protein kinase with decreasing substrate concentration has been reported by Lin and Key (1976) and was attributed to a heterogeneous substrate with one of the proteins in the mixture inhibiting the kinase.

Using more enzyme will increase phosphate incorporation for up to 3 units of the enzyme. As seen in Figure 8 the phosphate incorporation levels off with additional levels of the enzyme. As mentioned previously, there are only so many sites on the soy proteins with the appropriate sequence that can be phosphorylated with the enzyme so the presence of more enzyme will not increase the degree of phosphorylation after all available sites are phosphorylated and a steady state is attained.

The effects of enzymatic phosphorylation of soy proteins by protein kinase on alterations in the isoelectric points of these proteins is under investigation. Initial studies to determine whether the soy proteins and storage proteins like glycinin and β -conglycinin could be carried out enzymatically have proven successful. This study represents the optimization of methodology and reaction conditions for the phosphorylation of soy protein substrates with a commercial preparation of cAMPdPK. Future studies will focus on scaling up the reaction and characterizing the phosphorylated proteins in relation to their solubility under acidic conditions with a view to utilization of the economical soy proteins in various food products such as beverages, coffee whiteners, or mayonnaise.

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Identification by Two-Dimensional NMR of *myo*-Inositol Tris- and Tetrakis(phosphates) Formed from Phytic Acid by Wheat Phytase

Brian Q. Phillippy

The pathway of hydrolysis of phytic acid (myo-inositol hexakis(phosphate)) by wheat phytase from the tetrakis(phosphate) to the tris(phosphate) level was determined. Individual tetrakis(phosphate) isomers were hydrolyzed to tris(phosphates), which were purified by ion-exchange chromatography. Chemical shifts were determined by one-dimensional ¹H NMR, and structural assignments were confirmed by two-dimensional ¹H-¹H NMR. Hydrolysis of D-myo-inositol 1,2,5,6-tetrakis(phosphate) produced a mixture of D-myo-inositol 1,2,6-tris(phosphate) and D-myo-inositol 1,5,6-tris(phosphate). Hydrolysis of L-myo-inositol 1,2,3,4-tetrakis(phosphate) gave only myo-inositol 1,2,3-tris(phosphate). The role of phytic acid in inositol phosphate mediated calcium metabolism may depend on whatever functions its hydrolysis products are found to perform.

The recent discoveries of IP_6 (myo-inositol hexakis-(phosphate), phytic acid) in a variety of animal cells (Heslop et al., 1985; Morgan et al., 1987; Jackson et al., 1987; Tilly et al., 1987) bring the possibility that it plays a role in the inositol phosphate pathway regulating calcium metabolism in plant (Schumaker and Sze, 1987; Rincon and Boss, 1987) and animal (Streb et al., 1983) cells. D-I(1,4,5)P₃ has shown more potency than any other inositol phosphate in mobilizing calcium from intracellular stores (Irvine et al., 1984, 1986), specifically identified as endoplasmic reticulum (Delfert et al., 1986). D-I(1,3,4,5)P₄ can control entry of calcium into cells (Irvine and Moor, 1986) and can be dephosphorylated to D-I(1,3,4)P₃, which has

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a positive polarizing effect on membrane potential opposite to that of D-I(1,4,5)P₃ (Tertoolen et al., 1987). Compared to the other IPs, relatively large amounts of IP₅ have been found in cancer cells (Jackson et al., 1987; Tilly et al., 1987). This IP₅, assumed to be the I(1,3,4,5,6)P₅ isomer (Irvine and Moor, 1987), could be the precursor of IP₆.

Since IP_6 is present in large amounts in seeds, an appropriate enzyme to use in studying its breakdown is wheat phytase, a nonspecific acid phosphatase (Cou.tois, 1947). Wheat phytase produces predominantly L-I(1,2,3,4,5)P₅ in the initial dephosphorylation of phytic acid (Johnson and Tate, 1969). Tomlinson and Ballou (1962) used this enzyme to prepare IP₃ and IP₄ fractions from IP₆, which were identified by periodate oxidation, borohydride reduction, and dephosphorylation to alditols. They concluded that the IP₃ fraction contained I(1,2,3)P₃ and D-I(1,2,6)P₃ (configurations have been changed to correspond to currently accepted nomenclature). The IP₄ fraction contained D-I(1,2,5,6)P₄, and another IP₄ that was later identified as L-I(1,2,3,4)P₄ (Lim and Tate, 1973).

With use of improved separation techniques all of the above plus an additional IP₃ have been isolated and precursor-product relationships have been defined. Structural designations were made by two-dimensional ${}^{1}H{}^{-1}H$ correlation spectroscopy (COSY) based on data reported for other IP isomers (Cerdan et al., 1986; Lindon et al., 1987).

EXPERIMENTAL PROCEDURES

Materials. Sodium phytate and wheat phytase were obtained from Sigma Chemical Co. (St. Louis, MO). AG1-X8 200-400-mesh anion-exchange resin was from BioRad Laboratories (Richmond, CA).

Preparation of IPs. L-I(1,2,3,4)P₄ and D-I(1,2,5,6)P4 were prepared as described previously (Phillippy et al., 1987). A 30-mg portion of each IP₄ was dissolved in 10 or 20 mL of H₂O at room temperature, the pH was adjusted to 5.0, and 10 or 15 mg of



Figure 2. ${}^{1}H{}^{-1}H$ COSY of L-I(1,2,3,4)P₄ (A) and D-I(1,2,5,6)P₄ (B).

phytase was added. At hourly intervals, 0.2 mL of the mixture was added to 0.2 mL of 1.2% HCl, passed through a 0.45- μ m Millex HV-4 filter, and monitored by gradient ion chromatography (Phillippy and Bland, 1988). Additional phytase was added until most of the IP_4 had been converted to IP_3 . The sample was then diluted to 100 mL and applied to a 2×25 cm column of AG1-X8 200-400-mesh anion-exchange resin. IPs were eluted with a gradient of 2 L of 0-1 N HCl at a flow rate of 2 mL/min, and 20-mL fractions were collected in 100 test tubes. To obtain the elution profile, 1 mL from each tube was combined with 2 mL of 0.05% Fe(NO₃)₃·9H₂O in 1% HClO₄, and the absorbance was read at 290 nm. Five tubes corresponding to the center of each IP₃ peak were pooled, diluted to 500 mL, and applied to a 2-g column of AG1-X8, 200–400 mesh, at approximately 0.5 mL/min. IP₃ was eluted with 10 mL of 1 N HCl and lyophilized to remove the HCl. Samples were then dissolved in 3 mL of H_2O , and the pH was adjusted to 7.0. Following lyophilization, samples were dissolved in 99.8% ²H₂O and lyophilized once again.

NMR. ¹H NMR spectra were obtained by Spectral Data Services (Champaign, IL) on a Spectral Data Services 360-MHz NMR spectrometer at 25 °C. Approximately 5–10-mg portions of individual IPs were dissolved in 1 mL of 99.96% $^{2}H_{2}O$ and



Figure 3. Formation of IP₃s from L-I(1,2,3,4)P₄ (A) and D-I(1,2,5,6)P₄ (B) by hydrolysis with wheat phytase.

transferred to 5-mm NMR tubes. A 16000-point data set was obtained for the one-dimensional spectrum, while a 512-point data set with 256 increments and 32 transients/increment was obtained for the two-dimensional COSY. For the latter, the recycle time was 3 s. Sweep width was 2000 Hz.

RESULTS

In these studies one-dimensional ¹H NMR was used to confirm the purity of the IPs, to determine the chemical shifts of the six ring proton resonances, and to observe couplings. Correlated two-dimensional ¹H⁻¹H NMR was used to confirm the structural assignments. The one-dimensional spectrum of each IP₄ clearly indicated the presence of only one species (Figure 1). The two-dimensional spectra in Figure 2 confirmed the structural designations of L-I(1,2,3,4)P₄ and D-I(1,2,5,6)P₄ made previously (Tomlinson and Ballou, 1962; Lim and Tate, 1973). There were no cross peaks from the proton at position 2 possibly due to its distance downfield from protons 1 and 3 or interference from the large water shift at 4.8 ppm.

The fractionation patterns of the IP₃s obtained by the phytase hydrolysis of L-I(1,2,3,4)P₄ and D-I(1,2,5,6)P4 are shown in Figure 3. One peak was obtained from the former, whereas two were obtained from the latter. The one-dimensional spectra (Figures 4) indicate the purities and identifications of the three IP₃s. In Figure 5 are shown the two-dimensional spectra from which the structural assignments were made. The IP₃ from L-I(1,2,3,4)P₄ was identified as I(1,2,3)P₃. The larger IP₃ peak formed from D-I(1,2,5,6)P₄ was D-I(1,2,6)P₃ while the smaller peak proved to be D-I(1,5,6)P₃.

The chemical shifts of the IP_4s and IP_3s are listed in Table I. By comparison, it can be clearly seen that phosphorylation at any position caused the proton shift at the same position to move downfield several tenths of a ppm. Protons adjacent to phosphorylated positions also tended to move downfield. One exception, also observed by Cerdan et al. (1986), was that when position 2 was phosphorylated, the chemical shift of the adjacent proton

 Table I.
 ¹H NMR Chemical Shifts of Inositol Phosphates at pH 7

	proton position no.						
	1	2	3	4	5	6	
L-I(1,2,3,4)P4	4.07	4.91	4.14	4.32	3.61	3.93	
D-I(1,2,5,6)P ₄	4.15	4.72	3.60	3.95	4.00	4.44	
I(1,2,3)P ₃	3.90	4.96	3.90	3.68	3.19	3.68	
$D-I(1,2,6)P_3$	4.11	4.72	3.52	3.81	3.52	4.30	
$D-I(1,5,6)P_3$	4.09	4.23	3.67	3.84	4.01	4.40	

was decreased. In addition, when position 2 was phosphorylated, phosphorylation at position 3 caused the proton at position 4 to move upfield.

Couplings between trans-axial protons at adjacent positions produced the expected doublet of doublets, which collapsed into triplets with J_{H-H} of ≈ 10 Hz. However, couplings of the equatorial proton at position 2 with adjacent cis-axial protons on the order of J_{H-H} of ≈ 2 Hz (Cerdan et al., 1986) were too weak to observe. Phosphorylation at any position caused additional splitting similar to that of adjacent trans protons with J_{H-P} of approximately 10 Hz.

DISCUSSION

These results were consistent with the pattern that this enzyme displays by first removing the phosphates at positions 1 and 5 of L-I(1,2,3,4,5)P₅. In every case the phosphorylated positions were consecutive and either of the phosphates neighboring a free hydroxyl position was removed. This pattern allowed the IP₃s formed from D-I(1,2,5,6)P₄ to be assigned the D configuration with a fairly high degree of certainty. The absence of detectable D-I(1,2,6)P₃ (L-I(2,3,4)P₃) as a product from L-I(1,2,3,4)P₄ was unexpected. From Figure 3 it is evident that D-I(1,2,6)P₃ would have, if present, coeluted with I(1,2,3)P₃. Although there did appear to be some contaminant in the I(1,2,3)P₃ isolate (Figure 4A), it did not correspond to either of the other IP₃s in Figure 4B,C.



sio vis vis viv viz vio sis sis siv. Siz PPM Figure 4. ¹H NMR of $I(1,2,3)P_3$ (A), D- $I(1,2,6)P_3$ (B), and D- $I(1,5,6)P_3$ (C).

Although the biosynthetic pathway to IP_6 has yet to be determined, there is a good possibility that the intermediate IP_3 s and IP_4 s will include nonconsecutively phosphorylated isomers such as D-I(1,3,4,5)P₄ and I(1,3,4,6)P₄, which have been identified in animal cells (Balla et al., 1987). From a metabolic standpoint, separating the anabolic and catabolic pathways of IP_6 into those involving nonconsecutively and consecutively phosphorylated IPs, respectively, would seem logical.

While the levels of IP_5 and IP_6 do not appear to change as rapidly as the other IPs in cancer (Jackson et al., 1987; Tilly et al., 1987) cells, in pituitary gonadotrophs their



Figure 5. ${}^{1}H{}^{-1}H$ COSY of I(1,2,3)P₃ (A), D-I(1,2,6)P₃ (B), and D-I(1,5,6)P₃ (C).

responses were similar to that of $I(1,4,5)P_3$ (Morgan et al., 1987). The authors of the latter report suggested that a biphasic rise of $I(1,4,5)P_3$ might be caused by the coelution of an unknown isomer produced from higher IPs. If the IP₅ is predominantly $I(1,3,4,5,6)P_5$ as suggested (Irvine and Moor, 1987), the products should be different from those identified here. Hydrolysis according to the pattern observed above would lead to $I(1,4,5,6)P_4$, which has been found in turkey blood (Mayr and Dietrich, 1987), I- $(1,5,6)P_3$, and $I(4,5,6)P_3$.

The role of IP₆ in IP-mediated calcium metabolism may depend on whatever function its hydrolysis products are found to perform. Hydrolysis of the IPs derived from IP₆ could increase the levels of other isomers by increasing the levels of IP₂s and IP₁s, which could in turn be phosphorylated in different positions. A remote possibility is the conversion of D-I(1,2,5,6)P₄ to L-I(1,3,4,5)P₄ and $D-I(1,5,6)P_3$ to $L-I(1,4,5)P_3$ by the acid-catalyzed migration of cis phosphates (Tomlinson and Ballou, 1961). At this time it is unknown whether the L forms of the second messengers possess the biological activities of the D enantiomers. However, L-I(1,4,5)P_3 has recently been shown to display little if any second messenger activity (Polokoff et al., 1988; Strupish et al., 1988).

In germinating seeds, where abundant IP₆ hydrolysis occurs (Scott and Loewus, 1986), it would seem unlikely for its products not to participate to some degree in mediating calcium fluxes. If they are not restricted through compartmentation, they could compete for the kinases and phosphatases that regulate the concentrations of the biologically active isomers. It remains to be determined to what extent the isomers identified in this study accumulate in germinating seeds. Surprisingly, the most abundant IP₅ in ungerminated soybean seeds is $I(1,2,4,5,6)P_5$ of unknown enantiomeric composition (Phillippy and Bland, 1988). This IP₅, which tends to coelute with $I(1,3,4,5,6)P_5$ on ion-exchange columns (Phillippy et al., 1987; Cosgrove, 1969), could be formed from $I(1,2,4,5)P_4$ in the biosynthetic pathway of IP₆ (Igaue et al., 1982).

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ABBREVIATIONS USED

IP, inositol phosphate; IP_1 , IP_2 , IP_3 , IP_4 , IP_5 , and IP_6 , myo-inositol mono-, bis-, tris-, tetrakis-, pentakis-, and hexakis(phosphates), respectively, with isomeric lettering and numbering as appropriate; COSY, correlation spectroscopy.

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