato Ap_4A hydrolase. Corresponding nucleoside triphosphates appeared always as one of the reaction products. The tomato enzyme was unable to degrade Ap_3A but exhibited activity towards p_4A .

Fluoride anion (F⁻) proved to be a strong inhibitor of tomato Ap_4A hydrolase. Fifty per cent inhibition was found at 6.25 μ m. Similar values (2 - 3 μ M) were estimated for other Ap_4A hydrolases such as from yellow lupin, sunflower and marrow seeds as well (Guranowski, 1990). For the lupin Ap_4A hydrolase a noncompetitive inhibition by NaF was indicated (Guranowski, 1990).

All the properties of the tomato Ap_4A hydrolase described here are similar to those found for the enzyme from yellow lupin seeds (Guranowski, 1990; Jakubowski and Guranowski, 1983). The pH optima in the range of 6.5-9.0 was somewhat broader than that found for the lupin enzyme (pH 7.5-9.0).

^a Activity was assayed in a mixture containing of 50 mm HEPES/KOH buffer (pH 8.0), 100 μm dithiothreitol, 5 mm MgCl₂, 500 μm di[2,8-³H]-Ap₄A at 37 °C; ^b activity of all Ap₄A degrading enzymes (nmol/mg protein×min).

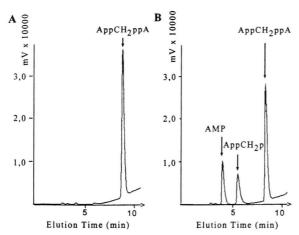


Fig. 2. HPLC analysis of the hydrolysis of AppCH₂ppA by tomato Ap₄A hydrolase, obtained after the hydroxyapatite purification step. Incubations were performed without (A) or with the enzyme (B) at 37 °C for 60 min. Aliquots were separated by HPLC on a Partisil 10-SAX column using a linear gradient of 5 to 60 % of buffer B to A (buffer A: 50 mM ammonium phosphate, pH 5.2; buffer B: 1 M ammonium phosphate, pH 5.7) at a flow rate of 1 ml per min during 20 min. After injecting 20 μ l samples onto a Partisil 10 SAX column (Merck, Darmstadt, Germany) elution profile was recorded at 254 nm and quantities were calculated using software GINA (Nuclear Interface, Münster, Germany).

Phosphonate analogues of DNOPs as substrates and inhibitors of Ap_4A hydrolase

 $\beta\beta'$ -Substituted or $\alpha\beta,\alpha'\beta'$ -disubstituted phosphonate analogues of Ap_nA (n = 3-5) were used to get some further insight on the active center of the enzyme (Guranowski et al., 1994; Guranowski et al., 1989; McLennan et al., 1989). We used compounds with substitution of the bridging oxygen(s) by methylene or halomethylene group(s) (e.g. AppCH₂ppA and ApCHClppCHClpA), and by ethylene group (e.g. AppCH2CH2ppA). In addition to that, we tested a compound with modified base moiety (DppCH₂ppD, D = diaminopurine) and ones which differed in the length of the oligophosphate chain (ApCH₂CH₂ppA, AppCH₂pCH₂ppA). As an example of the hydrolysis of Ap₄A analogues by tomato Ap₄A hydrolase, cleavage of the methylene group-containing analogue, AppCH₂ppA, analyzed by HPLC, is shown in Fig. 2. The products, AMP and pCH₂ppA were clearly detectable after 60 min of incubation, but the velocity of cleavage was 70 % lower than that of Ap₄A (Table II). The $\alpha\beta,\alpha'\beta'$ -

disubstituted phosphonate analogue of Ap₄A, which does not contain the oxygens between the αβ- and α',β'-phosphates, was not hydrolyzed (Table II). Interestingly, AppCH₂pCH₂ppA, an analogue of Ap₅A was not cleaved by the enzyme, too (Table II). With respect to the interaction with DppCH₂ppD, and AppCH₂ppA versus ApCHClppCHClpA, the tomato Ap₄A hydrolase behaved as other eukaryotic Ap₄A hydrolases (Guranowski *et al.*, 1994; McLennan *et al.*, 1989). Ap₃A is not a substrate of the tomato Ap₄A hydrolase. Interestingly, however, its analogue ApCH₂CH₂ppA is hydrolyzed to some extent (Table II).

Results of previous studies on the interaction of various Ap₄A analogues with (asymmetrical) Ap₄A hydrolases concerning the regiospecificity of hydrolysis allowed to propose a model of action of the eukaryotic Ap₄A hydrolases (Lazewska and Guranowski, 1990; McLennan *et al.*, 1989). The most important feature of this enzyme action is that it recognizes four phosphate residues and cleaves by addition of water at the "fourth" phosphate (P⁴) from the more strongly bound nucleotide residue with scission of the P⁴-O-P³ bond both in Ap₄A and Ap₅A (Guranowski *et al.*, 1994). Moreover, the enzyme site which recognizes the NTP moiety of a substrate tolerates some modifications in the oligophosphate chain of that moiety.

Lack of cleavage observed by us for AppCH₂pCH₂ppA is in line with that model. Neither of the two "fourth" phosphorus atoms of this symmetrical analogue can be attacked by a water oxygen because they have a CH₂ bridge to the adjacent phosphorus whose properties deny this mode of cleavage.

The much slower hydrolysis observed for the ethylene analogue of Ap₃A, ApCH₂CH₂ppA, suggests that the tomato Ap₄A hydrolase can also operate by a "frame shift" mechanism as proposed for the Ap₄A hydrolases acting on various analogues by McLennan *et al.* (1989). It is possible that the spatially extensive ethylene group may bridge the binding site for the "second" phosphorus in the NTP site of the hydrolase.

We have also examined inhibition of Ap₄A hydrolase activity by DNOP analogues described above, and estimated inhibition constants using the Ez-Fit software (Perella Scientific Inc., USA). All these compounds are competitive inhibitors.

	Compound									
АррррА	R-O-P-O-P-O-P-O-R O. O. O. O.	100	0.8 (K _m)							
Ap ₄ A-analogue: AppCH ₂ ppA (1)	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	29.3	0.6 (+/-0.11)							
ApCHCIppCHCIpA (2)	R-O-P-CHCI-P-O-P-CHCI-P-O-R	0	6.9 (+/-2.1)							
DppCH ₂ ppD (3)	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	5.3	0.4 (+/-0.08)							
Ap ₃ A-analogue: ApCH ₂ CH ₂ ppA (4)	O O O O O O O O O O O O O O O O O O O	0.5	735 (+/-188)							
Ap ₅ A-analogue: AppCH ₂ pCH ₂ ppA (5)	R-O-P-O-P-CH ₂ -P-CH ₂ -P-O-P-O-R	0	0.8 (+/-0.22)							

Table II. Kinetic constants of purified tomato Ap₄A hydrolase for Ap₄A and its analogues.

Most of them show K_i value in the range of the K_m value for Ap_4A , whereas for the Ap_3A analogue, $ApCH_2CH_2ppA$, the K_i value is two orders of magnitude higher (Table II).

Partial amino acid sequence of Ap₄A hydrolase

For the first time a peptide sequence of an asymmetrical cleaving Ap₄A hydrolase of plants was estimated by microsequencing of a dominant fragment obtained after CNBr cleavage. The sequence of 17 amino acids length is shown in Fig. 3A. Interestingly, a part of this sequence is in accordance with the consensus sequence for one part of a trimeric nucleotide binding motif, a so-called kinase II motif (Traut, 1994). This motif is characterised by an invariant aspartate which coordinates a divalent metal ion (e.g. Mg²⁺ of Mg-ATP) in order to fix the phosphate residue of NTP. The motif

was already found within the protein sequences of AMP kinase, ras p21 and actin (Traut, 1994). The detection of the kinase II motif in the partial sequence of Ap₄A hydrolase supports the above described model of its catalysis, in which the NTP moiety of a DNOP molecule is fixed in a pocket as part of the active center (McLennan *et al.*, 1989). In Fig. 3B a sequence comparison with other representative kinase II sequence motifs from different NTP-binding proteins is shown.

During preparation of this manuscript the first cDNA sequence of an asymmetrically cleaving Ap₄A hydrolase (human) was described (Thorne *et al.*, 1995). A comparison between the tomato peptide sequence and the deduced protein sequence of the human Ap₄A hydrolase shows 38.9 % identity (exact correspondence) and 72.2 % similarity (conservative substitution; Fig. 3C).

A

В

Protein	Source	Kinase-II-motif									
AMP kinase	porcine	⁸⁹ G F L I D G Y									
Actin	human	l:::l:. 152g I V L D S G D G V									
Ap ₄ A hydrolase	tomato	: . : : . : *G G V D D N(E)D P T									

C

Ap ₄ A hydrolase (tomato)	R	X	Α	Α	N	T	P	D	(E)	N	D	D	V	G	G	Q	P	Μ
	1	:	1	:	:			1	1	:		:			1	:		
Ap ₄ A hydrolase (human)	R	L	Α	T	E	L	D	D	E	G	P	\mathbf{E}	V	Н	G	K	P	P

Generation of an antiserum directed against an internal Ap₄A hydrolase peptide sequence

Fig. 3. (A) Partial amino acid sequence of Ap₄A hydrolase of tomato. The arrow indicates the CNBr cleaving site.

Residues in bold are part of a nucleotide binding site, a so-called kinase II motif (Traut, 1994), with an invariant aspartate (underlined). (B) Sequence comparison between the kinase II motifs of different NTP-binding proteins and the partial peptide sequence of Ap₄A hydrolase. Identical amino acids are marked by (I), conservative substitutions are marked by (•) and lack of similarities is marked by (•). (C) Se-

quence comparison between the partial amino acid sequence of tomato Ap₄A hydrolase and the corresponding sequence of human Ap₄A hydrolase

Our data related to the kinetic and molecular characteristics and the relation at amino acid level confirm the assumption, that Ap₄A hydrolases belong to a conserved protein family in higher eukaryotes.

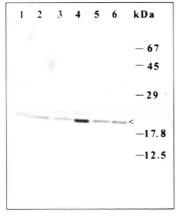


Fig. 4. Specificity of a rabbit-antibody raised against a peptide specific for tomato Ap₄A hydrolase. Different steps of purification of Ap₄A hydrolase were tested by Western blot analysis; lane 1, crude extract (15 µg); lane 2, ammonium sulphate precipitation, 35–50 %, 10 µg; lane 3, gel filtration on Sephadex G-75 superfine (5 µg); lane 4, ion exchange chromatography on DEAE-Sephacel (3 µg); lane 5, chromatography on hydroxyapatite (1 µg); lane 6, affinity chromatography on Ap₄A-Sepharose (20 ng). Ap₄A hydrolase position is marked by an arrow. Molecular weight markers are given on the right margin.

A polyclonal antiserum was raised against an internal peptide sequence of tomato Ap_4A hydrolase (see Material and Methods). The specificity of this antiserum was tested by Western blot analysis using probes of different purification steps of Ap_4A hydrolase. The antiserum recognized Ap_4A hydrolase (indicated by arrow) monospecifically in the crude extract as well as in the following steps of purification (Fig. 4, lane 1–6).

Influence of various environmental stresses on the intracellular level of tomato Ap₄A hydrolase

A significant increase of endogenous Ap₄A and related DNOPs upon environmental stress like heat shock or oxidative stress was reported several times (Brevet et al., 1985; Lee et al., 1983). This occurs in various prokaryotic and eukaryotic organisms and is thought to be a modulator in cellular responses to stress (Johnstone and Farr, 1991). Since Ap₄A is synthesized unspecifically by aminoacyl tRNA synthetases (for review see McLennan, 1992) but is cleaved by specific enzymes, its cellular level should be regulated mainly via Ap₄A degrading activities. Therefore, we studied Ap₄A hydrolase under conditions which are known to change dramatically intracellular level of Ap₄A. Using an antiserum directed against an internal peptide sequence of tomato Ap₄A hydrolase this

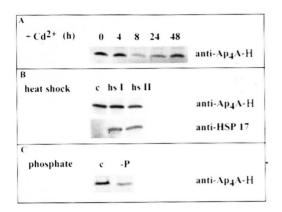


Fig. 5. Influence of environmental stress on the intracellular content of tomato Ap₄A hydrolase. Tomato cells grown in suspension were stressed according to different protocols. (A) Heavy metal stress was achieved by adding CdCl₂ to the final concentration of 100 µm to the culture medium at day 2 of culturing. At times indicated cells were harvested. (B) Heat shock was given subsequently to 3 days old tomato cell cultures using the following two types of treatment; hs I: 1 h 37 °C; 2 h 38,5 °C; 1 h 40 °C; hs II: 15 min 40 °C; 2,5 h 25 °C; 2 h 40 °C. (C) Phosphate deprivation (-P) was achieved by lack of KH₂PO₄ in the culture medium. Cells were harvested after 3 days of culturing. Western blot analysis was performed with an antiserum directed against an internal peptide of tomato Ap₄A hydrolase (anti-Ap₄A-H) or with a HSP 17-specific antiserum (anti-HSP 17), respectively. Equal amounts of protein (15 µg) were subjected to SDS-PAGE and blotted onto nitrocellulose.

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enzyme could be studied for the first time at protein level. Unexpected, the amount of Ap₄A hydrolase changed differently under the various stress. In response to CdCl₂ stress, Ap₄A hydrolase decreased transiently at about 8 h of treatment (Fig. 5A). Using two different types of heat shock treatments there was no change in the amount of Ap₄A hydrolase (Fig. 5B), whereas the heat shock response of the tomato cells is documented by appearance of the HSP 17 (Fig. 5B). Phosphate deprivation of tomato cells was accompanied by a slight, but significant decrease of Ap₄A hydrolase (Fig. 5C).

The different responses might be related to a specifically occurring cellular adaptation in response to various stress. Further studies has to elucidate a possible function of Ap₄A hydrolase in adaptive processes of plant cells.

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