

Evidence for new phosphorylation sites for protein kinase C and cyclic AMP-dependent protein kinase in bovine heart 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase

Mark H. Rider^a, Josef Van Damme^b, Didier Vertommen^a, Alain Michel^c, Joël Vandekerckhove^b and Louis Hue^a

^aHormone and Metabolic Research Unit, International Institute of Cellular and Molecular Pathology, and University of Louvain Medical School, Avenue Hippocrate 75, B-1200 Brussels, Belgium, ^bLaboratory of Physiological Chemistry, State University of Ghent, Ledeganckstraat 35, B-9000 Ghent, Belgium and ^cLaboratory of Biological Chemistry, Faculty of Sciences, University of Mons, 21 avenue Maistriau, B-7000 Mons, Belgium

Received 7 August 1992

Bovine heart 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PFK-2/FBPase-2) was phosphorylated by incubation with [γ -³²P]MgATP and cyclic AMP-dependent protein kinase (PKA) or protein kinase C (PKC). After digestion with chymotrypsin, the phosphorylation sites for the two protein kinases were identified by peptide mapping, and microsequencing. Evidence for new phosphorylation sites for PKA (Ser-483) and PKC (Ser-84 and Ser-466) was obtained.

6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase; Phosphorylation; Bovine heart

1. INTRODUCTION

The bifunctional enzyme 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PFK-2/FBPase-2) catalyses the synthesis and degradation of fructose 2,6-bisphosphate (Fru-2,6-P₂), which is an important regulator of glycolysis [1,2]. The liver (L-type) and heart (H-type) isozymes, but not the muscle (M-type) isozyme, are substrates of the cyclic AMP-dependent protein kinase (PKA) [3].

Phosphorylation by PKA has different effects on the activities of the L- and H-type isozymes: phosphorylation of the L-type leads to PFK-2 inactivation (increase in K_m^{app} for fructose 6-phosphate (Fru-6-P) and decrease in V_{max}) and FBPase-2 activation (increase in V_{max}) [4,5], whereas phosphorylation of the H-type results in a small activation of PFK-2 (decrease in K_m^{app} for Fru-6-P) with no effect on FBPase-2 activity [6,7]. H-Type PFK-2/FBPase-2 is also a substrate of protein kinase C (PKC), but phosphorylation has no effect on its enzyme activities [7,8].

In rat liver PFK-2/FBPase-2, the phosphorylation

site for PKA lies in the N-terminal domain at Ser-32 [9], while for bovine heart PFK-2/FBPase-2 the phosphorylation sites for PKA and PKC are in the C-terminal domain at Ser-466 and Thr-475, respectively [10]. Two forms of PFK-2/FBPase-2 have been identified in bovine heart with subunit M_r s of 58,000 and 54,000 [6,7,11], which result from alternative splicing of the same primary transcript [7]. The 54,000 M_r form of bovine heart PFK-2/FBPase-2 differs from the 58,000 M_r form in that it lacks a C-terminal peptide (residues 451–510), which is encoded by exon 15 in the rat gene [12] and which contains the phosphorylation sites for PKA and PKC; however, since the 54,000 M_r form is also phosphorylated by both PKA and PKC [7], phosphorylation sites other than Ser-466 (PKA) and Thr-475 (PKC) should be present in this form. In this paper we present evidence for new phosphorylation sites for PKA and PKC in bovine heart PFK-2/FBPase-2.

2. EXPERIMENTAL

Bovine heart PFK-2/FBPase-2, PKA, and PKC were purified as described previously [7,8]. One unit of enzyme activity is the amount which catalyses the formation of 1 μ mol of product/min under the assay conditions.

The bovine heart PFK-2/FBPase-2 preparation (100 μ g) was incubated in a final volume of 0.2 ml with 50 μ M [γ -³²P]MgATP and 1 mU of either PKA or PKC for 60 min as described in [7]. Proteins were precipitated by 10% (w/v) trichloroacetic acid and the mixture was allowed to stand in ice for 30 min. The precipitated proteins were collected by centrifugation (5,000 rpm for 5 min in an Eppendorf microfuge), washed twice with 1 ml of ice-cold acetone and dissolved

Correspondence address: M.H. Rider, ICP-UCL 7529, Av. Hippocrate 75, B-1200, Brussels, Belgium. Fax: (32) (2) 762 7455.

Abbreviations: FBPase-2, fructose-2,6-bisphosphatase (EC 3.1.3.46); Fru-6-P, fructose 6-phosphate; Fru-2,6-P₂, fructose 2,6-bisphosphate; PFK-2, 6-phosphofructo-2-kinase (EC 2.7.1.105); PKA, cyclic AMP-dependent protein kinase (EC 2.7.1.37); PKC, protein kinase C (EC 2.7.1.37); PTH, phenylthiohydantoin.

in 0.2 ml of 2 M urea, 100 mM NH_4HCO_3 , pH 8.0. The phosphorylated proteins were then digested with 2.5 μg of chymotrypsin for 4 h at 35°C.

Peptides were first separated on a Vydac C18 column (0.46 \times 25 cm) equilibrated in 0.1% (v/v) trifluoroacetic acid (solvent A) using the following gradient program: 5–100% B in 100 min (where B = 0.1% (v/v) trifluoroacetic acid/70% (v/v) CH_3CN) at a flow rate of 1 ml/min. Fractions (1 ml) were collected and those containing radioactivity were lyophilised. Radiolabelled peptides were dissolved in 200 μl of 0.1% (v/v) trifluoroacetic acid and purified by narrowbore HPLC as described in [7]. Where necessary, radiolabelled peptides were further purified by narrowbore HPLC in which the aqueous phase was 10 mM sodium phosphate, pH 6, and the organic phase was 10 mM sodium phosphate, pH 6, 60% CH_3CN [7]. Purified radiolabelled peptides were sequenced using an Applied Biosystems 477A pulsed liquid-phase sequencer equipped with a 120A PTH analyser.

Peptides, TKASLRISK [13], KKCSWASYM [13] and YRR-QAVKSYK [14], corresponding to residues 17–26, 26–34 and 77–86 of bovine heart PFK-2/FBPase-2, were synthesized as described. The peptides were phosphorylated with PKA and PKC as described in Table II. K_m^{pp} values were calculated by non-linear least squares fitting of the data to a hyperbola using a computer program [15].

3. RESULTS AND DISCUSSION

The purified preparation of bovine heart PFK-2/FBPase-2, which contains a mixture of the 58,000 and 54,000 M_r forms, was phosphorylated from $[\gamma\text{-}^{32}\text{P}]\text{MgATP}$ by either PKC or PKA and digested with chymotrypsin. Fig. 1 shows the elution profile of radioactivity obtained by HPLC separation of chymotryptic peptides. PKC treatment led to the labelling of three peaks (peaks I–III) while PKA treatment led to the labelling of two peaks (peaks IV and V). The labelled peaks were further purified by narrowbore HPLC using

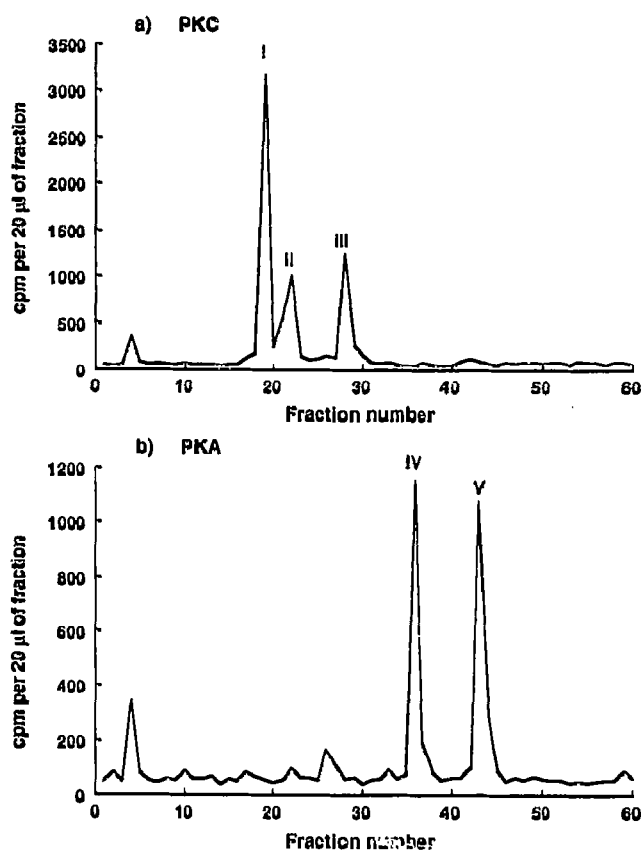


Fig. 1. HPLC of chymotryptic fragments of bovine heart PFK-2/FBPase-2 labelled with $[\gamma\text{-}^{32}\text{P}]\text{MgATP}$ and either PKC or PKA. Bovine heart PFK-2/FBPase-2 was incubated with $[\gamma\text{-}^{32}\text{P}]\text{MgATP}$ and either PKC (a) or PKA (b) for HPLC as described in section 2. Fractions (1 ml) were collected and aliquots (20 μl) were counted for radioactivity.

Table I

Amino acid sequences of phosphorylated peptides purified from bovine heart PFK-2/FBPase-2 incubated with $[\gamma\text{-}^{32}\text{P}]\text{MgATP}$ and either PKC or PKA

Peak	Amino acid sequence of purified phosphorylated peptide		Position in bovine heart PFK-2/FBPase-2 sequence
PKC	I ΔS/S	R(19.7), R(13.9), Q(31.1), A(37.9), V(33.6), K(19.3), S(1.7), Y(8.6) 8.0	78–85
	II ΔS/S	X, S(4.4), S(3.2), N(8.6), X, I(7.8), R(2.8), R(3.1), P(6.4), R(2.7), N(5.1), Y(1.8) 1.2 1.6	471–482
	III ΔS/S	R(18.8), R(11.3), N(14.7), S(1.7), F(13.9), T(3.3), P(2.4), L(1.6) 4.7	463–470
PKA	IV ΔS/S	R(2.9), R(3.3), N(12.0), S(0.5), F(19.9), T(5.0), P(5.7), L(3.2) 14.0	463–470
	V ΔS/S	X, V(15.9), G(22.0), S(4.1), R(4.4), P(6.2), L(3.4) 2.0	483–489

^{32}P -Labelled peptides from peaks I–V in Fig. 1 were purified as described for microsequencing. X represents a residue which could not be identified. ΔS/S represents the ratio of dehydroalanine/serine, calculated from the peak heights of their PTH derivatives. A low yield of PTH serine and a high ΔS/S ratio is indicative of a phosphorylated serine residue. PTH amino acid yields in pmol are given in parentheses.

Table II
Phosphorylation of synthetic peptides corresponding to sequences of bovine heart PFK-2/FBPase-2 by PKA and PKC

		Peptide sequence		
		TKASLRISEK	KKCSWASYM	YRRQAVKSYK
K_m^{pp} (μ M)	PKA PKC	N.M. 810	640 2910	N.M. 54
Stoichiometry of phosphorylation (mol/mol)	PKA PKC	0.06 0.73	0.73 0.20	0.01 0.35

The synthetic peptides were phosphorylated as described in [7]. For the measurements of K_m^{pp} , 0.2 mU of protein kinase was used and the concentration of peptide was varied from 0.01–5 mM. The stoichiometry of peptide phosphorylation was measured with 50 μ M peptide and 2 mU of protein kinase. N.M., not measured.

a linear gradient of acetonitrile as described in section 2. Table I shows the sequences of the radiolabelled peptides from peaks I–V. For each peak of radioactivity in Fig. 1 a single labelled peptide was isolated.

Table I shows that, as expected, PKC treatment led to the labelling of a peptide containing Thr-475, the phosphorylation site in the C-terminal domain described by Uyeda and co-workers [6,10]. Thr-475 was not detected in the PTH analyser, because it was phosphorylated. PKC treatment also led to the labelling of a peptide whose sequence was RRNSFTPL containing Ser-466 (Table I), the site previously shown to be phosphorylated by PKA [6,10].

In a previous study, we found that the 54,000 M_r form of bovine heart was phosphorylated by both PKA and PKC, suggesting the existence of other phosphorylation sites, and microsequencing revealed the three following peptides: 19-ASLR-22, 80-QAVKSYK-86 and 57-KLTR-60, but the phosphorylation site could not be identified [7]. Our present results show that treatment of bovine heart PFK-2/FBPase-2 with PKC led to the labelling of a chymotryptic peptide, 78-RRQAVKSY-85 (Table I), which overlaps with the sequence of the tryptic peptide, 80-QAVKSYK-86, previously described [7]. A synthetic peptide containing Ser-84 was phosphorylated by PKC with a low K_m^{pp} , whereas a peptide with the sequence ASLR, containing Ser-20, which

was previously identified as a potential phosphorylation site for PKC [7], was a poor substrate (Table II). Therefore, Ser-84 is the phosphorylation site for PKC in the 54,000 M_r form (Fig. 2).

PKA treatment of bovine heart PFK-2/FBPase-2 led to the labelling of two peptides (Table I), one of which contained Ser-466, the PKA phosphorylation site in the C-terminal domain described by Uyeda and co-workers [6,10]. The sequence of the other labelled peptide was 483-XVGSRL-489. From the published amino acid sequence, X corresponds to Ser-483 and lies in a favourable consensus sequence (RNYS-483) for phosphorylation by PKA [16]. Both Ser-466 and Ser-483 are located in the C-terminal peptide, which is deleted from the sequence of the 54,000 M_r form of bovine heart PFK-2/FBPase-2. Since, the 54,000 M_r form was phosphorylated by PKA, albeit with low stoichiometry, another phosphorylation site for PKA should exist outside the C-terminal peptide containing Ser-466 and Ser-483 [7]. Ser-29 is a potential phosphorylation site for PKA, since it is flanked on its N-terminal side by two basic lysine residues, however, a synthetic peptide containing Ser-29 was a poor substrate for PKA (Table II). The fact that Ser-29 is a poor substrate might be explained by the presence of the bulky C-adjacent tryptophan residue.

Bovine heart PFK-2/FBPase-2 is a multi-site phosphorylated enzyme (Fig. 2). PKC phosphorylates Thr-475 and Ser-84, whereas PKA phosphorylates Ser-466 and Ser-483. The interactions between the phosphorylation sites are currently being studied.

Acknowledgements: This work was supported by the Belgian State Prime Minister's Office-Science Policy Incentive Program in Life Sciences 99/93-122, Grant 20, by grants from the Belgian Fund for Medical Scientific Research (to L.H.) and from the Belgian National Fund for Scientific Research (to J.V.). We thank V. Henry for her skilled typing assistance and V. Feytons of the University of Leuven for synthesis of the peptide, YRRQAVKSYK.

REFERENCES

- [1] Hue, L. and Rider, M.H. (1987) *Biochem. J.* 245, 313–324.

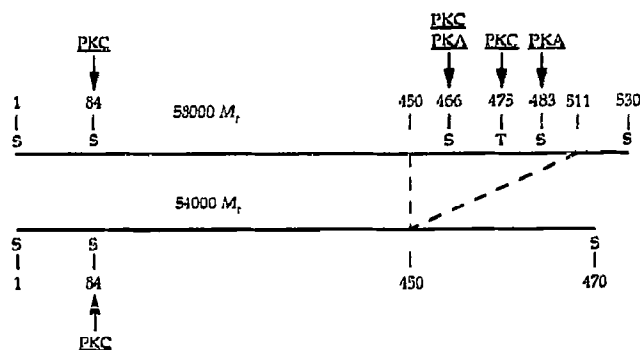


Fig. 2. Schematic representation of the phosphorylation sites in the two forms of bovine heart PFK-2/FBPase-2.

- [2] Pilkis, S.J., El-Maghrabi, M.R. and Claus, T.H. (1988) *Annu. Rev. Biochem.* 57, 755-783.
- [3] Hue, L., Rider, M.H. and Rousseau, G.G. (1990) in: *Fructose 2,6-bisphosphate* (Pilkis, S.J., ed.) pp. 173-192, CRC Press, Boca Raton, FL.
- [4] Van Schaftingen, E., Davies, D.R. and Hers, H.G. (1981) *Biochem. Biophys. Res. Commun.* 103, 362-368.
- [5] El-Maghrabi, M.R., Claus, T.H., Pilkis, J. and Pilkis, S.J. (1982) *Proc. Natl. Acad. Sci. USA* 79, 315-319.
- [6] Kitamura, K., Kangawa, K., Matsuo, H. and Uyeda, K. (1988) *J. Biol. Chem.* 263, 16976-16801.
- [7] Rider, M.H., Van Damme, J., Lebeau, E., Vertommen, D., Vidal, H., Rousseau, G.G., Vandekerckhove, J. and Hue, L. (1992) *Biochem. J.* 285, 405-411.
- [8] Rider, M.H. and Hue, L. (1986) *Biochem. J.* 240, 57-61.
- [9] Murray, K.J., El-Maghrabi, M.R., Kountz, P.D., Sukas, T.J., Soderling, T.R. and Pilkis, S.J. (1984) *J. Biol. Chem.* 259, 7673-7681.
- [10] Sakata, J. and Uyeda, K. (1990) *Proc. Natl. Acad. Sci. USA* 87, 4951-4955.
- [11] Kitamura, K. and Uyeda, K. (1988) *J. Biol. Chem.* 263, 9027-9033.
- [12] Darville, M.I., Chikri, M., Lebeau, E., Hue, L. and Rousseau, G.G. (1991) *FEBS Lett.* 288, 91-94.
- [13] Crepin, K.M., Darville, M.I., Michel, A., Hue, L. and Rousseau, G.G. (1989) *Biochem. J.* 264, 151-160.
- [14] Agostinis, P., Derua, R., Sarno, S., Goris, J. and Merlevede, W. (1992) *Eur. J. Biochem.* 205, 241-248.
- [15] Barlow, R.B. (1983) *Biodata Handling with Microcomputers*, pp. 116-121, Elsevier, Cambridge.
- [16] Kennelly, P.J. and Krebs, E.G. (1991) *J. Biol. Chem.* 266, 15555-15558.