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Tetrahymena Elongation Factor-1α Binds to Hsp70 Family Proteins

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ABSTRACT—Translation elongation factor 1α (EF-1α) catalyzes the GTP-dependent binding of aminoacyl-tRNA to the ribosome. We previously reported that Tetrahymena EF-1α induced bundles of rabbit skeletal muscle F-actin as well as Tetrahymena F-actin (Kurasawa et al., 1996) and that Ca²⁺/calmodulin (CaM) regulated the F-actin-bundling activity of EF-1α without inhibition of the binding between EF-1α and F-actin (Kurasawa et al., 1996a). In this study, we investigated EF-1α-binding proteins in Tetrahymena using a Tetrahymena EF-1α affinity column. Tetrahymena EF-1α bound directly to 74 kDa, 77 kDa, and 78 kDa proteins, in addition to CaM. The bindings of 74 kDa, 77 kDa, and 78 kDa proteins to Tetrahymena EF-1α were Ca²⁺-independent and ATP-sensitive. The N-terminal amino acid sequence of the 74 kDa protein was similar to those of 70 kDa heat shock protein (hsp70) family.

INTRODUCTION

Translation elongation factor-1α (EF-1α) catalyzes the GTP-dependent binding of aminoacyl-tRNAs to their respective mRNAs anticodons in the A site of ribosomes in the peptide elongation phase of protein synthesis (Kaziro, 1978; Moldave, 1985; Riis et al., 1990). Several recent reports indicate that EF-1α appears to have a second role as a regulator of microtubule rearrangements (Kuriyama and Borisy, 1985; Kuriyama et al., 1990; Ohta et al., 1990; Shiina et al., 1994). On the other hand, direct and indirect evidence shows that EF-1α also participates in the regulation of actin cytoskeleton (Demma et al., 1990; Yang et al., 1990; Dharmawardhane et al., 1991; Itano and Hatano, 1991). In previous paper, we demonstrated that Tetrahymena EF-1α could also bind to F-actin and form F-actin bundles (Kurasawa et al., 1996a; Kurasawa et al., 1996b; Numata, 1996). Thus, the EF-1α is regarded as regulators in the organization of microfilaments as well as microtubules.

A carrot EF-1α homolog bundled microtubules in vitro, and moreover, this bundling was modulated by the addition of Ca²⁺ and CaM together (Ca²⁺/CaM) (Durso and Cry, 1994). Kaur and Ruben demonstrated the direct interaction between CaM and the EF-1α from Trypanosoma brucei (Kaur and Ruben, 1994). Using EF-1α, actin and CaM separately purified from Tetrahymena, we demonstrated that Ca²⁺/CaM directly bound to EF-1α and did not effect on the formation of EF-1α/F-actin complex (Kurasawa et al., 1996a). In addition, Ca²⁺/CaM completely inhibited the formation of F-actin bundles by EF-1α (Kurasawa et al., 1996a). These findings suggest that the EF-1α mediates the formation of F-actin bundles and microtubule bundles by a Ca²⁺/CaM-sensitive mechanism. These reports suggest that associations between EF-1α and cytoskeleton have significance beyond translation.

To ascertain associations between EF-1α and cytoskeleton, we examined EF-1α-binding proteins using the Tetrahymena EF-1α affinity column. In this paper, we report direct binding of Tetrahymena EF-1α to 74 kDa, 77 kDa and 78 kDa proteins in Ca²⁺-independent and ATP-sensitive manner, and similarity between an N-terminal amino acid sequence of the 74 kDa protein and those of hsp70 family proteins.

MATERIALS AND METHODS

Cell culture

Cultivation of Tetrahymena pyriformis (strain W) was performed as described previously (Watanabe et al., 1994).

Electrophoresis

SDS-PAGE was performed on a 10 or 15% running gel with a 3% stacking gel according to Laemmli (Laemmli, 1970). Two-dimensional gel electrophoresis was carried out according to the method of Hironaga et al. (1981). Gels were stained with silver or Coomassie Brilliant Blue R-250.

Preparation of Tetrahymena EF-1α

Tetrahymena EF-1α was purified by the method described previously (Takeda et al., 1995).
Preparation of Tetrahymena extract

T. pyriformis cells cultivated in 500 ml culture medium for 41 hr were harvested by centrifugation at 1200g for 1 min. The cell pellet was washed twice with cold NKC solution (0.2% NaCl, 0.008% KCl, 0.012% CaCl₂, and divided into two parts. One part was resuspended in 2 volumes of extraction buffer (10 mM MES, 10% glycerol, 1 mM MgCl₂, 5 μg/ml leupeptin, 10 μM Nε-p-tosyl-L-lysine chloro-methyl ketone (TLCK), 3.1 mM NaN₃, pH 7.0) containing 1 mM CaCl₂ (E-Ca buffer). Another part was resuspended in 2 volumes of extraction buffer containing 1 mM EGTA (E-EGTA buffer). Each suspension was sonicated for 4 min at an output setting of 8 using a cell distributor (Ultra sonic Inst., Toyko, Japan). Each sonicated suspension was centrifuged at 100,000g for 1.5 hr at 0°C. The resultant supernatant prepared in the presence of 1 mM CaCl₂ or 1 mM EGTA was designated as a Ca extract or an EGTA extract, respectively.

Column chromatography

Preparations of Tetrahymena EF-1α affinity column and control BSA column were carried out using the HiTrap NHS-activated (Pharmacia Biotech, Uppsara, Sweden), according to the manufacturer’s instructions. One ml Tetrahymena EF-1α (2 mg/ml) was applied to a HiTrap NHS-activated sepharose column. The column volume was 1 ml. The coupling efficiency was about 2 mg/ml resin. Coupling of BSA to the HiTrap NHS-activated was carried out in the same manner. Column chromatography was carried out in the presence of 1 mM CaCl₂ or 1 mM EGTA. In the presence of 1 mM CaCl₂, each 25 ml of the Ca extract was applied to a Tetrahymena EF-1α column or a control BSA column equilibrated with E-Ca buffer at a flow rate of 0.1 ml/min. After loading, each column was rinsed with E-Ca buffer containing 50 mM KCl (EK-Ca buffer) at 0.1 ml/min for 270 min. Then the columns were eluted successively with EK-Ca buffer containing 1 mM ATP, EK-Ca buffer containing 1 mM GTP, EK-Ca buffer containing 1 mM EGTA, E-Ca buffer containing 150 mM KCl, E-Ca buffer containing 0.4 M KCl and E-Ca buffer containing 1.0 M KCl. On the other hand, in the presence of 1 mM EGTA, 25 ml of the EGTA extract was applied to the Tetrahymena EF-1α column equilibrated with E-EGTA buffer. After loading, the column was rinsed with EK-EGTA buffer at 0.1 ml/min for 120 min. Then the column was eluted successively with EK-EGTA buffer containing 1 mM ATP, EK-EGTA buffer containing 1 mM GTP, EK-EGTA buffer containing 1 mM EGTA, E-Ca buffer, E-EGTA buffer containing 150 mM KCl, E-EGTA buffer containing 0.4 M KCl and E-EGTA buffer containing 1.0 M KCl.

Polyclonal antibodies

Rabbit antiserum against T. pyriformis actin, tubulin and 14 nm filament protein had been previously prepared and characterized (Hirono et al., 1987; Takagi et al., 1991; Numata et al., 1983)

Amino acid sequencing

The 1 mM ATP-eluted fraction was subjected to two-dimensional SDS-PAGE and transferred to a polyvinylidene difluoride filter (Millipore, Bedford, USA). The filter was stained with Coomassie Brilliant Blue R-250. The spot containing only the 74-kD protein was excised from the membrane. N-terminal amino acid sequence of the 74-kD protein was determined by automated Edman degradation with an Applied Biosystems gas-phase sequencer (Foster City, CA, USA).

RESULTS

Tetrahymena EF-1α column-binding proteins from the Tetrahymena extract

To investigate a second role of EF-1α as a regulator of cytoskeleton organization, we examine EF-1α-binding proteins in Tetrahymena. Aliquots of T. pyriformis cell extract, prepared in a low ionic strength buffer containing 1 mM CaCl₂, were passed through the Tetrahymena EF-1α column and the control BSA column. Proteins absorbed to those columns were eluted successively with 1 mM ATP, 1 mM GTP, 1 mM EGTA, 150 mM KCl, 0.4 M KCl, and 1 M KCl, because EF-1α is a GTP-binding protein and the F-actin bundling activity of EF-1α is regulated by Ca²⁺/CaM. Fig. 1A shows SDS-PAGE of each eluate from the Tetrahymena EF-1α column. Proteins of apparent molecular weights of 78 kDa, 74 kDa, 60 kDa, 52 kDa and 50 kDa were eluted with 1 mM ATP (ATP eluate) (Fig. 1A, lane 3). The 78 kDa, 60 kDa, 52 kDa and 50 kDa proteins were eluted with 1 mM GTP (GTP eluate) (Fig. 1A, lane 5). In the ATP eluate, the 74 kDa protein was not detected, and the amount of the 78 kDa protein was less than that in the ATP eluate. On the contrary, the amounts of the 52 kDa and 50 kDa proteins in the GTP eluate increased. These results indicate that the bindings of 78 kDa and 74 kDa proteins to Tetrahymena EF-1α are ATP-sensitive. A 16.7 kDa protein was a major protein eluted with 1 mM EGTA (Fig. 1A, lanes 7 and 8). Protein of apparent molecular weight of 90 kDa, the 52 kDa and 50 kDa proteins were eluted with 150 mM and 0.4 M KCl (Fig. 1A, lanes 10, 11 and 13).

On the other hand, when Tetrahymena cell extract prepared in a low ionic strength buffer containing 1 mM EGTA was passed through the Tetrahymena EF-1α column, the 78 kDa and 74 kDa proteins were absorbed to the column, but the 16.7-kD protein was not (data not shown). These results indicate that the bindings of 78 kDa and 74 kDa proteins to Tetrahymena EF-1α are Ca²⁺-independent and ATP-sensitive, while the binding between the 16.7 kDa protein and Tetrahymena EF-1α is Ca²⁺-dependent. The major proteins seen in the Tetrahymena EF-1α column eluate were not significantly absorbed to the control BSA column (Fig. 1B).

Immunoblot analysis of the proteins in the EF-1α column eluate was performed using antibodies against Tetrahymena actin, tubulin and 14nm filament protein. We could not identify those proteins in the EF-1α column eluate (data not shown). Since Tetrahymena extract was prepared by centrifugation at 100,000 g for 1.5 hr, almost all F-actin, microtubules and 14nm filament might be removed from the extract.

The 74-kD protein is homologous to hsp70 superfamily proteins

The 1 mM ATP-eluted fraction was subjected to two-dimensional gel electrophoresis. As a result, we demonstrated that the fraction contained 78, 77, and 74 kDa proteins (Fig. 2), and that the 78 kDa protein in Fig. 1A, lane 3 contained the 78- and 77 kDa proteins in Fig. 2. The isoelectric points of these proteins were approximatory 6.0. The amino acid sequences of these proteins were then analyzed. Although only N-terminal 25 amino acid sequence of the 74 kDa protein was determined, the sequence was found to be similar to the predicted N-terminal amino acid sequences of hsp70 superfamily proteins (Craig et al., 1989; Heschl and Baillie, 1989; Domanico et al., 1993; Rubin et al., 1993; Bardwell and Craig, 1984) (Fig. 3). Previously, we detected Tetrahymena hsp70 family proteins in the cell extract of heat-shocked cells using
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Fig. 1. SDS-PAGE analysis of the proteins eluted from the *Tetrahymena* EF-1α affinity column which was loaded with a *Tetrahymena* cell extract. The *Tetrahymena* cell extract prepared with E-Ca buffer was applied to the *Tetrahymena* EF-1α affinity column (A) or the control BSA column (B). Protein fractions eluted from the *Tetrahymena* EF-1α affinity column were run on a 15% gel. The gels were silver-stained. Lanes 1 and 2, flow-through fractions; lanes 3 and 4, 1 mM ATP-eluted fractions; lanes 5 and 6, 1 mM GTP-eluted fractions; lanes 7, 8 and 9, 1 mM EGTA-eluted fractions; lanes 10, 11 and 12, 150 mM KCl-eluted fractions; lanes 13, 14, and 15, 0.4 M KCl-eluted fractions; lanes 16, 17 and 18, 1 M KCl-eluted fractions. One mM ATP-eluted fractions from the *Tetrahymena* EF-1α affinity column (A, lanes 5 and 6) contained 78 kDa and 74 kDa proteins. One mM EGTA-eluted fractions (A, lanes 7 and 8) contained 16.7 kDa protein. These proteins could not bind to the control BSA column (B). Arrowheads a, b and c indicate the 78, 74 and 16.7 kDa proteins, respectively. The apparent molecular weights (kDa) are shown on the right.
two-dimensional gel electrophoresis (Takamatsu et al., 1986). The isoelectric points and molecular weights of these hsp70 family proteins almost corresponded to those of the 78, 77, and 74 kDa proteins (data not shown). On the other hand, the 16.7 kDa protein was identified to the Tetrahymena CaM, in terms of apparent molecular weight, antigenecity, and a Ca\(^{2+}\)-dependent shift in electrophoretic mobility (see other submitted paper).

**DISCUSSION**

In this study, we found that the 74 kDa, 77 kDa and 78 kDa proteins bound to Tetrahymena EF-1\(\alpha\) in ATP-sensitive manner (Fig. 1A). The 74 kDa protein was a hsp70 homolog (Fig. 3). This is the first report of direct binding between EF-1\(\alpha\) and hsp70 homolog, although the possibility of association between EF-1\(\alpha\) and hsp70 was reported by Marchesi and Ngo (1993). They isolated multiprotein complexes from supernatants of nocodazole-arrested CHO cells. The complexes, assembled in vitro after a 37\(^\circ\)C incubation in the presence of ATP or GTP, was composed of equivalent amounts of \(\alpha\)-, \(\beta\)- and \(\gamma\)-tubulin, EF-1\(\alpha\) and hsp70. However, tubulin isoforms were not detected to bind the Tetrahymena EF-1\(\alpha\) affinity column.

The interaction of the hsp70 family member with its target proteins is transient, because release of the target proteins from the hsp 70 depend on ATP-binding (Palleros et al., 1993). We showed here that the 74 kDa, 77 kDa and 78 kDa proteins were eluted with 1 mM ATP from the EF-1\(\alpha\) column, suggesting that the 77 kDa and 78 kDa proteins may be also the hsp70 family members because they probably have an ATP-binding activity. Williams and Nelsen (1997) have reported that three members of the hsp70 family (hsp72, 73 and 78) and one member of the hsp90 family (hsp82) formed a high molecular mass complex (\(\sim 700\) kDa) with tubulin in Tetrahymena. Although we could not detect tubulin and hsp90 in eluate from the Tetrahymena EF-1\(\alpha\) column, it is possible that the 74 kDa hsp70 homolog, 77 kDa and 78 kDa proteins in the 1 mM ATP-eluted fraction may correspond to hsp72, 73, and 78 respectively and that these members of the hsp70 family may form complexes and function as chaperons.

Hsp70 has been shown to associate with newly synthesized protein during translation and there is ample evidence indicating that hsp70 binds to unfolded proteins (Beckmann et al., 1990). Thus, it appears likely that hsp70 associates with nascent cytosolic proteins to aid in their folding and pre-

**Fig. 2.** A two-dimensional gel electrophoresis pattern of the 1 mM ATP fraction eluted from the Tetrahymena EF-1\(\alpha\) column. First-dimension is isoelectric focusing (horizontal). Second-dimension SDS-PAGE (vertical) was performed on a 10% running gel. Only the region of the 78 kDa and 74 kDa proteins is shown. Arrowheads a, b, and c indicate the 78 kDa, 77 kDa, and 74 kDa proteins, respectively.

**Fig. 3.** N-terminal amino acid sequence of the 74 kDa protein. Comparison of the N-terminal amino acid sequence of the 74 kDa protein with the predicted amino acid sequences of hsp70 family. (a) N-terminal amino acid sequence of the 74 kDa protein, (b) residues 26-50 of Saccharomyces cerevisiae hsp70 related protein SSC1 precursor (accession No., A32943) (Craig et al., 1989), (c) residues 47–71 of kidney bean hsp70 (S25005), (d) residues 27–51 of Caenorhabditis elegans hsp70F precursor (B32475) (Heschl and Baillie, 1989), (e) residues 49–73 of human mitochondrial hsp70 precursor (B48127) (Domanico et al., 1993), (f) residues 48–72 of Drosophila melanogaster heat-shock cognate protein 5 precursor (JN0667) (Rubin et al., 1993), (g) residues 1–22 of Escherichia coli dnaK protein (A03311) (Bardwell and Craig, 1984). Dots and underlines indicate identity and similarity, respectively.
vent aberrant protein-protein interactions. The yeast SSB 70 kDa heat shock proteins (Ssb1/2p) have been shown to be associated with translating ribosomes (Nelson et al., 1992). This association was disrupted by puromycin, suggesting that Ssb1/2p can bind directly to the nascent polypeptides. This association was disrupted by puromycin, suggesting that a portion of the slow growth phenotype of Ssb1/2p may bind directly to the nascent polypeptides. The yeast Ssb1/2p have been shown to be associated with translating ribosomes (Nelson et al., 1992). At the present time it is not clear to what degree hsp70 and EF-1α interact. The multifunctional ability into full play, as the translation elongation factor, the hsp70-binding and the actin cross-linker protein.

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