Structure and Subunit Arrangement of the A-type ATP Synthase Complex from the Archaeon *Methanococcus jannaschii* Visualized by Electron Microscopy

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From the ‡Universität des Saarlandes, Fachrichtung 2.5-Biophysik, D-66421 Homburg, Germany, §Department of Biophysics Chemistry, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, 9747 AG Groningen, The Netherlands, and ¶Institut für Mikrobiologie, Johann Wolfgang Goethe-Universität Frankfurt, D-60439 Frankfurt, Germany

In Archaea, bacteria, and eukarya, ATP provides metabolic energy for energy-dependent processes. It is synthesized by enzymes known as A-type or F-type ATP synthase, which are the smallest rotary engines in nature (Yoshida, M., Muneyuki, E., and Hisabori, T. (2001) *Nat. Rev. Mol. Cell. Biol.* 2, 669–677; Imamura, H., Nakano, M., Noji, H., Muneyuki, E., Ohkuma, S., Yoshida, M., and Yokoyama, K. (2003) *Proc. Natl. Acad. Sci. U. S. A.* 100, 2312–2315). Here, we report the first projected structure of an intact A$_1$A$_0$ ATP synthase from *Methanococcus jannaschii* as determined by electron microscopy and single particle analysis at a resolution of 1.8 nm. The enzyme with an overall length of 25.9 nm is organized in an A$_1$ headpiece (9.4 $\times$ 11.5 nm) and a membrane domain, A$_0$ (6.4 $\times$ 10.6 nm), which are linked by a central stalk with a length of $\sim$8 nm. A part of the central stalk is surrounded by a horizontal-situated rod-like structure (“collar”), which interacts with a peripheral stalk extending from the A$_0$ domain up to the top of the A$_1$ portion, and a second structure connecting the collar structure with A$_1$. Superposition of the three-dimensional reconstruction and the solution structure of the A$_1$ complex from *Methanosarcina mazei* Gø1 have allowed the projections to be interpreted as the A$_1$ headpiece, a central and the peripheral stalk, and the integral A$_0$ domain. Finally, the structural organization of the A$_1$A$_0$ complex is discussed in terms of the structural relationship to the related motors, F$_1$F$_0$ ATP synthase and V$_1$V$_0$ ATPases.

ATP synthases/ATPases are present in every life form and are the most important enzymes for the energy metabolism of the cell (1). They catalyze the formation of ATP at the expense of the transmembrane electrochemical ion gradient. They arose from a common ancestor that underwent structural and functional changes leading to three distinct classes of A$_1$A$_0$, F$_1$F$_0$, and V$_1$V$_0$ ATP synthases/ATPases. The V$_1$V$_0$ ATPases, found in organelles of eukaryotes, lost their ability to synthesize ATP. Their function is to create steep ion gradients at the expense of ATP hydrolysis (2). Archaea contain ATPases, the A$_1$A$_0$ ATP synthases, that are structurally similar to the V$_1$V$_0$ ATPases but synthesize ATP like the F$_1$F$_0$ ATPases. For example, the A$_1$A$_0$ ATP synthases contain duplicated and even triplicated K subunits (proteolipids) (3, 4). The A$_1$A$_0$ ATP synthase has at least nine subunits (A$_3$B$_3$CDFHIIK$_3$), but the actual subunit stoichiometry, especially regarding the proteolipid subunits K in A$_1$ ATPases, is different in various organisms (12, 6, 4, or as suggested by genomic data, only 1 (5)). The A$_1$A$_0$ ATP synthase is composed of a water-soluble A$_1$ ATPase and an integral membrane subcomplex, A$_0$. ATP is synthesized or hydrolyzed on the A$_1$ headpiece consisting of an A$_3$B$_3$ domain, and the energy that is provided for or released during that process is transmitted to the membrane-bound A$_0$ domain (4). The energy coupling between the two active domains occurs via the so-called stalk part, an assembly proposed to be composed of the subunits C, D, and F (6, 7).

Insight in the molecular structure of the A$_1$ ATPase from *Methanosarcina mazei* Gø1 whose A$_1$ domain is made up of the five different subunits, A$_3$B$_3$CDF (8). The data have shown that the hydrated A$_1$ ATPase is rather elongated with a headpiece of $10 \times 9.4$ nm in dimension and a stalk of $\sim$8.4 nm in length. A comparison of the central stalk of this A$_1$ complex with bacterial F$_1$ and eukaryotic V$_1$ ATPase indicates different lengths of the stalk domain (8, 9). Image processing of electron micrographs of negatively stained A$_1$ ATPase from *M. mazei* Gø1 (7) has revealed that the headpiece consists of a pseudohexagonal arrangement of six masses surrounding a seventh mass. These barrel-shaped masses of $\sim$3.2 and 2.8 nm in diameter and 7.5 and 5.0 nm in length, which consist of the major subunits A and B, are arranged in an alternating manner (7). The hexagonal barrel of subunits A and B encloses a cavity of $\sim$2.3 nm in the middle in which part of the central stalk is asymmetrically located. The stalk protrudes from the bottom side of the headpiece forming an angle of $\sim$20$^\circ$ with the vertical axis of the molecule. At the upper end of the hexagonal barrel, extensions can be observed that are assumed to belong to the N termini of subunit A (7). Further insights into the topology of the A$_1$ ATPase were obtained by differential protease sensitivity (8) and cross-linking studies (6, 7). These studies...
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resulted in a model in which the subunits C, D (partly), and F form the central stalk domain (7).

However, in contrast to the related F- and V-type ATP synthases/ATPases, little is known regarding the overall structure of the A₁A₀ molecule, which is largely due to the instability of the isolated complexes (10). Most recently, an isolation procedure of the A₁A₀ ATP synthase of the hyperthermophilic Archaea *Methanococcus jannaschii* resulted in a complete and functionally coupled enzyme (11). Besides the property of being an enzyme of a hyperthermophilic organism whose multienzyme complexes are believed to be more stable than those of mesophiles, the *M. jannaschii* A₁A₀ ATP synthase is of particular interest because it has a K subunit three times the size of that of most bacteria and Archaea. Furthermore, this subunit has lost one of the ion translocating residues (12). Here, we used electron microscopy to visualize directly the structure of the A₁A₀ ATP synthase from *M. jannaschii*. A comparison with the low resolution structure of the A₁ ATPase from *M. mazei* G60, derived from small-angle x-ray scattering data and single particle electron microscopy, allowed the unambiguous identification of most of the densities in the stalk domain and the A₀ part. The structure of the complete A₁A₀ ATP synthase also facilitates, for the first time, a comparison with structural models of the related F₁F₀ ATP synthase and V₁V₀ ATPase holoenzymes.

**EXPERIMENTAL PROCEDURES**

**Materials**—All of the chemicals were of reagent grade and were obtained from Merck (Darmstadt, Germany), BIOMOL (Hamburg, Germany), Roth (Karlsruhe, Germany), or Sigma (Deisenhofen, Germany).

**Protein Preparation**—The A₁A₀ ATP synthase of *M. jannaschii* was purified by sucrose density centrifugation and anion-exchange chromatography (DEAE-Sepharose) as described previously (11). ATPase-active fractions were pooled and concentrated on Centricon 100-kDa concentrators (Millipore). The concentrated sample was loaded on a Superose 6 column (10/30, Amersham Biosciences) and eluted with 50 mM Tris-HCl (pH 7.5), 5 mM MgCl₂, 10% glycerine, 150 mM NaCl, 0.1% Triton X-100, 0.1 mM phenylmethylsulfonyl fluoride, and Pefabloc SC (a final concentration of 1 mM, BIOMOL). The peak fractions, which were stained with silver, were collected and analyzed by SDS-PAGE (13, 14). Mg²⁺-dependent ATPase activity was determined as described earlier (15).

**Electron Microscopy and Image Analysis**—Protein was prepared on freshly glow-discharged carbon-coated copper grids stained with 2% uranyl acetate. Images of the negatively stained A₁A₀ ATP synthase were collected on a Philips CM20FEG electron microscope operating at 200 kV and liquid N₂-cooled specimen to reduce radiation damage. Images of 2,048 × 2,048 pixels (after a binning of 2) were recorded at ×67,200 magnification at a pixel size of 30 µm with a Gatan 4000 SP 4K slow-scan CCD camera with GRACE software for semi-automated specimen selection and data acquisition (16). Single particle analysis was performed with the GRIP (Groningen image processing) software package on a PC cluster. A total of 17,238 single particle projections (128 × 128 pixel frame; pixel size of 0.34 nm) from 331 images were obtained by selecting all of the discernable particles. For each micrograph, the defocus value was determined and a simple contrast transfer function correction by phase reversal was done (17). After band-pass filtering, the images were subsequently subjected to multireference alignment, multivariate statistical analysis, and hierarchical ascendant classification. This dataset was divided into two subsets including either one or two peripheral stalks to obtain a more homogenous dataset for a refinement of these classes. The subsets were analyzed in parallel by reference-free alignment (18). Each rotational and translational alignment was repeated four times, and classification was done by multivariate statistical analysis. Datasets were again divided and aligned as described above. The final classification of the homogenous datasets was performed by multivariate statistical analysis and hierarchical classification to extract the key structural features of the enzyme (19). The resolution of the class averages was measured according to van Heel (20).

**RESULTS**

**Subunit Composition and Electron Microscopy**—A characteristic gel of the preparation of the A₁A₀ ATP synthase from *M. jannaschii* is presented in Fig. 1A showing the nine subunits, A–F, H, I, and K, with apparent molecular masses of 66, 51, 45, 25, 23, 11, 10, 77, and 21 kDa, respectively. A typical electron microscopy raw image of the enzyme yields monodisperse particles with almost no contamination by smaller particles that could represent dissociated complexes or fragments (Fig. 1B). A total of 17,238 such molecular images were subjected to image processing. Fig. 2 demonstrates different class sums of the A₁A₀ ATP synthase projections obtained after several steps of reference-free translational/rotational alignment, multivariate statistical analysis, and multireference alignment. All of the projections reveal a tripartite structure consisting of a headpiece, a membrane-embedded domain, and a connecting stalk region. The classes can be grouped in respect

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**Fig. 1.** SDS-PAGE of isolated A₁A₀ ATP synthase from *M. jannaschii* and an electron micrograph of the negatively stained complex. A, A₁A₀ ATP synthase was applied to SDS-PAGE (10%). To separate the subunits D (25 kDa) and E (23 kDa), the enzyme was loaded on a 17.5% gel (B). Both gels were stained with silver. The K-oligomer is SDS-resistant as shown recently (11) (C). Bar represents 50 nm.
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Fig. 2. A gallery of selected classes resulting from the last multivariate statistical analysis and classification of 17,238 particles of the A1:A0 ATP synthase. Four classes (1–4) showing either one (A) or two (B) peripheral stalks in addition to the central stalk are shown.

Fig. 3. Total averages calculated from 410 (A), 497 (B), and 316 (C) images. C, a projection at around 40° compared with that in B. Bar represents 20 nm. Labels: black arrows, masses of the peripheral stalks connected with the A1 headpiece; white arrowhead, asymmetric upper part of the central stalk; black asterisk, mass connecting the A0 with the collar like domain; white arrows, mass extending from the collar and the A0 domain.

Localization of the Subunits Inside the A1:A0 ATP Synthase—A known three-dimensional reconstruction of the asymmetrical A1 complex from M. mazei G61 (7) determined from tilt pairs of negatively stained molecules was superimposed on the projection of the A1:A0 ATP synthase from M. jannaschii (Fig. 4, panel C) by rotating the A1 subcomplex in 5° steps through 360°. One of the projections of the A1 from M. mazei G61 is well accommodated within the A0 headpiece, composed of the A0B3D subassembly (7) and the upper central stalk, which is only partially (35%) solved in the three-dimensional reconstruction of the A1 ATPase from M. mazei G61 (7). In this projection, one of the catalytic A subunits is on the right of the A0 domain, implying that the peripheral stalk on the right may be close to this major A subunit. Nevertheless, from the superposition of the A1 profile with the A0 part in the A1:A0 ATP synthase images, it is clear that the cap at the top of the A1 headpiece (Figs. 3B and 4C) does not belong to the A0B3D subassembly. To further examine the composition of the central stalk, the projection of the A1:A0 ATP synthase from M. jannaschii (7) was compared with the solution structure of the A0B3CDF complex of the A1 ATPase from M. mazei G61 deduced from solution x-ray scattering data (8). The central stalk of the hydrated A0B3CDF complex, which consists of the subunits C, F, and a part of subunit D, is 8.4 nm in length (8) and fits well to the dimensions (8 nm) of the elongated central stalk of the negative-stained A1:A0 ATP synthase, indicating that the central stalk is made up by the subunits C, D (partly), and F.

DISCUSSION

The A1:A0 ATP synthase has been described as a chimeric enzyme combining the structural and functional features of F1F0 ATP synthases and V1V0 ATPases (4). Single particle analysis resulted in the visualization of projections of the A1:A0 ATP synthase from M. jannaschii consisting of an A1 headpiece and an A0 domain linked by a central stalk and two peripheral stalks. The A1 headpiece fits well with the projection of the recently determined three-dimensional reconstruction with the A1 complex from M. mazei G61 composed of the hexagonal A0B3 domain surrounding a cavity in which the central stalk subunit D is located (7, 8). The subunit is displaced toward an A-B-A triplet (7), allowing the rearrangements of the central D sub-
unit as demonstrated for the A1 ATPase from M. mazei Gö1 (6, 7) and the related Thermus thermophilus \( A_{\text{N-1}} \) ATPase (21). A key feature from the superposition of the A1 complex from \( M. \) mazei Gö1 and the A1A0 ATP synthase is the close fit at the top of the A1 headpiece showing the knoblike structures. These knobs, also found in the related V-type ATPase (22–25) but absent in the F-type ATP synthases (26–28), are formed by the N-terminal non-homologous inserts (80–90 amino acids) of the three catalytic A subunits, which alternate with the nucleotide-binding B subunits (7, 29). They point out that the cap at the top of the A1 headpiece is rather elongated (7, 30).

The comparison of the A1A0 ATP synthase with the recently determined envelope of the hydrated \( A_{\text{B}_{2}}C_{D}F \) complex derived from small-angle x-ray scattering data (8) from \( M. \) mazei Gö1 is superimposed on the projection of the A1A0 ATP synthase from \( M. \) jannaschii, respectively.

The question that now arises is, which subunits of the A1A0 ATP synthase as isolated has nine subunits (A1–I, K). Five of them form the A1 part and are assembled in the stoichiometry \( A_{2}B_{2}C_{D}F \) (see above). The I and K subunits form the membrane domain, \( A_{0} \). Subunit I (70 kDa) is very similar to subunit a of V1V0 ATPases with a hydrophilic N-terminal and a hydrophobic C-terminal domain. The C terminus of subunit I is predicted to have seven transmembrane helices and is assumed to be functionally similar to subunit a of the V1V0 ATPases and F1F0 ATP synthases (3). A and B subunits are labeled in dark and light grey, respectively. The subunit topology in the A-type ATP synthase is based on biochemical (6–8) and structural data (Refs. 8, 9, and this work). The tricapped proteolipids of \( M. \) jannaschii arose by gene triplication followed by a fusion of the gene copies and resulting in the proposed stoichiometry of four K subunits (4).

Stalks, and the additional mass on top of A1. The A1A0 ATP synthase is predicted as isolated has nine subunits (A1–I, K). Five of them form the A1 part and are assembled in the stoichiometry \( A_{2}B_{2}C_{D}F \) (see above). The I and K subunits form the membrane domain, \( A_{0} \). Subunit I (70 kDa) is very similar to subunit a of V1V0 ATPases with a hydrophilic N-terminal and a hydrophobic C-terminal domain. The C terminus of subunit I is predicted to have seven transmembrane helices and is assumed to be functionally similar to subunit a of the V1V0 ATPases and F1F0 ATP synthases (3). The N-terminal domain is predicted to be highly α-helical and assumed to be the functional homolog of the soluble domain of peripheral stalk subunit b of F1F0 ATP synthases. Because only one of the peripheral stalks is clearly attached to the outside of the \( A_{0} \) domain, we conclude that the hydrophilic N terminus of subunit I emerges from the membrane-embedded \( A_{0} \) part and may go up along the side of A1 until the top of the A1 headpiece (Fig. 5). Whether the N-terminal domain might partly contribute to the cap on the top of the A1A0 molecule can only be speculated. In the presented average, the peripheral stalk (right) has a kinked structure in the lower part, giving this domain the flexibility to wrap around the A1 headpiece and end up as the cap on the top (Fig. 3, B and C). Insertion and deletion of altered length in the so-called “tether” domain of the peripheral stalk subunit b of the Escherichia coli F1F0 ATP synthase, which is located above the membrane service, can be tolerated by the enzyme, indicating that this related connecting stalk has an inherent flexible structure (31).

It has been suggested for the F1F0 ATP synthases that flexibility of the domain might allow reorientation of the stalk to act as a stator for rotation in one direction during ATP synthesis and in the opposite direction during ATP hydrolysis (31, 32).

Subunit K is a homolog of the F-type subunit c with two transmembrane helices. It consists of fused tandem repeats of sequences corresponding to the F-type subunit. \( M. \) jannaschii has a subunit K with six membrane-spanning helices (27 kDa) but with only two active carboxylates per monomer (12), which are involved in ion conduction along the membrane. As in the case of the F-type ATP synthases (33, 34) and V-type ATPases (35), the K subunits (or c in the F- and V-type ATPases) are thought to form a ring, which belongs to the rotary element inside the A1A0 ATP synthase. As shown in Fig. 4, the bottom of the central CDF-stalk domain spans the upper center of the \( A_{0} \) domain, facilitating the direct contact of the rotary el-

**Fig. 4.** A, C, and D, comparison of the A1A0 ATP synthase from \( M. \) jannaschii (A) with the projection of the three-dimensional reconstruction of the A1 complex (C) (7) and the low resolution structure of the hydrated A1B3CDF complex (D) (8) from \( M. \) mazei Gö1. B, side and top view of the surface representation of the three-dimensional reconstruction of the A1 ATPase from \( M. \) mazei Gö1 at a 3.2-nm resolution (7). The black arrow points at the groove of the A1 headpiece. The side view of the A1 complex (gold; C) and the envelope of the hydrated A1B3CDF complex derived from small-angle x-ray scattering data (green; D) from \( M. \) mazei Gö1 are superimposed on the projection of the A1A0 ATP synthase from \( M. \) jannaschii, respectively.

**Fig. 5.** Model of the subunit topology in the A1A0 ATP synthase from \( M. \) jannaschii. A1 and A0 subunits are labeled in dark and light grey, respectively. The subunit topology in the A-type ATP synthase is based on biochemical (6–8) and structural data (Refs. 8, 9, and this work). The tricapped proteolipids of \( M. \) jannaschii arose by gene triplication followed by a fusion of the gene copies and resulting in the proposed stoichiometry of four K subunits (4).
ments, which consists of an ensemble made from the central stalk (CDP domain) and a ring of hydrophobic K subunits in the A1 membrane domain (21).

The second peripheral stalk appears to be connected to the collar domain and goes up to the A1 headpiece. Probable candidates for this stalk are the remaining A1A0-hydrophilic subunits H (12 kDa) and E (25 kDa) with the latter predicted to be highly α-helical (12). The modest contact area of this peripheral stalk with the A1 headpiece, which is also evident in electron micrographs of the related bacterial V1V0 ATPase from *Caloramator fervidis* (36), might be caused partially by stain accumulation. The top view projection of the rotated A1F1/F0 ATP synthase is uncertain, these classes of ATPases/V1V0 ATPases, such as the catalytic A1 headpiece and the central stalk domain. Although the F1F0 ATP synthases and V1V0 ATPases, such as the catalytic A1/F1/V1 headpiece and the central stalk domain. Although the positions of the second peripheral stalk appears to be connected to the collar domain and goes up to the A1 headpiece. Probable connections, because such projection are not present in significant numbers if intact A1A0 molecules are prepared.

In summary, the first two dimensional projection maps of the A1A0 ATP synthase from *M. jannaschii* presented provides the structural basis toward a fuller understanding of the mechanistic events occurring in this class of enzymes. The reconstruction at a 1.8-nm resolution shows similarities and diversities between the structural modules to the evolutionary-linked F1F0 ATP synthases and V1V0 ATPases, such as the catalytic A1/F1/V1 headpiece and the central stalk domain. Although the existence of one (26, 37) or two (27) peripheral stalk(s) in the F1F0 ATP synthase is uncertain, these classes of ATPases/synthases might need at least one peripheral stalk acting as a stator that prevents the major hexameric arranged subunits (α3β3 or A6B6) from following the rotation of the central stalk domain. Whether the visualized second peripheral stalk in the V1V0 ATPase and in the presented A1A0 ATP synthase might act as a regulatory domain in the A-type ATP synthase as described for the plant V ATPase (25) can now be addressed.

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