Purification and Properties of an ATPase from *Sulfolobus solfataricus*

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A sulfite-activated ATPase isolated from *Sulfolobus solfataricus* had a relative molecular mass of 370,000. It was composed of three subunits whose relative molecular masses were 63,000, 48,000, and 24,000. The enzyme was inhibited by the vacuolar ATPase inhibitors nitrate and *N*-ethylmaleimide; 4-chloro-7-nitrobenzofurazan (NBD-Cl) was also inhibitory. *N*-Ethylmaleimide was predominately bound to the largest subunit while NBD-Cl was bound to both subunits. ATPase activity was inhibited by low concentrations of *p*-chloromercuriphenyl sulfonate and the inhibition was reversed by cysteine which suggested that thiol groups were essential for activity. While the ATPase from *S. solfataricus* shared several properties with the ATPase from *S. acidocaldarius* there were significant differences. The latter enzyme was activated by sulfate and chloride and was unaffected by *N*-ethylmaleimide, whereas the *S. solfataricus* ATPase was inhibited by these anions as well as *N*-ethylmaleimide. These differences as well as differences that occur in other vacuolar-like ATPases, isolated from the methanogenic and the extremely halophilic bacteria suggest the existence of several types of archaeal ATPases, none of which have been demonstrated to synthesize ATP. © 1992 Academic Press, Inc.

**F**₀**F**₁ and vacuolar ATPases are membrane-bound proton translocating enzymes. The **F**₀**F**₁ ATPases are associated with bacterial cytoplasmic membranes, mitochondrial membranes, and thylakoids, where they function as ATP synthases. The vacuolar ATPases are located on the endomembranes of eukaryotic cells, where they hydrolyze ATP and generate gradients of protons that are subsequently used to transport solutes into intracellular vacuoles. These enzymes are also differentiated on the basis of the sensitivity of vacuolar ATPases to nitrate, *N*-ethylmaleimide; and the antibiotic bafilomycin (1), agents that do not affect **F**₀**F**₁ ATPases. In addition, the enzymes' subunits differ with respect to their number and relative molecular masses (for recent reviews of **F**₀**F**₁ and vacuolar ATPases see Refs. (2) and (3), respectively). Although the amino acid sequences of the largest of the subunits of **F**₀**F**₁ and vacuolar ATPases suggest that they are related, the overall identity is low (4).

Archaeal ATPases are structurally unlike **F**₀**F**₁ ATPases. The catalytic portion consists of from two to five subunits (5–9) whose relative molecular masses are considerably higher than are those for the analogous subunits from **F**₀**F**₁ ATPases. In addition, there is no evidence for the presence of a membrane component equivalent to the **F**₂ moiety, although in the case of *Sulfolobus acidocaldarius* a low molecular mass DCCD-reactive proteolipid (10) exhibits considerable amino acid sequence homology with subunit c from **F**₀**F**₁ ATPases (11). The amino acid sequence of the α and β subunits of the ATPases from *Methanosarcina barkeri* (5) and *S. acidocaldarius* (12), and the two major subunits from the ATPase from *Halobacterium salinarium* (13) display considerable homology with sequences from subunits B and A, respectively, of vacuolar ATPases (14) which suggests that these enzymes are more closely related to vacuolar rather than **F**₀**F**₁ ATPases. On the other hand, antiserum prepared against the β subunit of the ATPase from *S. acidocaldarius* cross-reacts with the β subunit from various **F**₀**F**₁ ATPases as well as subunit II from *H. saccharovorum* (9).

The ATPases from *H. saccharovorum* and *H. salinarum* (formerly designated *H. halobium*) are similar with respect to the relative molecular masses of the native enzymes

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Abbreviations used: DCCD, dicyclohexylcarbodiimide; NEM, *N*-ethylmaleimide; NBD-Cl, 4-chloro-7-nitrobenzofurazan (or 4-chloro-7-nitrobenzo-2-oxa-1,3-diazole); PAGE, polyacrylamide gel electrophoresis; PCMS, *p*-chloromercuriphenyl sulfonate; SDS, sodium dodecyl sulfate; Caps, 3-(cyclohexylamino)propanesulfonic acid; PMSF, phenylmethylsulfonyl fluoride; Seph 6G, Sepharose 6G.
and their two major subunits (6, 15). Their sensitivity to nitrates and NEM suggests that they may be vacuolar ATPases (16). However, the situation in the halobacteria is complicated in that these ostensibly similar ATPases differ in several significant properties (17). An analogous situation exists in the case of S. acidocaldarius, where two ATPases have been described which possess very different properties (8, 18). We recently purified an ATPase from S. solfataricus whose several properties suggest that this enzyme is yet another type of *Sulfolobus* ATPase. We wish to report on these observations, suggest that they are consistent with the notion that there may be a multiplicity of Archaeal vacuolar-like ATPases, and emphasize that none has been demonstrated to synthesize ATP (i.e., act as an ATP synthase).

**MATERIALS AND METHODS**

*Growth and preparation of cell-free extracts.* Sulfolobus strain 98/2 was obtained from T. Langworthy and identified as *S. solfataricus* (N. Pace, personal communication). It was grown at 70°C in a medium consisting of the following additions (in grams per liter of deionized water): (NH4)2SO4 (1.3), MgSO4·7H2O (0.25), CaCl2·2H2O (0.07), KH2PO4 (0.28), 1-glutamic acid (0.5), and yeast extract (1.0). The pH was adjusted at room temperature to 3.2 with 5 N sulfuric acid. The medium was autoclaved for 15 min at 21 psi and after it had cooled, sterile glucose was added to a final concentration of 0.2% (w/v). Cells were grown in a three-necked 3-liter round bottom flask containing 2 liters of medium. The flask, which was placed in a heating mantle, had a condenser connected to one of the outlets; a gas dispersion tube fitted with a coarse glass-fritted cylinder was connected to the second outlet for the purposes of aerating the culture; and the third outlet was closed and used as a sampling port. The culture was vigorously aerated with sterile air which was first passed through a vacuum/pressure pump and any precipitate was removed by centrifugation at 39,000g for 10 min at 4°C. The supernatant was decanted and used to determine the subunit structure of the enzyme. SDS-PAGE was carried out with 11% gels as described by Laemmli (24). Gels containing isotopes were soaked in Amplify and dried under reduced pressure and the radioactivity was detected on Kodak XAR 5 film by exposing the film at –70°C.

*Determinations of relative molecular mass.* The *M* r of the native enzyme was determined by gel filtration using a 1.5 × 84-cm UltroGel AcA434 column equilibrated in Buffer B. The following standards (with their *M* r s) were used: urease (486,000), catalase (232,000), aldolase (157,000), bovine serum albumin, dimer and monomer (134,000 and 67,000), and ovalbumin (45,000). The *M* r of the subunits was determined by SDS–PAGE using the Sigma SDS-70 low molecular weight kit standards.

*Materials.* Na2 ATP, Na2 ADP, PuMPS, and the SDS-70 low molecular weight kit were obtained from the Sigma Chemical Co. (St. Louis, MO). The Na2 ATP contained 0.02% ATP which represented a quantity whose hydrolysis would not be detected given the conditions we employed to assay for *P* i production. *N*-[2,3-14C]Ethylmaleimide (7 mCi/mmol) was obtained from Amersham Corp. (Arlington Heights, IL) while [*-14C]NBD-Cl (109 mCi/mmol) was purchased from Research Products International Corp. (Mount Prospect, IL). *Hepes* was obtained from Cal Biochem (La Jolla, CA). Proteins were determined with reagents obtained from the Pierce Chemical Co. (Rockford, IL). The PD-10 desalting columns and Centricon 30 microconcentrators were obtained from Pharmacia Fine Chemicals (Piscataway, NJ) and the Amicon Corp. (Lexington, MA), respectively. UltroGel AcA434 was a product of LKB Instruments, Inc. (Gaithersburg, MD).

**RESULTS**

**Purification of the Enzyme**

ATPase activity was present in the membrane and cytoplasmic fractions. This distribution was directly related to the force used to disrupt the cells. In addition, storage of the membranes at 4°C resulted in the gradual appearance of soluble ATPase activity and was associated with the concomitant loss of membrane-bound ATPase activity. Preliminary experiments indicated the membrane and soluble activities were similar with respect to their response to anions, inhibitors, and pH and temperature optima (K. Meier and L. I. Hochstein, unpublished data).

The enzyme in the soluble fraction was unstable and was immediately processed at least through the amo-
TABLE I
Purification of the *S. Solfataricus* ATPase

<table>
<thead>
<tr>
<th>Fraction</th>
<th>Units (μmol/min)</th>
<th>Protein (mg)</th>
<th>Yield (% of total in the soluble fraction)</th>
<th>Specific activity (units/mg protein)</th>
<th>Purification (fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Soluble</td>
<td>91</td>
<td>190</td>
<td>100</td>
<td>0.48</td>
<td>1.0</td>
</tr>
<tr>
<td>AmSO₄</td>
<td>70</td>
<td>65</td>
<td>77</td>
<td>1.1</td>
<td>2.3</td>
</tr>
<tr>
<td>UG</td>
<td>56</td>
<td>17</td>
<td>62</td>
<td>3.3</td>
<td>6.9</td>
</tr>
<tr>
<td>Seph 6B</td>
<td>19</td>
<td>0.43</td>
<td>21</td>
<td>44</td>
<td>92</td>
</tr>
</tbody>
</table>

nium sulfate fractionation step. The soluble fraction was adjusted to a protein concentration of 4 mg/ml with Buffer A and made 50% saturated with respect to ammonium sulfate. This mixture was stirred for 30 min at room temperature (ca. 22°C) and then centrifuged at 10,000g for 30 min at 22°C. The sediment was made up to a protein concentration of about 12 mg/ml in Buffer A and made 50% saturated with respect to ammonium sulfate. This mixture was stirred for 30 min at room temperature (ca. 22°C) and then centrifuged at 10,000g for 30 min at 22°C. The sediment was made up to a protein concentration of about 4 mg/ml with Buffer A (AS fraction) and passed through an UltraGel AcA34 column (1.5 × 85 cm) equilibrated in pH 7.4 Buffer B (20 mM Hepes/6 mM NaOH). Those fractions that contained ATPase activity (Ve/V₀ = 1.42) were combined and designated the UG fraction. The UG fraction was made 18% with respect to (NH₄)₂SO₄ and applied to a Sepharose 6B column (1.6 × 29 cm) that was previously equilibrated in Buffer B that was also 18% with respect to (NH₄)₂SO₄. The column was washed with 100 ml of 18% (NH₄)₂SO₄/Buffer B followed by a decreasing linear (NH₄)₂SO₄ gradient (18 to 6% ammonium sulfate in Buffer B over 200 ml). ATPase activity, which appeared between 13 and 11.5% (NH₄)₂SO₄, was combined, passed through a PD-10 desalting column, concentrated in a Centriicon 30 microconcentrator, and designated as the Seph 6B fraction. The enzyme was stored at 4°C as it was unstable at -19°C and lost approximately 80% of its initial activity within 2 days at that temperature.

Table I summarizes a typical purification of the soluble ATPase starting with 3.5 g of cells. In this particular case, 75% of the total activity was associated with the soluble fraction. The soluble fraction also contained an active pyrophosphatase, the bulk of which remained soluble in 50% ammonium sulfate and which did not adsorb to Sepharose 6B in the presence of 18% ammonium sulfate. Following hydrophobic chromatography on Sepharose 6B and the removal of ammonium sulfate, the ATPase (i.e., the Seph 6B fraction) hydrolyzed 44 μmol of ATP/min/mg of protein which represented a 92-fold purification and a 21% recovery of the activity present in the soluble fraction. Once purified, the enzyme from *S. solfataricus* was extremely stable and could be stored at 4°C for at least 3 months with little loss of activity.

Several proteins were detected in the Seph 6B fraction by PAGE. Only one, which corresponded to the major constituent, exhibited in situ ATPase activity in the gels. To determine the subunit structure of the enzyme, the Seph 6B fraction was further "purified" by PAGE. For this experiment, 4.5 units of ATPase were subjected to PAGE and 3.2 units were subsequently recovered after extraction and concentration. The protein concentration following PAGE could not be determined as some component in the procedure interfered with the protein determination. The electrophoretically purified enzyme was composed of three subunits (Fig. 1a) whose Mᵣ were 63,000, 48,000, and 24,000 (Fig. 1b). This compares with values of 65,000, 51,000, and 20,000 (9) and 69,000, 54,000, and 28,000 (8) for the subunits from the *S. acidocaldarius* ATPase. The Mᵣ of the native enzyme was 370,000 which was consistent with the 3:3:1 subunit stoichiometry proposed for the *S. acidocaldarius* ATPase (18).

**Properties of the Enzyme**

As shown in Fig. 2, ATP hydrolysis took place most rapidly at pH 6.6 when the enzyme was assayed at 86°C which was the temperature at which maximum ATPase activity occurred. There was no measurable activity at 30°C. The enzyme exhibited an absolute requirement for

![FIG. 1. Subunit structure of the *S. solfataricus* ATPase. The Seph 6B fraction (100 μg protein) was "purified" by PAGE and subsequently dissociated with SDS, and examined by SDS-PAGE. (a) Lane 1, molecular mass standards; lane 2, *Sulfolobus* ATPase. (b) Relative mobility (Rᵢ) vs log Mᵣ.](image-url)
Effect of Anions

ATPase activity was variously affected by anions (Fig. 3). Sulfite was stimulatory, with maximum activation taking place between 5 and 10 mM sulfite. Concentrations greater than 10 mM sulfite resulted in a progressive decrease in the extent of activation and eventual inhibition of ATP hydrolysis. This was an effect not previously reported for the other Sulfolobus ATPases. Nitrate also inhibited the enzyme. A 50% inhibition occurred in the presence of 8 mM nitrate, and 50 mM nitrate resulted in maximum inhibition (87%) of ATPase activity. The enzyme was inhibited by sulfate. A 50% inhibition was produced by 25 mM sulfate. The ATPase was inhibited by chloride although it was not too sensitive to that anion and was unaffected by 50 mM sodium bicarbonate. Replacing sodium with ammonium ion had no significant effect on sulfate or chloride inhibition (data not shown). This suggests that the anion inhibition was neither quantitatively nor qualitatively related to the cation.

Effect of Inhibitors

The *S. solfataricus* ATPase was inhibited by NEM (Fig. 4a), an alkylationing reagent that reacts with sulphydryl groups, although the reagent will react with amino residues when conditions are mildly alkaline (25). Maximum inhibition occurred between 500 mM and 1 mM NEM (Fig. 4a). Divalent cations. Magnesium and manganese were equally effective, whereas calcium was ineffective. ATPase activity increased with the Mg/ATP ratio (ATP = 12.5 mM), reaching a maximum between 0.25 and 0.5; higher ratios resulted in a marked inhibition of ATPase activity. An apparent $K_m$ of 0.6 mM ATP was determined from Lineweaver-Burke plots (Mg/ATP = 0.5). The enzyme hydrolyzed the magnesium salts of ATP, GTP, and ITP at approximately the same rate which was about 5 and 50 times the rates observed with the magnesium salts of UTP and CTP, respectively. The Seph 6B fraction hydrolyzed Mg-ADP and MgP$_4$O$_7$ at 9 and <1% of the rate observed with Mg-ATP when assayed using conditions optimal for ATP hydrolysis. Since the Seph 6B fraction contained several minor components, the portion of ADP hydrolyzing activity associated with the *Sulfolobus* was not certain. Mg-ADP also inhibited ATPase activity but determining a precise value for $K_i$ was complicated by the simultaneous hydrolysis of Mg-ADP. A 57% inhibition of ATPase activity was observed at ATP and ADP concentrations of 12.5 and 6.2 mM, respectively (Mg/nucleotides = 0.5). Plots of $1/v$ versus $1/S$ at different concentrations of ADP affected the slopes but not the intercepts indicating that Mg-ADP was a competitive inhibitor with respect to Mg-ATP.

![FIG. 2. The effect of pH on ATPase activity. The Seph 6B fraction (2.5 µg protein) was assayed in the presence of the following buffers which were adjusted to the desired pH at 86°C: Mes (○), Hepes (●), and Caps (□). 100% activity equals the production of 1.08 µmol P/O/10 min.](image)

![FIG. 3. Effect of anions on ATPase activity. The Seph 6B fraction (2.5 µg protein) was preincubated for 2 min at 86°C in the presence of the indicated concentrations of the sodium salts of sulfite (●), bicarbonate (□), chloride (●), sulfate (○), and nitrate (▲) and subsequently assayed for ATPase activity. The results are reported as % of the activity observed in the absence of added anions which was assigned a value of 100% and was equal to the production of 1.15 µmol P/O/10 min.](image)
The enzyme was extremely sensitive to PCMS. As shown in Fig. 4b, 500 nM PCMS produced a 35% inhibition and enzyme activity was totally inhibited in the presence of 20 μM PCMS. Preincubating the enzyme for 10 min in the presence of 5 μM PCMS and subsequently for 2 min in the presence of 500 μM cysteine reduced the inhibition from 88 to 8%. The low concentrations of PCMS that inhibited the enzyme as well as the reversal of inhibition by cysteine were consistent with the involvement of thiols and by extension suggested that NEM also inhibited by reacting with thiol residues.

NBD-Cl inhibits FoF1 ATPases by reacting with a single tyrosinyl residue in the β subunit, and the inhibition can be reversed by thiols (26). In the case of vacuolar ATPases the mode of action is not known and the inhibitor binds to a number of subunits. The ATPase from S. solfataricus was also inhibited by NBD-Cl. Preincubating the enzyme with 1 mM NBD-Cl for 15 min at 86°C inhibited ATPase activity 83% which was the maximum inhibition attained under these conditions (Fig. 5a). When the enzyme was preincubated at 86°C in the presence of 125 μM NBD-Cl, the inhibition, which was 25% after 15 min, was 77% after 2 h and appeared to continue to increase after that time (Fig. 5b). As also shown in Fig. 5b, the enzyme did not lose activity when incubated in buffer at 86°C for 120 min. As in the case of FoF1 ATPases (26), cysteine reversed NBD-Cl inhibition of the Sulfolobus ATPase. In addition, cysteine activated the enzyme. These effects are shown in Table II. The extent of reversal was inversely related to the time the enzyme was exposed to NBD-Cl. Virtually all the ATPase activity was recovered when the enzyme was first incubated with 250 μM NBD-Cl for 15 min (which resulted in 52% inhibition) and then 1 mM cysteine for 10 min. When the enzyme was incubated for 3 h with 250 μM NBD-Cl (which resulted in a 96% inhibition) before the addition of cysteine, 42% of the activity was recovered. This suggested the existence of at least two NBD-Cl derivatives of the enzyme, only one of which was reversed by cysteine, and recalled the behavior of NBD-Cl with FoF1 ATPases (26). The presence of Mg-ATP did not protect the Sulfolobus ATPase against NBD-Cl or NEM inhibition, which was unlike the ATPase from H. saccharovorum (16).

When the ATPase was incubated with [14C]NEM so that the enzyme was maximally inhibited, the bulk of the radioactivity was associated with the 63,000-Da subunit with some radioactivity found with the 45,000- and 24,000-Da subunits (Fig. 6). When the enzyme was incubated in the presence of [14C]NBD-Cl, the inhibitor appeared to be the equally distributed between the two largest subunits (Fig. 6). It is not clear if this distribution reflected non-specific interactions due to the reactive nature of NBD-Cl (26) or if the high temperature during the assay exacerbated the reactivity and lack of specificity of NBD-Cl.
FIG. 5. Inhibition of ATPase activity by NBD-CI. (a) The Seph 6B fraction (2.5 µg protein) was preincubated for 2 min at 86°C in the presence of the indicated concentrations of NBD-CI and subsequently assayed for ATPase activity. (b) The effect of preincubation on inhibition. The enzyme was incubated at 86°C for the indicated times in the presence (●) and absence (○) of 125 µM NBD-CI and assayed for residual ATPase activity as described under Materials and Methods. The results in both cases are reported as % of the activity observed in the absence of added NBD-CI, where 100% equals the production of 880 nmol of P10/min.

ATPase activity was not affected by azide (10 mM), quercetin (200 mM), or vanadate (10 mM). DCCD (100 µM) was not inhibitory when incubated with the enzyme overnight at pH 6 at room temperature (22°C), conditions which inhibit the ATPase from H. saccharovorum and result in the binding of the inhibitor to subunit II (27).

Cl and resulted in intersubunit migration of the inhibitor subsequent to initial binding.

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DISCUSSION

The enzyme from S. solfataricus, like other archaeal ATPases, resembled vacuolar ATPases more than the F0F1 ATPase. The S. solfataricus ATPase was inhibited by NEM and nitrate, and the number and the relative molecular masses of its subunits was more in character with vacuolar ATPases. In addition, NEM was bound to the largest of the Sulfolobus ATPase subunits, as is true with the ATPase from H. saccharovorum (Sulzner et al., manuscript in preparation) and vacuolar ATPases, which in the latter case is proposed to be the catalytic subunit (28, 29). However, unlike the vacuolar and halobacterial ATPases, where the presence of ATP repressed NEM inhibition and decreased the incorporation of inhibitor, no substrate protection was observed in the case of the Sulfolobus enzyme.

The ATPase from S. solfataricus shared a number of properties with the S. acidocaldarius ATPase. The specific activities of the purified S. solfataricus and S. acidocaldarius (18) ATPases were similar; both ATPases were inhibited by similar concentrations of nitrate; and the relative molecular masses of the native enzymes and three of their subunits were in reasonable agreement. Recently, the enzyme from S. acidocaldarius was reported to contain a fourth subunit (9). Although we did not detect such a subunit, the composition of the S. solfataricus ATPase cannot be unequivocally established at this time. Proteolytic activity as well as the electrophoretic method used

![Graph showing inhibition of ATPase activity by NBD-CI.](image)

TABLE II
Reversal of NBD-CI Inhibition by Cysteine

<table>
<thead>
<tr>
<th>Preincubation time</th>
<th>Additions during preincubation</th>
<th>15 min</th>
<th>3 h</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard</td>
<td></td>
<td>0.88</td>
<td>0.98</td>
</tr>
<tr>
<td>+ NBD-CI</td>
<td></td>
<td>0.42</td>
<td>0.04</td>
</tr>
<tr>
<td>+ Cysteine</td>
<td></td>
<td>1.51</td>
<td>1.54</td>
</tr>
<tr>
<td>+ NBD-CI/cysteine</td>
<td></td>
<td>1.38</td>
<td>0.64</td>
</tr>
</tbody>
</table>

Note. The Seph 6B fraction (2.5 µg protein) was preincubated in 50 mM Na-Hepes buffer at room temperature. The pH of the buffer was 7.2 at room temperature and 6.6 at 86°C. Where indicated, NBD-CI (250 µM) or cysteine (1 mM) was present. After the indicated preincubation time, cysteine (1 mM) was added and after an additional 10 min at room temperature, the reaction mixtures were incubated for 2 min at 86°C and Mg-ATP was added to start the reaction. The results are presented as micromoles P10, produced in 10 min.

![Radioautograph showing NEM and NBD-CI labeling of the S. solfataricus ATPase.](image)
to prepare the ATPase could have individually or collectively led to the loss of that subunit.

However, the Sulfolobus ATPases differ in ways to suggest they are not identical enzymes. Sulfate and chloride, which stimulate the ATPases from \textit{S. acidocaldarius}, inhibit the \textit{S. solfataricus} enzyme. Bicarbonate, which stimulates the enzyme from \textit{S. acidocaldarius}, does not affect the ATPase from \textit{S. solfataricus}. The Sulfolobus ATPases are also dissimilar with respect to their sensitivity to NEM and PCMS. The enzyme from the \textit{S. acidocaldarius} is not significantly inhibited by NEM (8) and is considerably less sensitive to mercurials (18) than is the ATPase from \textit{S. solfataricus}. The enzymes also differ with respect to their pH optima. In the absence of sulfite, the \textit{S. acidocaldarius} ATPase exhibits acidic and alkaline maxima with a minimum at approximately pH 6.5. The addition of sulfite to the enzyme isolated by Lübben \textit{et al.} (18) results in a single and relatively broad maximum (pH 5.5 to 7.0) with a 300% increase in enzyme activity. This stimulation is due to the increase in activity at the pH minimum. There is no stimulation at the alkaline pH maximum and only a 20% enhancement at the acidic pH maximum. The addition of sulfite to the ATPase described by Konishi \textit{et al.} (8) enhances the activity at both optima so that the enzyme still exhibits two optima with the maximum stimulation of absolute activity occurring at the acidic maximum. The ATPase from \textit{S. solfataricus} displayed a single pH optimum located between pH 6.5 and 7.2, regardless of the presence of sulfite, and the maximum sulfite stimulation was of the order of 60%. These and additional differences are summarized in Table III.

Differences also exist among ostensibly similar ATPases from other \textit{Archaea}. The enzymes from \textit{H. saccharovorum} and \textit{H. halobium} have the same relative molecular masses as do their two major subunits, and both are equally sensitive to nitrate and NBD-Cl. On the other hand, the enzymes differ with respect to their pH optima, detergent activation, and, most significantly, the effect of anions. The enzyme from \textit{H. saccharovorum} is activated by chloride and detergent, whereas the enzyme from \textit{H. halobium} exhibits very little activity in the presence of chloride, is activated by sulfate, sulfite, and citrate, and is unaffected by detergent. In addition, the enzyme from \textit{H. saccharovorum} is unaffected by the nature of the cation, unlike the ATPase from \textit{H. halobium} (15, 17). The ATPases isolated from methanogens also appear to differ. The enzyme from \textit{M. barkeri} (30) is composed of two subunits (\textit{M}, 62,000 and 49,000) and is activated by sulfite which causes a shift in the pH optimum to a more alkaline value. By way of contrast, the ATPase from \textit{Methanoblobus tindarius} is not activated by sulfite and is composed of four subunits whose relative molecular masses are 67,000, 52,000, 20,000, and <10,000 (31).

While archael ATPases appear similar, these differences suggest that they may be functionally different enzymes. It should be pointed out that, although ATP synthase has been demonstrated in various \textit{Archaea} (10, 31, 32), there is no direct evidence that such synthesis is caused by any of the archaeal ATPases which have been isolated to date. Whether \textit{Archaea} synthesize ATP using an enzyme closely related to vacuolar ATPases, an \textit{F}_\text{o}\text{F}_\text{ATP synthase, or a third type of enzyme has yet to be established.

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REFERENCES


