

Purification and characterization of the inhibitory subunit (δ) of the ATP-synthase from *Micrococcus luteus*

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Abstract Subunit δ was isolated from the ATP-synthase from *Micrococcus luteus* strain (ATCC 4698). δ , in the case of *M. luteus* F_0F_1 -ATPase, acts as an inhibitor of ATP hydrolysis and thus resembles subunits in *E. coli* and chloroplast ATP-synthase. After treatment with 1.5 M LiCl the ATP-synthase dissociated, and subsequently subunit δ (27 kDa) was purified by hydrophobic interaction chromatography. Inhibition of ATP-synthase lacking δ by addition of δ showed non-competitive kinetics with a K_i of ~ 5.9 nM. Subunit ϵ from chloroplast F_1 , which corresponds functionally to the *M. luteus* F_0F_1 - δ , and chloroplast δ were tested for ATPase inhibitory activity by addition to the partially δ -depleted ATP-synthase from *M. luteus*. CF_1 - ϵ inhibited *M. luteus* ATP-synthase up to 80%, whereas CF_1 - δ did not show any influence.

Key words: ATP-synthase; *Micrococcus luteus*; CF_1 ; δ subunit; ϵ subunit; Inhibitor protein; Reconstitution

1. Introduction

ATP-synthases of mitochondria, eubacteria and chloroplasts synthesize ATP from ADP and P_i by using a proton electrochemical gradient. The enzyme can also function reversibly to hydrolyze ATP and to generate a proton electrochemical gradient. F_0F_1 -synthases consist of two parts, an intrinsic membrane component, F_0 , conducting protons, and an extrinsic component, F_1 , containing the catalytic sites for ATP-synthesis and hydrolysis [1,2].

The ATP-synthase is regulated by several inter-related factors, including the proton-motive force, the ATPase inhibitor protein and divalent cations [3]. F_1 -ATPase inhibitor proteins have been isolated from bovine heart [4], *Saccharomyces cerevisiae* [5], rat liver [6], and plant mitochondria [7]. In the case of chloroplast and *Escherichia coli* ATP-synthases the ϵ subunit of F_1 acts as an inhibitor of ATPase activity [8,9].

We have shown earlier that in *M. luteus*, subunit δ acts like an inhibitor of the F_1 -ATPase and the F_0F_1 ATP-synthase complex [10–12]. Apart from functional homologies the δ subunit from *M. luteus* shows N-terminal sequence homologies to the ϵ subunits from other organisms [12].

In the present study, by using a new preparation of subunit δ and of ATP-synthase ($-\delta$) [12], several aspects of the inhibitory subunit (δ) were investigated. We also studied the interaction of the δ and ϵ subunits from chloroplast F_1 with partially δ -depleted ATP-synthase from *M. luteus*.

2. Materials and methods

2.1. Materials

LiCl was purchased from Fluka (Buchs), ATP from Serva (Heidelberg) and Tris (2-amino-2-[hydroxymethyl]-1,3-propanediol) from

Boehringer (Mannheim). All other chemicals were at least of analytical grade and obtained from Merck, Darmstadt.

2.2. Isolation of the δ subunit from purified *M. luteus* ATP-synthase

M. luteus ATP-synthase was isolated as described previously [12]. The δ subunit was isolated from the purified ATP-synthase as follows. ATP-synthase (2 mg of protein) was dissociated by treatment with a chaotropic medium containing 1.5 M LiCl, 4 mM ATP, 50 mM Tris and 10% (v/v) glycerol at pH 7.5, for 30 min. The resulting mixture was applied to a hydrophobic interaction chromatography (HIC) column of Fractogel (R) EMD Propyl 650 (S). Material was eluted with a flow of 0.5 ml/min by a linear gradient of 100–0% LiCl. Protein was analyzed by the SDS-PAGE system of Laemmli [13] using a 12–15% linear acrylamide gradient.

2.3. Protein analysis

Protein was determined according to Lowry [14] and Dulley [15]. Dissociation products from the LiCl treatment of *M. luteus* ATP-synthase were analysed by Blue native PAGE of Schägger and von Jagow [16].

2.4. Purification of the small subunits from CF_1

Subunits δ and ϵ from chloroplast F_1 were over-expressed in *E. coli* and purified as described [17].

2.5. Measurement of ATPase activity

ATP hydrolysis was measured via released phosphate from 1 mM Ca-ATP (5:1) according to the method of Fiske and Subbarow [18] with a continuous analysis system [19]. One ATPase unit hydrolyzed 1 μ mol of ATP/min. The specific reaction conditions are given in the legends to the figures.

3. Results

3.1. Preparation of *M. luteus* F_0F_1 - δ

Purified ATP-synthase from *Micrococcus luteus* was dissociated as described in section 2. Dissociation was controlled by native page. The mixture of dissociated F_0F_1 subunits was applied to a hydrophobic interaction chromatography-column of Fractogel (R) EMD 650 (S), and six peaks were eluted (Fig. 1). The first peak around 1.4 M LiCl contained subunits α and β , (Fig. 2), followed by undissociated F_1 -ATPase at 1.2 M LiCl. F_0F_1 ($-\beta$) eluted in the third peak around 1.1 M LiCl, whereby the undissociated F_0F_1 was contained in peak four. Subunit δ eluted from the column at 0.7 M LiCl (peak 5); peak 6 contained a mixture of subunit γ and β .

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Abbreviations: ATP-synthase (EC3.6.1.34) from *M. luteus*; ATP-synthase($-\delta$), ATP-synthase lacking the δ -subunit; F_0 , F_0 subcomplex of ATP-synthase; F_1 , F_1 subcomplex of ATP-synthase; CF_1 , chloroplast ATPase; CF_0 , chloroplast proton channel; CF_1 - ϵ , ϵ subunit of chloroplast ATPase.

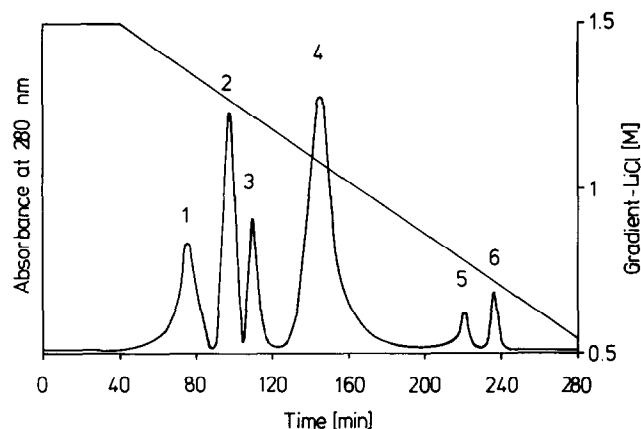


Fig. 1. Elution profile of hydrophobic interaction chromatography of 2 mg dissociated *M. luteus* ATP-synthase on Fractogel (R) EMD 650 (S). The sample was pretreated as described in section 2. Elution was by a linear gradient (1.5–0 M) of LiCl in 4 mM ATP, 50 mM Tris, 10% (v/v) glycerol, pH 7.5, at 0.5 ml/min. Absorption at 280 nm was detected and the salt gradient is shown as a straight line.

200 μ g of subunit δ were obtained from 12 mg ATP-synthase. Since δ represents only about 5% of the total protein (540 kDa), the overall yield of the δ subunit is about 33%.

3.2. Reconstitution

Previously we have shown that the time-dependent increase in ATPase activity of *M. luteus* ATP-synthase is due to the slow dissociation of the δ subunit from the enzyme [12]. If the interaction between δ and the ATP-synthase ($-\delta$) of *M. luteus* is

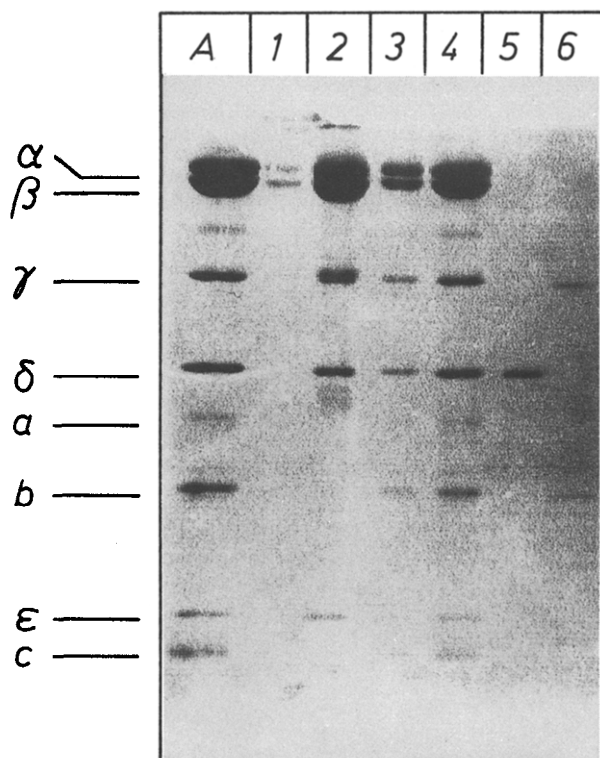


Fig. 2. SDS electrophoresis of samples obtained during preparation of dissociated *M. luteus* ATP-synthase. A 12–15% gradient gel (Coomassie blue stained) was run with the following samples: lane A, 20 μ g of purified ATP-synthase; lanes 1–6 correspond to peaks 1–6 in Fig. 1.

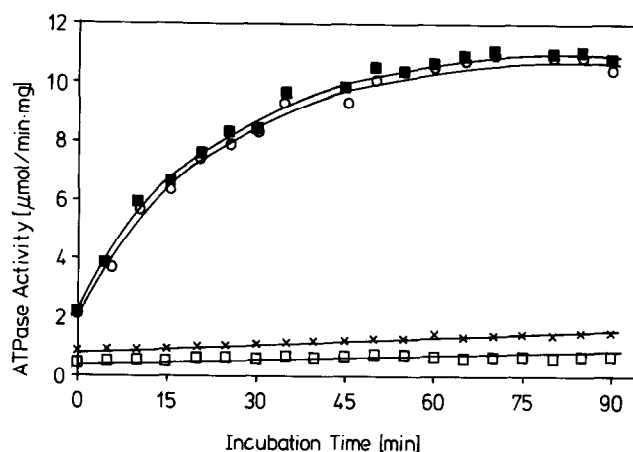


Fig. 3. ATP-hydrolysis after addition of δ - (O) and ϵ subunit (x) from CF_1 and δ subunit (□) from *M. luteus* ATP-synthase. The time-course of activation was measured by diluting 100 μ g ATP-synthase with 100 ml of 0.1 M Tris-HCl (pH 8.0) at 37°C. Five minutes before the ATP hydrolysis was initiated by addition of 1 mM Ca-ATP, 1.0 μ g of each subunit was added. The measurement without an addition of subunit is symbolized by (■).

governed by an association–dissociation equilibrium then inhibition should be reversed by addition of inhibitory subunit δ . Fig. 3 shows that incubation of diluted ATP-synthase resulted in an increase in its hydrolytic activity, whereas addition of *M. luteus* δ subunit inhibited ATP-hydrolysis by 90%. In analogy, hybrid reconstitution with CF_1 - ϵ reduced the rate of ATP-hydrolysis by about 80%. In contrast, no inhibition was observed by addition of the chloroplast F_1 - δ .

3.3. Kinetics of inhibition of ATP-hydrolysis by *M. luteus* δ

The effect of ATP concentration on ATPase activity was determined for ATP-synthase ($-\delta$) and *M. luteus* F_0F_1 - δ plus a saturating concentration of δ subunit (Fig. 4). V_{max} and K_m values for uninhibited ATP-synthase ($-\delta$) were 7.75 ± 0.45 units/mg and 168.6 ± 6.7 μ M, respectively. The values for δ subunit-inhibited ATP-synthase ($-\delta$) were 2.99 ± 0.1 units/mg for V_{max} and 159.7 ± 6.4 μ M for K_m . These data demonstrate that the *M. luteus* δ subunit is a non-competitive inhibitor. A plot of the ATP-synthase ($-\delta$) hydrolytic activity vs. δ subunit concentration (Fig. 4B) shows a maximal inhibition of 90%. Half-maximal inhibition occurs at a δ -concentration of about 4.4 nM, $K_i = 5.9$ nM.

4. Discussion

In the present work, the function of *M. luteus* has been studied by reconstitution experiments with purified δ and *M. luteus* ATP-synthase lacking δ . Increase in the rate of ATP-hydrolysis by *M. luteus* ATP-synthase was reversed by addition of subunit and the chloroplast CF_1 - ϵ , while addition of CF_1 - δ was without effect.

The dissociation constant for the non-competitive inhibitor *M. luteus* δ with ATP-synthase ($-\delta$) is in the nanomolar range, and enzyme in the presence of δ has about 10% of the activity of ATP-synthase lacking δ .

Apparently, the δ subunit of *M. luteus* acts as an inhibitor of *M. luteus* ATPase just like chloroplast- and *E. coli* F_1 - ϵ [8,9,20]. In what way *M. luteus* δ occupies a role as a dissociation

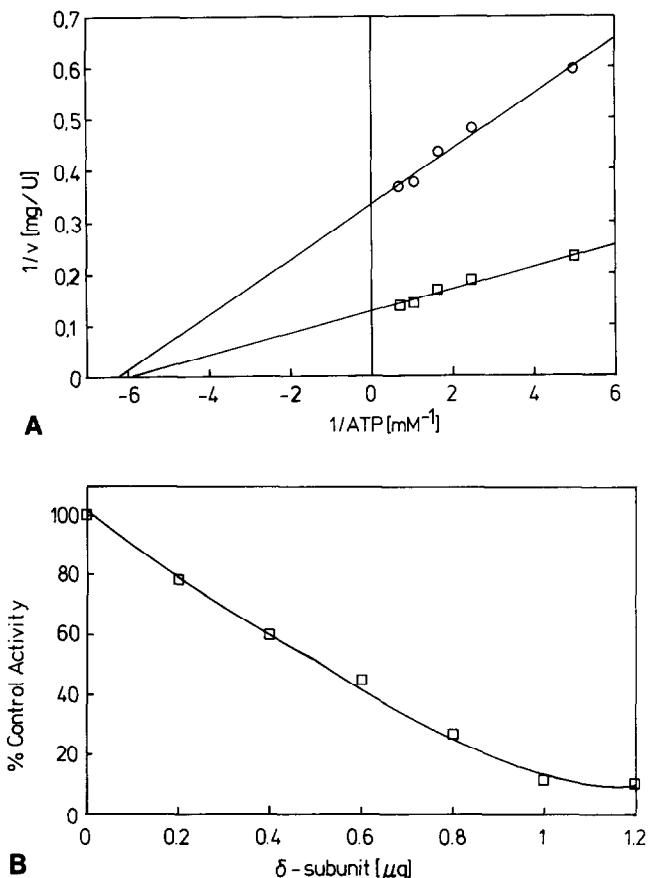


Fig. 4. (A) Effect of ATP concentration on ATPase activity of the inhibited and uninhibited ATP-synthase($-\delta$). ATP-synthase($-\delta$) was prepared as described [12]. 1 μ g ATP-synthase was incubated in 0.1 M Tris-HCl (pH 8.0) at 37°C with (○) or without (□) 1 μ g of δ subunit from *M. luteus*. After 5 min the ATPase reaction was started by addition of Ca-ATP and phosphate release was determined as described in section 2. (B) Activity vs. *M. luteus* δ concentration. 1 μ g of ATP-synthase($-\delta$) was incubated with varying concentrations of subunit δ from *M. luteus* and ATPase activities were determined as described in section 2. Control activity was 7.5 μ mol \cdot min⁻¹ \cdot mg⁻¹.

table inhibitor in the membrane-bound enzyme remains to be investigate. However, indications of a reversible dissociation/association of the δ -ATP-synthase($-\delta$) complex are revealed by investigations with reconstituted *M. luteus* ATP-synthase [12], where time-dependent incubation induced an increase in hydrolytic activity. In this context, it could be shown for the soluble ATP-synthase that the time dependence of ATPase activity is due to the dissociation of the δ subunit from the enzyme [12].

In comparison with *M. luteus* δ , dissociation of chloroplast ϵ from CF₁ is not a part of ATPase activation in the thylakoid

membrane. The ϵ subunit from chloroplast F₁ strongly interacts with the γ subunit of CF₁ [21]. The electrochemical proton gradient induces changes in the position of ϵ relative to the γ subunit [21,22]. Furthermore, the ϵ subunit from CF₁ is required for reconstitution of phosphorylation in the thylakoid membrane [23,24]. However, the fact that the ATPase activity of *M. luteus* ATP-synthase is inhibited by ϵ subunit from CF₁ and δ subunit from *M. luteus* reveals their functional homology as an inhibitor.

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