FOR THE RECORD

Crystallization and preliminary X-ray analysis of fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase

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Abstract: Diffraction-quality crystals of the bifunctional enzyme fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase from rat testis have been obtained. The crystals were grown in the presence of ATP γ S, fructose 6-phosphate, the detergent *n*-octylglucoside, and the precipitant polyethylene glycol 4000. The crystals have the symmetry of the trigonal space group P3_{1/2}21 with a = b = 83.0 Å and c = 130.6 Å. Flash-frozen crystals diffract to beyond 2.2 Å, and native data have been collected.

Keywords: bifunctional enzyme; enzyme mechanism; kinase; phosphatase glycolysis regulation

Fructose 2,6-bisphosphate is the most potent activator of phosphofructokinase, which is a key regulatory enzyme of glycolysis. Synthesis and degradation of this unique sugar bisphosphate are catalyzed by fructose 6-phosphate, 2-kinase (Fru 6-P + ATP = Fru 2,6-P₂ + ADP) and fructose 2,6-bisphosphatase (Fru 2,6-P₂ \rightarrow Fru 6-P + P_i). Both these activities reside on a single protein, fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase. Different tissues contain tissue-specific isozymes of the

bifunctional enzyme, and these isozymes have differing relative activities of kinase and phosphatase (Uyeda, 1991). Several of these isozymes from various mammalian tissues have been characterized. They are all homodimers, consisting of subunits with M_r ranging from 54,000 to 60,000 Da. The amino acid sequences of the enzymes from liver (Darville et al., 1987; Algaier & Uyeda, 1988; Lively et al., 1988), skeletal muscle (Crepin et al., 1992), heart (Sakata & Uyeda, 1990), testis (Sakata et al., 1991), and brain (Watanabe et al., 1994) have been determined. The amino acid sequences of both catalytic domains are highly conserved among these isozymes, but the amino and carboxyl termini are completely different. These differences in the terminal peptides appear to regulate the relative activities of the kinase and the phosphatase, which in turn determine the Fru 2,6-P2 concentrations in each tissue. The activity ratio of the kinase can also be modulated by phosphorylation/dephosphorylation of either the N- or the C-terminus. Phosphorylation of the N-terminus of the liver enzyme results in inhibition of the kinase and activation of the phosphatase (van Schaftingen et al., 1981; el-Maghrabi et al., 1982; Furuya et al., 1982). In contrast, phosphorylation of the C-terminus of the heart enzyme results in activation of the kinase without any effect on the phosphatase activity (Kitamura & Uyeda, 1987; Kitamura et al., 1988). Other isozymes including the rat testis bifunctional enzyme lack such phosphorylation sites. It is known that the kinase domain resides in the amino-terminal half and the phosphatase domain in the carboxyl-terminal half of the enzyme. The kinetics of the reaction catalyzed by Fru 6-P,2-kinase follow ternary complex formation (Kitajima et al., 1984).

Enzyme mechanisms can be understood through knowledge of catalytic residues and substrate binding sites (Knowles, 1991). We are attempting to solve the crystal structure of Fru 6-P,2-kinase:Fru 2,6-Pase in order to more clearly determine the mechanism of this bifunctional enzyme and to understand the interplay of the two opposing activities. Lee et al. (1994) reported the crystallization of a truncated form of the rat liver enzyme consisting of amino acid residues 227-470. This truncated en-

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Abbreviations: Fru 6-P,2-kinase:Fru 2,6-Pase, fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase; Fru 6-P, fructose 6-phosphate; Fru 2,6-P₂, fructose 2,6-bisphosphate; Tris, tris(hydroxymethyl)aminomethane; ATPγS, adenosine-5'-(γ-thio)triphosphate; HEPES, N-(2-hydroxyethyl)piperazine-N'-ethanesulfonic acid; PEG, polyethylene glycol; n-ocylglucoside, 1-o-n-octyl- β -D-glucopyranoside; MES, morpholinoethanesulfonic acid.

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zyme contains only the Fru 2,6-Pase domain and lacks the Fru 6-P,2-kinase domain. Here we report the crystallization of the full-length Fru 6-P,2-kinase:Fru 2,6-Pase from the rat testis in the presence of ATP γ S and Fru 6-P. The crystals diffract to high resolution and are suitable for the determination of the molecular structure of the enzyme.

Initially, we attempted to crystallize wild-type rat testis Fru 6-P,2-kinase:Fru 2,6-Pase expressed in Escherichia coli (Sakata et al., 1991) and purified as described by Tominaga et al. (1993). Previously published crystallization conditions for various kinases were tried on the bifunctional enzyme. Several crystals of the enzyme were obtained using modified crystallization conditions that have yielded rabbit muscle pyruvate kinase crystals (Schmidt-Bäse et al., 1991). However, these crystals diffracted to only moderate resolution, and the crystallization was difficult to reproduce. A mutant form of the rat testis Fru 6-P,2kinase:Fru 2,6-Pase in which all four Trp residues were changed to Phe is expressed in much higher levels in E. coli than the wildtype enzyme. The mutant enzyme shows kinetic properties nearly identical to the wild-type enzyme; the only differences are a twofold higher K_m for Fru 6-P of Fru 6-P,2-kinase and a twofold higher V_{max} for Fru 2,6-P₂ of Fru 2,6-Pase (F. Watanabe, D.M. Jameson, & K. Uyeda, Enzymatic and fluorescent studies of four single tryptophan mutants of rat testis fructose 6-phosphate, 2-kinase:fructose-2,6-bisphosphatase, in prep.). Using this mutant enzyme, we were able to grow well-diffracting crystals more reproducibly. The best crystals were obtained at 4 °C using the sitting drop vapor diffusion method. Typically, a 10-mg/mL protein solution in 50 mM Tris-PO₄, pH 7.5, 5-10% glycerol, 0.5 mM EDTA, 1% PEG 400, 10 mM dithiothreitol, 3 mM MgCl₂, 1 mM ATPγS (tetralithium salt), 1 mM Fru 6-P was mixed with an equal volume of the vapor diffusion reservoir containing 50 mM succinate, pH 6.0-6.3, 10 mM HEPES, pH 7.0, 12-18% PEG 4000, 1-2% n-octylglucoside. Some crystals were also grown without 0.5 mM EDTA and 1% PEG 400 in the protein buffer. The crystals are diamond-shaped or rhombic and grow to maximal dimensions of $0.6 \times 0.25 \times 0.15$ mm within 2-7 days (Fig. 1). Crystals also grow without the kinase substrate Fru 6-P and when the succinic acid/HEPES buffer is replaced by 100 mM MES, pH 7.0, but not if ATP γ S is omitted from the solution. The detergent appears to be essential for reproducible crystal growth. When it is not included in the crystallization solution, the protein tends to precipitate. It is possible that hydrophobic surfaces on the enzyme cause it to aggregate at high concentrations, and the detergent may interact with these hydrophobic surfaces and shield them from one another.

X-ray diffraction experiments were performed on a Xuong–Hamlin area detector using graphite monochromated CuK α radiation from a Rigaku RU-300 rotating anode generator. The generator was operated at 50 kV and 100 mA. At room temperature, the crystals diffracted beyond 2.8 Å, but decayed rapidly. Upon soaking the crystals in cryoprotectant solutions (50 mM Tris-PO₄, pH 7.5, 10 mM dithiothreitol, 3 mM MgCl₂, 50 mM succinic acid, pH 6.2, 10 mM HEPES, pH 7.0, 0.5 mM EDTA, 1% PEG 400, 16% PEG 4000) containing increasing concentrations of glycerol (from 10% to 25%) for 5 min in each solution, we were able to flash-freeze the crystals in liquid nitrogen at 120 K. The frozen crystals diffract beyond 2.2 Å resolution. A native data set was collected and the space group was determined as P3_{1/2}21. The unit cell constants of the crystals as determined by the program XDS (Kabsch, 1988) are a = b = 83.0 Å, c =

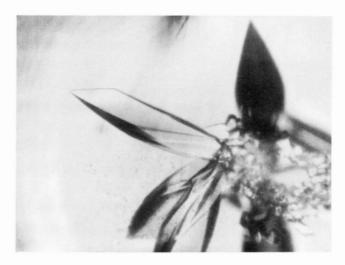


Fig. 1. Crystals of fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase. The crystals were grown at 4 °C in a 5.4- μ L drop initially containing 5 mg/mL Fru 6-P,2-kinase:Fru 2,6-Pase in 25 mM Tris-PO₄, pH 7.5, 2.5% glycerol, 5 mM dithiothreitol, 1.5 mM MgCl₂, 0.5 mM ATPγS, 0.5 mM Fru 6-P, 0.25 mM EDTA, 0.5% PEG 400, 25 mM succinic acid, pH 6.3, 5 mM HEPES, pH 7.0, 7% PEG 4000, 0.5% *n*-octylglucoside, equilibrated against a 1-mL reservoir containing 14% PEG 4000, 50 mM succinic acid, pH 6.2, and 10 mM HEPES. Dimensions of the centered crystal are 0.6 × 0.25 × 0.15 mm.

130.6 Å, and $\alpha = \beta = 90^\circ$, $\gamma = 120^\circ$. For the native data set, 144,982 reflections were measured and reduced to 26,474 unique reflections with the program Scalepack (Otwinowski, 1993) with $R_{merge}{}^6 = 0.071$. Assuming one Fru 6-P,2-kinase:Fru 2,6-Pase molecule per asymmetric unit, the Matthews coefficient is 2.41 Å³/Da, which corresponds to a solvent content of 48.9% (Matthews, 1968). Several heavy-atom derivatives of the Fru 6-P,2-kinase:Fru 2,6-Pase crystals have been prepared as part of our efforts to solve the structure by the method of multiple isomorphous replacement.

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 $^{^6}R_{merge} = \sum_{hkl} \left[\sum_i \left(\left| I_{hkl,i} - \langle I_{hkl} \rangle \right| \right) \right] / \sum_{hkl,i} \langle I_{hkl} \rangle$, where $I_{hkl,i}$ is the intensity of an individual measurement of the reflection with Miller indices h, k, and l, and $\langle I_{hkl} \rangle$ is the mean intensity of that reflection.

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