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Unisite ATP hydrolysis by soluble *Rhodospirillum rubrum* F_1 -ATPase is accelerated by Ca^{2+}

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Abstract

At saturating concentrations of ATP, soluble F_1 from the *Rhodospirillum rubrum* (RF₁) exhibits a higher rate of hydrolysis with Ca²⁺ than with Mg²⁺. The mechanisms involved in the expression of a higher catalytic activity with Ca²⁺ were explored by measuring the ATPase activity of RF₁ at substiochiometric concentrations of ATP (unisite conditions). At a ratio of 0.25 [γ -³² P]ATP per RF₁, the enzyme exhibited a 50 times higher hydrolytic rate with Ca²⁺ than with Mg²⁺. The rate of [γ -³² P]ATP binding to RF₁ was in the same range with the two divalent metal ions. Centrifugation–filtration of RF₁ exposed to substoichiometric [γ -³² P]ATP concentrations and Mg²⁺ through Sephadex columns yielded an enzyme that contained [γ -³² P]ATP and [³² P]phosphate in a stoichiometry that was close to one. In the presence of Ca²⁺, the eluted enzyme did not contain [γ -³² P]ATP nor [³² P]phosphate. This indicated that the rate of product release was faster with Ca²⁺ than with Mg²⁺. It was also observed that the ratio of multisite to unisite hydrolysis rates was of similar magnitude with both divalent cations. This suggests that they do not affect differently the cooperative mechanisms that may exist between catalytic sites. In consequence, the higher ATPase activity of RF₁ in presence of Ca²⁺ strongly suggests that the retention time of products is decreased in the presence of this cation. © 1998 Elsevier Science B.V.

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1. Introduction

The ATP synthase of energy transducing membranes catalyzes the synthesis of ATP from ADP and P_i (for reviews, see [1,2]). The energy for the synthesis of ATP is provided by electrochemical H⁺ gradients derived from electron transport that is initiated by substrate oxidation, or by light in photosynthetic organisms. The ATP synthase of the photosynthetic bacterium *Rodospirillum rubrum* has been extensively studied [3–6]. The enzyme from *R. rubrum* is similar to ATP synthases from other sources; it consists of a membrane moiety (F₀) whose function is to channel H⁺ to a portion of the ATP synthase known

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as F_1 , the site where the catalytic events that lead to ATP synthesis take place. The latter segment has been isolated from chromatophores of *R. rubrum* (RF₁) and its properties and structure have been studied in several laboratories [6–9].

One of the most apparent characteristics of soluble F_1 is its ability to catalyze hydrolysis of ATP through a process that is Mg²⁺ dependent. The ATPase activity of RF_1 is also supported by Mg^{2+} , but at variance with for example mammalian mitochondrial F₁, its ATPase activity with Ca^{2+} is strikingly higher than with Mg^{2+} [7]. This is not unique to RF_1 . F_1 from Chromatium [10], chloroplast [11], turnip mitochondria [12], Rhodobacter sphaeroides [13], Bacillus subtillis [14], Micrococcus luteus [15], and Streptomyces lividans [16], and other organisms also exhibit a higher ATPase activity with Ca^{2+} than with Mg^{2+} . Thus, this characteristic of F_1 seems to be rather widespread in ATP synthases of energy transducing membranes. This is rather peculiar, particularly if it is considered that light-driven ATP synthesis in chromatophores from R. rubrum or chloroplast membranes, is supported by Mg²⁺, but not by Ca²⁺ [17,18]. This has raised a number of questions on how the hydrolytic events that occur in soluble RF₁ are related to ATP synthesis in intact chromatophores.

In this work, the mechanisms that lead to the expression of a higher ATPase activity of RF_1 in presence of Ca^{2+} were explored. The purpose of the experiments was to gain further information on some of the factors that operate in the kinetics of the enzyme. Specifically, we studied ATP hydrolysis under conditions in which ATP concentration is lower than that of RF_1 (unisite hydrolysis). As shown by various authors [19–22], under unisite conditions, only the catalytic site with the highest affinity for ATP carries out hydrolysis. The following is the accepted sequence of the reactions of unisite ATP hydrolysis

$$F_{1} + ATP \Leftrightarrow F_{1} \cdot ATP \Leftrightarrow F_{1} \cdot ADP \cdot P_{i}$$
$$\Leftrightarrow F_{1} \cdot ADP + P_{i} \Leftrightarrow F_{1} + ADP$$

The results show that in presence of Ca^{2+} , unisite ATP hydrolysis is many-fold higher than with Mg^{2+} and that this is consequence of a higher rate of product release from the high affinity catalytic site.

2. Materials and methods

All non-radioactive reagents were purchased from Sigma. [³²P]P_i was from New England Nuclear; this was used for the preparation of $[\gamma^{-32}P]ATP$ according to reference [23]; its specific activity was $2-3 \times$ 10^6 cpm/nmol. Soluble RF₁ was prepared from *R*. rubrum strain S1. Bacteria were grown photosynthetically in the medium described by Sistrom [24]. Chromatophores were isolated from R. rubrum harvested in the logarithmic phase of growth [25]. Soluble RF₁ was extracted from chromatophores by the chloroform method and purified according to Norling et al. [8]. RF₁ dissolved in 50 mM Tris-HCl, 1 mM MgCl₂ and 15% glycerol, pH 7.5 at a concentration of about 20 mg/ml was stable for months at -70° C. Before use, the enzyme was thawed and passed through a column of Sephadex G-50 by centrifugation [26] equilibrated with the reaction medium without ATP. The molecular weight of RF_1 (384 kDa) was deduced from its nucleotide sequence [4].

2.1. Multisite hydrolysis

Multisite Ca^{2+} and Mg^{2+} -ATPase activities of RF_1 were assayed in 25 mM Tris-acetate pH 8.0, 30 mM K-acetate, 3 mM $CaCl_2$ or $MgCl_2$ and 3 mM ATP. P_i formed was measured colorimetrically [27].

2.2. Unisite $[\gamma^{-32}P]ATP$ hydrolysis and coldchase experiments

In the standard method for measuring unisite $[\gamma^{32}P]ATP$ hydrolysis, 50 µl of RF₁ at a concentration of 2 µM in a mixture of 40 mM MES, 0.25 mM KH₂PO₄ and 2 mM MgCl₂ or 2 mM CaCl₂ pH 8.0 was mixed with 50 µl of 0.5 µM of $[\gamma^{-32}P]ATP$. At the desired times, the reaction was arrested with 300 µl of cold trichloroacetic acid (TCA) 6% final concentration. Carrier Ca²⁺- or Mg²⁺-ATP (4 mM, final concentration) were added to the arrested mixtures. The final volume was completed to 0.5 ml. $[^{32}P]P_i$ was extracted twice with butyl acetate after formation of the phosphomolybdate complex as described elsewhere [28]. The amount of $[\gamma^{-32}P]ATP$ that remained in the water phase was used to calculate the amount of $[\gamma^{-3^2}P]ATP$ hydrolyzed. In coldchase experiments [19], 100 µl of non-radioactive Ca²⁺- or Mg²⁺-ATP (4 mM final concentration) were added to RF₁ undergoing unisite $[\gamma^{-3^2}P]ATP$ hydrolysis. When Ca²⁺ was used, the reaction was allowed to proceed for 6s; with Mg²⁺ the reaction was arrested after 1 min. The amount of $[\gamma^{-3^2}P]ATP$ that was not hydrolyzed was determined as described above.

2.3. Determination of $[\gamma^{-32}P]ATP$ bound to RF_1 by the hexokinase-glucose trap method

 $[\gamma^{-3^2}P]$ ATP binding to RF₁ under unisite conditions was determined by the hexokinase-glucose trap method [29]. For these experiments, RF₁ was incubated with Ca²⁺ or Mg²⁺ in the standard mixture for unisite $[\gamma^{-3^2}P]$ ATP hydrolysis, except that the final volume was 40 µl. At the desired times, the samples were supplemented with 300 µl of a mixture at pH 8.0 that contained 20 units of hexokinase, 10 mM glucose and 10 mM MgCl₂; the reactions were arrested 30 s later with HCl (1.3 N, final concentration). The activity of hexokinase added was around 5 × 10³-folds higher than the hydrolytic activity of RF₁ at saturating ATP concentrations. To determine the amount of $[\gamma^{-3^2}P]$ ATP that had been converted into

glucose 6-[³²P]phosphate, the samples were placed in boiling water (92°C) for 30 min. Subsequently, [³²P]P_i was extracted twice as described above, and the radioactivity in the aqueous phase was determined; this was considered to correspond to the amount of glucose 6-[³²P]phosphate formed. From the data, the rate of $[\gamma^{-32}P]$ ATP binding was calculated according to reference [30]. Prior to the experiments two assays were carried out: (i) In the experiments with Ca^{2+} , Mg^{2+} had to be added with hexokinase in order to support hexokinase action; experiments in the absence of RF₁ showed that under these conditions, hexokinase converted around 97% of $[\gamma^{-32}P]ATP$ into glucose $6 = [^{32}P]$ phosphate in less than 2 s; (ii) the effect of heat treatment on $[\gamma^{-32}P]ATP$ and glucose 6-[³²P]phosphate was determined; it was observed that heat treatment produced cleavage of more than 97% of $[\gamma^{-32}P]$ ATP; and that on the average 98% of glucose 6-[³²P]phosphate was heat resistant.

2.4. Determination of $[\gamma^{-32}P]ATP$ and $[^{32}P]$ phosphate bound to RF_1 by the centrifugation-filtration method

In other experiments, the unisite mixture was centrifuged through Sephadex G-50 columns. The eluate was received in 100 μ l of 12% TCA, an aliquot was used to determine total radioactivity. Another identi-



Fig. 1. Time course ATP hydrolysis by RF₁ at saturating (A) and substitichiometric (B) ATP concentrations. In (A), the reaction was carried out with 3 mM ATP and 3 mM of Mg²⁺ (\blacktriangle) or Ca²⁺ (\bigcirc); the reaction was initiated by adding 12 µg (\bigstar) or 2 µg (\bigcirc) RF₁ to the reaction medium (final volume = 100 µl) as indicated under Section 2. At the times indicated, the reactions were arrested and the amount of P₁ formed was determined. Unisite ATPase activity (B) was started by mixing of equal volumes of RF₁ (2 µM) and [γ -³²P]ATP (0.5 µM) in the unisite standard buffer, in the presence of 2 mM of Mg²⁺ (\triangle) or Ca²⁺ (\bigcirc); at the times shown the reactions were arrested with TCA, and the amount of [γ -³²P]ATP that remained was determined.



Fig. 2. Effect of different concentrations of azide on ATP hydrolysis by RF₁ under multisite (\bigcirc) and unisite (\bigcirc) conditions in presence of Ca²⁺ (A) or Mg²⁺ (B). The experimental mixtures were as in Fig. 1 except that azide was added at the indicated concentrations. Under unisite conditions, (\bigcirc) represent the fraction of [γ -³²P]ATP hydrolyzed after 8 s of incubation with Ca²⁺ (panel A) or after 5 min of incubation with Mg²⁺ (panel B). In the absence of azide, the fractions of hydrolyzed [γ -³²P]ATP, were 0.18 and 0.13 mol [γ -³²P]ATP/mol RF₁ with Ca²⁺ and Mg²⁺, respectively. Under multisite conditions (\bigcirc), without azide, the ATPase activity (100%) was 6 and 0.1 µmol/min/mg with Ca²⁺, and Mg²⁺, respectively.

cal sample was extracted twice with butyl acetate after formation of the phosphomolybdate complex. The radioactivity in the aqueous phase was considered as $[\gamma-^{32}P]ATP$ bound to RF_1 . The difference between total radioactivity and $[\gamma-^{32}P]ATP$ was equal to $[^{32}P]P_i$ bound to RF_1 . Protein was determined, according to Smith et al. [31], in eluates of identical samples, except that these were received in $100 \ \mu 1$ of 10% SDS.

3. Results

The ATPase activity of RF1 was measured at saturating and substoichiometric concentrations of ATP (Fig. 1(A) and (B), respectively) in presence of Ca^{2+} and Mg^{2+} . In confirmation of previous data [7] ATP hydrolysis was higher with Ca²⁺ under multisite conditions. Under unisite conditions in presence of Mg²⁺, there was a rapid initial burst of $[\gamma^{-32}P]ATP$ hydrolysis that was followed by a relatively slow phase of hydrolysis that continued until $[\gamma^{-32}P]ATP$ was exhausted (Fig. 1(B)). This pattern has been observed with F_1 from various sources [19,20,32]. With Mg²⁺ the rapid phase reflects binding and splitting of $[\gamma^{-32}P]$ ATP at the high affinity catalytic site, where an equilibrium between $[\gamma^{-32}P]ATP$ and ADP and $[^{32}P]P_i$ is established. The slow phase of hydrolysis is consequence of a slow rate of product dissociation from the catalytic site [33].

The time course of unisite ATP hydrolysis by RF_1 in the presence of Ca^{2+} differed markedly from that observed with Mg^{2+} (Fig. 1(B)). With Ca^{2+} , there was a continuous relatively rapid rate of $[\gamma^{-32}P]ATP$



Fig. 3. Accesibility of $[\gamma^{-3^2}P]$ ATP to hexokinase in RF₁ incubated under unisite conditions. In (A), $[\gamma^{-3^2}P]$ ATP was incubated under unisite conditions with Mg²⁺ (\bigcirc) or Ca²⁺ (\bigcirc). At the times shown, hexokinase (20 units) and 10 mM glucose was added. In the tubes incubated with Ca²⁺, hexokinase and glucose were added together with 10 mM MgCl₂. The presence of Ca²⁺ did not affect hexokinase action (see Section 2). After 30 s of the addition of hexokinase, the reaction was arrested. (B) shows the data in (A) plotted in the form of a second order rate equation as in reference [38]; the $[\gamma^{-3^2}P]$ ATP binding rate constants (k_{+1}) were calculated from the slopes ($k_{+1} = m/RF_{1(0)} - ATP_{(0)}$). Calculated k_{+1} was 2.5 × 10⁵ M⁻¹ s⁻¹ with Ca²⁺ (\square), and 1.6 × 10⁵ M⁻¹ s⁻¹ with Mg²⁺ (\blacksquare).

hydrolysis that lasted until the totality of $[\gamma - {}^{32}P]ATP$ was consumed i.e. approximately 1 min.

It has been reported that at substoichiometric ATP concentrations, F_1 may still work as under multisite conditions [34]. The sensitivity of ATP hydrolysis to azide has been used to distinguish between multisite and unisite hydrolysis i.e. the former, but not the latter, is inhibited by azide [35–37]. Therefore, to determine if the high ATPase activity observed with Ca²⁺ at substoichiometric ATP concentrations was indeed due to RF₁ working under unisite conditions, the effect of azide was determined at low and saturating [γ -³²P]ATP concentrations. For comparison, the experiments were also carried out in presence of Mg²⁺.

With Ca²⁺, azide inhibited hydrolysis at high ATP concentrations, but it did not affect hydrolysis when the concentration of ATP was lower than that of RF₁ (Fig. 2(A)). This indicates that with Ca²⁺ at substoichiometric ATP concentrations, only the high affinity catalytic site carried out hydrolysis. In presence of Mg²⁺, azide inhibited hydrolysis at high ATP concentrations, but not at substoichiometric ATP concentrations. However, it was unexpectedly observed that azide enhanced unisite hydrolysis by about 50% (Fig. 2(B)). We have no explanation for these latter results.

3.1. Binding of $[\gamma^{-3^2}P]ATP$ to R. rubrum F_1 incubated under unisite conditions with Mg^{2+} and Ca^{2+}

The finding that in presence of Ca^{2+} , RF_1 exhibits a higher rate of unisite ATP hydrolysis than with Mg^{2+} led us to study the effect that these divalent metal ions have on the various steps of the catalytic cycle. In a first approach, the binding of $[\gamma^{-32}P]ATP$ to RF_1 was determined. RF_1 was incubated with Ca^{2+} or Mg²⁺ and substoichiometric concentrations of $[\gamma^{-32}P]$ ATP; at various times, a large excess of hexokinase (+ glucose) was added to trap $[\gamma^{-32}P]ATP$ that was not bound to RF₁. It should be noted that when Ca²⁺ was used, hexokinase was added together with Mg²⁺ in order to support hexokinase action. Controls in which $[\gamma^{-32}P]ATP$ was added to a mixture that contained hexokinase, RF1 and Mg2+, with and without Ca²⁺, showed that in the two conditions, 97% of $[\gamma^{-32}P]ATP$ was transformed into glucose $6 - \begin{bmatrix} 3^{2} P \end{bmatrix}$ phosphate in less than 2 s.

With Mg²⁺ and Ca²⁺, there was a progressive decrease in the amount of $[\gamma^{-32}P]ATP$ that was accessible to hexokinase (Fig. 3(A)). With the two divalent metal ions, the time curves were markedly similar. From the amount of $[\gamma^{-32}P]ATP$ that was accessible to hexokinase, the rate of $[\gamma^{-32}P]ATP$ binding to RF₁ was calculated (Fig. 3(B)) according to references [30,38]. With Ca²⁺ and Mg²⁺ the rates were in the same range i.e. 2.5 and $1.6 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$, respectively. Therefore, the large difference in the rate of unisite $[\gamma^{-32}P]ATP$ hydrolysis with the two divalent metal ions is not due to differences in the rate of $[\gamma^{-32}P]ATP$ binding.

3.2. Product release from R. rubrum F_1 undergoing unisite hydrolysis in presence of Mg^{2+} and Ca^{2+}

It has been shown in F_1 from various sources, that under unisite conditions, ATP at the catalytic site is continuously hydrolyzed and synthesized with an equilibrium constant that is near unity [19,21]. In RF_1



Fig. 4. Amount of $[\gamma^{-32}P]ATP((\blacktriangle, \triangle) \text{ and } [{}^{32}P]\text{phosphate}$ (\blacksquare, \square) bound to RF₁ under unisite conditions with Ca²⁺ (\triangle, \square) or Mg²⁺ ($\blacktriangle, \blacksquare$). At the times shown 100 µl of the reaction mixture were passed through Sephadex centrifugation–elution columns and received in a tube containing 100 µl of 12% TCA. An aliquot was used to determine total radioactivity (the sum of $[\gamma^{-32}P]ATP$ and $[^{32}P]P_i$), and another aliquot was to determine $[\gamma^{-32}P]ATP$. The difference between total radioactivity and $[\gamma^{-32}P]ATP$ was considered as $[^{32}P]P_i$ bound to RF₁. The *inset* show the ratio of bound $[\gamma^{-32}P]ATP:[^{32}P]$ phosphate in presence of Mg²⁺. These values were calculated from the data ($\blacktriangle, \blacksquare$) in the main plot.

undergoing unisite hydrolysis of $[\gamma^{-3^2}P]ATP$, it was studied if Ca²⁺ and Mg²⁺ yield different ratios of $[\gamma^{-3^2}P]ATP$ to $[^{3^2}P]P_i$ at the catalytic site. In these experiments, RF₁ was exposed to unisite conditions, and at various times the reaction mixture was passed through Sephadex columns. In the eluates, the amount of protein, $[\gamma^{-3^2}P]ATP$ and $[^{3^2}P]P_i$ was determined. With Mg²⁺, the amount of $[\gamma^{-3^2}P]ATP$ and $[^{3^2}P]P_i$ bound to RF₁ (Fig. 4), yielded an ATP:P_i ratio slightly higher than one (Fig. 4 inset). In presence of Ca²⁺ (Fig. 4), hardly any $[\gamma^{-3^2}P]ATP$ or $[^{3^2}P]P_i$ was detected in the eluates, indicating that the lifetime of $[^{3^2}P]P_i$ at the catalytic site was shorter than with Mg²⁺.

3.3. Effect of excess ATP on $[\gamma^{-32}P]ATP$ bound to RF_1 under unisite conditions

It has been shown that the addition of excess ATP to F_1 undergoing unisite hydrolysis promotes a hydrolytic burst of the $[\gamma^{-32}P]ATP$ bound under unisite conditions [20,32,39]. This results from the filling of empty catalytic sites which, through a cooperative reaction, produces a large increase in the rate of

product release. This reaction was studied in RF₁ incubated with Mg²⁺ or Ca²⁺ (Fig. 5). RF₁ was incubated under unisite conditions and at various times, excess non-radioactive ATP was added. With Mg²⁺, the results (Fig. 5(A)) were similar to those described in F₁ from other sources i.e. excess ATP produced a burst of hydrolysis of the previously bound [γ -³²P]ATP [20,39]. Nonetheless, it must be noted that excess ATP added in the first seconds of reaction time induced a relatively small enhancement of [γ -³²P]ATP hydrolysis. This is because at those times, not all [γ -³²P]ATP added had been bound to the enzyme (see Fig. 3).

With Ca²⁺, notwithstanding the time of incubation under unisite conditions, the addition of excess ATP produced a small enhancement of $[\gamma^{-32}P]$ ATP hydrolysis (Fig. 5(B)). This again indicates that with Ca²⁺, $[\gamma^{-32}P]$ ATP bound to the catalytic site is rapidly hydrolyzed, and thus there is hardly any bound $[\gamma^{-32}P]$ ATP committed to hydrolysis.

The magnitude of the hydrolytic burst of $[\gamma^{-32}P]ATP$ bound to F_1 under unisite conditions, has been used to determine the rate at which $[\gamma^{-32}P]ATP$ binds to the catalytic site [19]. When the data of Fig.



Fig. 5. Cold-chase experiments with RF₁ undergoing unisite $[\gamma^{-32}P]$ ATP hydrolysis in the presence of Mg²⁺ (A) and Ca²⁺ (B). RF₁ was incubated with $[\gamma^{-32}P]$ ATP (0.25 μ M) under the standard conditions for unisite hydrolysis. At different reaction times, the samples were arrested with 300 μ l of cold TCA (\bigcirc), or alternatively 100 μ l of non-radioactive ATP (4 mM) was added (\bigoplus). With Mg²⁺ (A), the reaction was allowed to proceed for 1 min, or for 6s with Ca²⁺ (B). At these times, the reactions were arrested and the amount of $[\gamma^{-32}P]$ ATP hydrolyzed was determined (see Section 2, for details). The amount of cold ATP hydrolyzed was below 1% in presence of Mg²⁺ (A), and 3% in the samples with Ca²⁺ (B). Panel (C) is the graphical determination of k_{+1} using the data of cold-chase (\bigoplus) in (A) and (B). The constants were calculated from the slopes using the equation described by Penefsky [30]: $k_{+1} = \text{slope}/F_{1(0)} \cdot \text{ATP}_{(0)}$, where $F_{1(0)}$ and ATP₍₀₎ are the initial concentrations of F₁ and $[\gamma^{-32}P]$ ATP respectively. F₁ · ³²P is the concentration of F₁ · ³²P complex at the indicated times. The obtained constants were 1.26 × 10⁵ M⁻¹ s⁻¹ and 9.8 × 10⁴ M⁻¹ s⁻¹ for the conditions with Ca²⁺ (\square) and Mg²⁺ (\blacksquare), respectively.

5(A) and (B) were used to determine the rate of $[\gamma^{-3^2}P]ATP$ binding (Fig. 5(C)), the values obtained $(1.26 \times 10^5 \text{ and } 9.8 \times 10^4 \text{ M}^{-1} \text{ s}^{-1} \text{ with } \text{Ca}^{2+}$ and Mg²⁺, respectively) were lower than those obtained with the hexokinase method $(2.5 \times 10^5 \text{ M}^{-1} \text{ s}^{-1} \text{ with } \text{Ca}^{2+}$, and $1.6 \times 10^5 \text{ M}^{-1} \text{ s}^{-1} \text{ with } \text{Mg}^{2+}$). It has been described [28] that the hydrolytic burst induced by excess ATP, is accompanied by release of a fraction of previously bound $[\gamma^{-32}P]ATP$. Therefore, it is possible that the value obtained by the cold-chase technique is underestimated.

4. Discussion

In chromatophores of R. rubrum, Mg²⁺, but not Ca²⁺, supports ADP phosphorylation driven by electron transport [17,40-42]. Also it has been shown that at saturating ATP concentrations, particulate RF_0F_1 exhibits a higher hydrolytic activity with Mg^{2+} than with Ca^{2+} [43]. Thus, the observation that soluble RF₁ shows multisite ATPase activity several-fold higher with Ca^{2+} than with Mg^{2+} [7] raises a number of questions concerning the mechanisms that operate during catalysis in particulate and soluble RF₁. In principle, the differences in hydrolytic rates of soluble RF₁ with Ca²⁺ and Mg²⁺ could reflect a difference in cooperativity among the three catalytic sites of RF₁, or alternatively, a difference in the kinetics of the events that occur at the catalytic sites. Our results show that the rate of unisite ATP hydrolysis by soluble RF_1 is several times higher with Ca^{2+} . Since under unisite conditions, only the high affinity catalytic site of a portion of the enzymes carries out ATP hydrolysis, the results indicate that independently of cooperativity, Ca²⁺ and Mg²⁺ affect differently the kinetics of ATP hydrolysis at the high affinity catalytic site of RF₁.

4.1. Mg^{2+} -dependent unisite $[\gamma^{-32}P]ATP$ hydrolysis by RF_1

Most of the studies on unisite ATP hydrolysis by soluble F_1 from several sources have been made in presence of Mg²⁺ [2]. These results have shown that at substoichiometric concentrations of ATP to F_1 , there is a rapid binding of $[\gamma$ -³²P]ATP to the catalytic site of highest affinity [19]. At this site, the bound

 $[\gamma^{-32}P]$ ATP is continuously hydrolyzed and resynthesized with an equilibrium constant that is near unity [19,20]. Indeed, if F_1 undergoing unisite [γ -³²P]ATP hydrolysis in presence of Mg²⁺ is filtered through Sephadex columns, the eluted enzyme contains $[\gamma^{-32}P]ATP$, as well as $[^{32}P]P_i$, the ratio between the two being close to one. Another relevant feature of unisite Mg^{2+} – ATP hydrolysis is that the rate limiting step of the catalytic cycle is product release [19,21]. In fact, upon the addition of excess ATP to F_1 undergoing unisite $[\gamma^{-32}P]$ ATP hydrolysis, the rate of hydrolysis of bound $[\gamma^{-32}P]$ ATP increases several orders of magnitude. This results from the occupancy of other adenine nucleotide binding sites which in turn induce a 10⁵-fold increase in the rate of product release [21].

In RF₁ incubated with Mg²⁺ and substoichiometric concentrations of $[\gamma$ -³²P]ATP, there is a rapid binding of $[\gamma$ -³²P]ATP to RF₁, and it was observed that in RF₁ undergoing unisite $[\gamma$ -³²P]ATP hydrolysis, $[^{32}P]P_i$ derived from $[\gamma$ -³²P]ATP hydrolysis remains bound to RF₁ after passage through centrifuge columns. The ratio of $[\gamma$ -³²P]ATP: $[^{32}P]P_i$ at the catalytic site was 1.2 (see Fig. 4 inset). Likewise, the addition of high ATP concentrations to RF₁ undergoing unisite $[\gamma$ -³²P]ATP hydrolysis produces a hydrolytic burst of the previously bound $[\gamma$ -³²P]ATP. This set of observations indicates that in presence of Mg²⁺. RF₁ does not behave differently from F₁ from other sources.

4.2. Ca^{2+} -dependent unisite $[\gamma^{-32}P]ATP$ hydrolysis by RF_1

Our data show that with Ca²⁺, unisite hydrolysis is significantly higher than with Mg²⁺, albeit the binding of $[\gamma^{-3^2}P]$ ATP to RF₁ with both divalent cations is in the same time range. It was also found that the passage of RF₁ undergoing unisite hydrolysis of $[\gamma^{-3^2}P]$ ATP in presence of Ca²⁺ through Sephadex columns yielded an enzyme that did not contain $[^{3^2}P]P_i$. Therefore, it would appear that in comparison to Mg²⁺, the high rate of unisite $[\gamma^{-3^2}P]$ ATP hydrolysis that is observed with Ca²⁺ is consequence of a high rate of product release from the catalytic site. This in turn suggests that the affinity of the catalytic site for phosphate with Ca²⁺ is lower than with Mg²⁺. Thermodynamics analysis of the catalytic cy-

Table 1 Rate promotion from the unisite to multisite catalysis in RF_1

Unisite hydrolysis (s ⁻¹)	Multisite hydrolysis (s ⁻¹) ^a	Rate promotion (fold) ^b
$6.8 \times 10^{-5 \text{ c}}$	0.54	8×10^{3} Mg ²⁺ -ATPase
$3.7 \times 10^{-3 \text{ d}}$	48	1.3×10^{4} Ca ²⁺ -ATPase

^a Multisite turnover rates were calculated from linear rates of P_i formation.

^b Rate promotion is expressed as the ratio of multisite turnover to unisite turnover.

^c Mg²⁺-dependent unisite turnover was calculated from the slope of $[\gamma^{-3^2}P]ATP$ hydrolysis between 14s to 20min. At 14s all $[\gamma^{-3^2}P]ATP$ added had bound to RF₁ (see Fig. 3).

^d The turnover in the unisite Ca²⁺-ATPase activity was calculated in the slope between 14–30 s.

cle of ATP synthesis shows that phosphate binding is a major energy requiring step [44]. Therefore, it is possible that with Ca^{2+} , energy requirements for phosphate binding are exceedingly high, and in consequence, light-driven ATP synthesis cannot take place.

In RF₁ ATP hydrolysis with Ca²⁺ is faster than with Mg²⁺. However, this does not necessarily imply that in the presence of Ca²⁺, the rate limiting step shifts to another step of the catalytic cycle. In this context, it is instructive to compare the rates of unisite and multisite by RF₁ with Ca²⁺ and Mg²⁺. As shown in Table 1 the ratio of multisite:unisite hydrolysis was of similar extent with the two divalent cations. Thus, it appears that the rates of product release vary in parallel with Ca²⁺ and Mg²⁺. Acceleration of [³²P]phosphate release by the occupancy of other sites in chloroplast F₁ in presence of Ca²⁺ has been reported [45,46].

Miwa and Yoshida [47] and Yokoyama et al. [48] showed that in $F_1-\alpha_3\beta_3$ complexes that lack γ -subunit, the ATPase activity is two-fold higher with Ca^{2+} than with Mg^{2+} ; this suggested that interactions of the catalytic subunits with the γ -subunit are not necessarily involved in the expression of high catalytic rates with Ca^{2+} . The latter reports are in consonance with the present data, since our overall results indicate that Ca^{2+} bears directly on the events and/or molecular rearrangements that occur at the high affinity catalytic site of RF_1 . However, it is noted that in V_c -ATPase, the interactions between subunits affect strongly the response to Ca^{2+} and Mg^{2+} [49].

In regard to the action of Ca^{2+} and Mg^{2+} on the retention time of the products of unisite ATP hydrolysis, knowledge of the structure of the catalytic site

loaded with Mg^{2+} -ADP or Ca^{2+} -ADP would be valuable, but these data are not available. However, the crystal structure of F_1 with one of its sites occupied by Mg^{2+} -ADP (β_{DP} subunit, in the terminology of Abrahams et al. [50]), and that of dethiobiotin synthetase in complex with Ca^{2+} -ADP show that Ca^{2+} and Mg^{2+} are coordinated differently at the active sites [51]. Moreover in the crystal structure of the ATPase fragment of the 70 kDa heat shock protein, Flaherty et al. [52] observed that the active site occupied by AMP–PNP, Ca^{2+} and Mg^{2+} bind to locus 2.3 Å apart. Therefore, these findings suggest that the rate of ADP release may be related to differences in the coordination of Ca^{2+} and Mg^{2+} at the catalytic site.

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References

- A.K. Souid, H.S. Penefsky, J. Bioenerg. Biomembr. 26 (1994) 627–630.
- [2] J. Weber, A.E. Senior, Biochim. Biophys. Acta 1319 (1997) 19–58.

- [3] A. Baccarini-Melandri, D. Zannoni, J. Bioenerg. Biomembr. 10 (1978) 109–138.
- [4] G. Falk, A. Hampe, J.E. Walker, Biochem. J. 228 (1985) 391–407.
- [5] L. Slooten, S. Vandenbranden, Biochim. Biophys. Acta 976 (1989) 150–160.
- [6] Z. Gromet-Elhanan, J. Bioenerg. Biomembr. 24 (1992) 447–452.
- [7] B.C. Johansson, M. Baltscheffsky, H. Baltscheffsky, Eur. J. Biochem. 40 (1973) 109–117.
- [8] B. Norling, Å. Strid, P. Nyrén, Biochim. Biophys. Acta 935 (1988) 123–129.
- [9] S. Weiss, R.E. McCarty, Z. Gromet-Elhanan, J. Bioenerg. Biomembr. 26 (1994) 573–581.
- [10] A. Gepshtein, C. Carmeli, Eur. J. Biochem. 44 (1974) 593–602.
- [11] V.K. Vambutas, E. Racker, J. Biol. Chem. 240 (1965) 2660–2667.
- [12] J.F. O'Rourke, S.B. Wilson, Biochim. Biophys. Acta 1098 (1992) 224–232.
- [13] H. Muller, H. Neufang, K. Knobloch, Eur. J. Biochem. 127 (1982) 559–566.
- [14] D.B. Hicks, T.A. Krulwich, J. Bacteriol. 169 (1987) 4743– 4749.
- [15] E. Muñoz, M.R.J. Salton, M.H. Ng, M.T. Schor, Eur. J. Biochem. 7 (1969) 490–501.
- [16] M. Hensel, G. Deckers-Hebestreit, K. Altendorf, Eur. J. Biochem. 202 (1991) 1313–1319.
- [17] M. Nishimura, Biochim. Biophys. Acta 64 (1962) 345–352.
- [18] M. Avron, J. Biol. Chem. 237 (1962) 2011–2017.
- [19] C. Grubmeyer, R.L. Cross, H.S. Penefsky, J. Biol. Chem. 257 (1982) 12092–12100.
- [20] T.H. Duncan, A.E. Senior, J. Biol. Chem. 260 (1985) 4901–4907.
- [21] D. Cunningham, R.L. Cross, J. Biol. Chem. 263 (1988) 18850–18856.
- [22] S. Zhang, A.T. Jagendorf, J. Biol. Chem. 270 (1995) 6607– 6614.
- [23] I.M. Glynn, J.B. Chapell, Biochem. J. 90 (1964) 147-149.
- [24] W.R. Sistrom, J. Gen. Microbiol. 28 (1960) 607-616.
- [25] Z. Gromet-Elhanan, D. Khananshvili, Methods Enzymol. 126 (1986) 528–538.
- [26] H.S. Penefsky, Methods Enzymol. 56 (1979) 527-530.
- [27] P.A. Lanzetta, L.J. Alvarez, P.S. Reinach, O.A. Candia, Anal.Biochem. 100 (1979) 95–97.
- [28] J.J. Garcia, A. Gómez-Puyou, M. Tuena de Gómez-Puyou, J. Bioenerg. Biomembr. 29 (1997) 61–70.

- [29] H.S. Penefsky, Proc. Natl. Acad. Sci. U.S.A. 82 (1985) 1589–1593.
- [30] H.S. Penefsky, Methods Enzymol. 126 (1986) 608–618.
- [31] P.K. Smith, R.I. Krohn, G.T. Hermanson, A.K. Mallia, F.H. Gartner, M.D. Provenzano, E.K. Fujimoto, N.M. Goeke, B.J. Olson, D.C. Klenk, Anal. Biochem. 150 (1985) 76–85.
- [32] D.M. Mueller, J. Biol. Chem. 264 (1989) 16552–16556.
- [33] H.S. Penefsky, R.L. Cross, Adv. Enzymol. 64 (1991) 173– 214.
- [34] E. Muneyuki, M. Yoshida, D.A. Bullough, W.S. Allison, Biochim. Biophys. Acta 1058 (1991) 304–311.
- [35] S.G. Dagget, T.A. Tomaszek, S.M. Schuster, Arch. Biochem. Biophys. 236 (1985) 815–824.
- [36] T. Noumi, M. Maeda, M. Futai, FEBS Lett. 213 (1987) 381–384.
- [37] D.M. Mueller, V. Indyk, L. Mcgill, Eur. J. Biochem. 222 (1994) 991–999.
- [38] A.K. Souid, A.H. Penefsky, J. Biol. Chem. 270 (1995) 9074–9082.
- [39] R.L. Cross, C. Grubmeyer, H.S. Penefsky, J. Biol. Chem. 257 (1982) 12101–12105.
- [40] Z. Gromet-Elhanan, S. Weiss, Biochemistry 28 (1989) 3645–3650.
- [41] Å. Strid, P. Nyrén, Biochemistry 28 (1989) 9718–9724.
- [42] M. Montero-Lomelí, O.B. Martins, G. Dreyfus, J. Biol. Chem. 264 (1989) 21014–21017.
- [43] C. Bengis-Garber, Z. Gromet-Elhanan, Biochemistry 18 (1979) 3577–3581.
- [44] M.K. Al-Shawi, D. Parsonage, A.E. Senior, J. Biol. Chem. 265 (1990) 4402–4410.
- [45] P.J. Andralojc, D.A. Harris, Biochim. Biophys. Acta 1016 (1990) 55–62.
- [46] P.J. Andralojc, D.A. Harris, Biochim. Biophys. Acta 1184 (1994) 54–64.
- [47] K. Miwa, M. Yoshida, Proc. Natl. Acad. Sci. U.S.A. 86 (1989) 6484–6487.
- [48] K. Yokoyama, T. Hisabori, M. Yoshida, J. Biol. Chem. 264 (1989) 21837–21841.
- [49] X.-S. Xie, J. Biol. Chem. 271 (1996) 30980–30985.
- [50] J.P. Abrahams, A.G.W. Leslie, R. Lutter, J.E. Walker, Nature (London) 370 (1994) 621–628.
- [51] W. Huang, J. Jia, K.J. Gibson, W.S. Taylor, A.R. Rendina, G. Schneider, Y. Lindqvist, Biochemistry 34 (1995) 10985– 10995.
- [52] K.M. Flaherty, S.M. Wilbanks, C. DeLuca-Flaherty, D.B. McKay, J. Biol. Chem. 269 (1994) 12899–12907.