Demonstration of Phosphoryl Group Transfer Indicates That
the ATP-binding Cassette (ABC) Transporter Cystic Fibrosis
Transmembrane Conductance Regulator (CFTR) Exhibits
Adenylate Kinase Activity*

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Background: Electrophysiological studies indicated that Cl− channel function of cystic fibrosis transmembrane conductance regulator (CFTR) can be coupled to adenylate kinase activity (ATP+AMP ⇄ 2 ADP).

Results: CFTR catalyzes phosphoryl group transfer between a nucleotide triphosphate and a photoactivatable AMP analog.

Conclusion: CFTR exhibits adenylate kinase activity.

Significance: These data demonstrate biochemically that a membrane-bound ABC transporter can function as an adenylate kinase.

Cystic fibrosis transmembrane conductance regulator (CFTR) is a membrane-spanning adenosine 5′-triphosphate (ATP)-binding cassette (ABC) transporter. ABC transporters and other nuclear and cytoplasmic ABC proteins have ATPase activity that is coupled to their biological function. Recent studies with CFTR and two nonmembrane-bound ABC proteins, the DNA repair enzyme Rad50 and a structural maintenance of chromosome (SMC) protein, challenge the model that the function of all ABC proteins depends solely on their associated ATPase activity. Patch clamp studies indicated that in the presence of physiologically relevant concentrations of adenosine 5′-monophosphate (AMP), CFTR Cl− channel function is coupled to adenylate kinase activity (ATP+AMP ⇄ 2 ADP). Work with Rad50 and SMC showed that these enzymes catalyze both ATPase and adenylate kinase reactions. However, despite the supportive electrophysiological results with CFTR, there are no biochemical data demonstrating intrinsic adenylate kinase activity of a membrane-bound ABC transporter. We developed a biochemical assay for adenylate kinase activity, in which the radioactive γ-phosphate of a nucleotide triphosphate could transfer to a photoactivatable AMP analog. UV irradiation could then trap the 32P on the adenylate kinase. With this assay, we discovered phosphoryl group transfer that labeled CFTR, thereby demonstrating its adenylate kinase activity. Our results also suggested that the interaction of nucleotide triphosphate with CFTR at ATP-binding site 2 is required for adenylate kinase activity. These biochemical data complement earlier biochemical studies of CFTR and indicate that the ABC transporter CFTR can function as an adenylate kinase.

Cystic fibrosis transmembrane conductance regulator (CFTR) is an apical membrane anion channel that mediates chloride and bicarbonate flux across several epithelia (1). Loss of CFTR function causes the recessive genetic disease cystic fibrosis (2). CFTR is a member of the adenosine 5′-triphosphate (ATP)-binding cassette (ABC) family of proteins (3). ABC proteins are defined by two highly conserved ABC-type nucleotide-binding domains (NBDs) (4) that dimerize and form two ATP-binding sites (site 1 and site 2) (5–7). This family includes membrane-spanning ABC transporters, such as CFTR, that translocate an array of substrates across cell membranes and a variety of nuclear and cytoplasmic proteins involved in many essential biological functions, such as DNA repair and mRNA translation (3). It is well established that ABC proteins are ATPases (8, 9), i.e. they can hydrolyze ATP to adenosine 5′-diphosphate (ADP) and inorganic phosphate (P) (ATP + H2O → ADP + P). The conformational changes associated with ATP binding and hydrolysis are coupled to the biological function of the ABC protein (10–13); in CFTR, this is opening and closing of the channel (14–17).

Recent studies with CFTR (18, 19) and two other ABC proteins, the DNA repair enzyme Rad50 (20) and a structural maintenance of chromosome (SMC) protein (21), challenge the model that the function of all ABC proteins depends solely on

The abbreviations used are: CFTR, cystic fibrosis transmembrane conductance regulator; ABC, ATP-binding cassette; 2-N3-AMP, 2-azidoadenosine 5′-monophosphoramidate; AMPPNP, adenosine 5′-adenosyl) pentaphosphate; Gp5G, adenosine 5′-monophosphoramide; AMP-PNP, adenosine 5′-(β,γ-imido)triphosphate; ApA, P5′-(5′-guanosyl) pentaphosphate; Gp5A, P5′-(5′-adenosyl) pentaphosphate; Gp5Gp5A, P5′-(5′-guanosyl) pentaphosphate; NBD, nucleotide-binding domain; SMC, structural maintenance of chromosome; Tricine, N-(2-hydroxyethyl)amino-4-guanidinobutane.

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their associated ATPase activity. CFTR opening and closing depends on ATPase activity if ATP is the only nucleotide present (14–17). However, patch clamp studies using excised membrane patches containing CFTR indicated that in the presence of physiologically relevant concentrations of adenosine 5'-monophosphate (AMP), adenylate kinase activity is coupled to channel function (18). Adenylate kinases are enzymes that bind ATP and AMP at separate sites and catalyze the transfer of the γ-phosphoryl group of ATP onto the α-phosphate of AMP (ATP + AMP ⇌ 2 ADP) (22). The ABC proteins Rad50 (20) and SMC (21), which are not transporters, but nuclear proteins involved in DNA repair and chromosome maintenance, have been shown to catalyze both ATPase and adenylate kinase reactions. Furthermore, Bhaskara et al. (20) showed that a yeast strain with a Rad50 mutation that reduced its adenylate kinase but not its ATPase activity resembled a Rad50 null strain with regard to meiosis and telomere maintenance. This result suggests an important physiologic role for Rad50 adenylate kinase activity.

Lammens and Hopfner (21) solved the crystal structure of the ABC-NBD of the Pyrococcus furiosus SMC protein in complex with the adenylate kinase inhibitor Ap₅A, providing the first structural view of the active center of an ABC adenylate kinase. Ap₅A contains two adenosine groups connected by five phosphate groups allowing it to bind simultaneously to an ATP- and an AMP-binding site (23). The structure showed the two adenosine moieties of Ap₅A attached to two binding sites separated by ~15 Å. A Mg²⁺ ion, one adenosine, plus α, β, and γ-phosphates of Ap₅A bound the canonical Mg²⁺-ATP-binding site on lobe I of the SMC NBD. The other adenosine, the “AMP” adenosine group, stacked onto the side chain of a conserved glutamine of the Q-loop at the interface of lobe I and lobe II.

A recent study measured ATPase and adenylate kinase activity of recombinant CFTR after solubilizing it from membranes using 8% (v/v) pentadecafluorooctanoic acid (24). The study failed to detect adenylate kinase activity, and the authors concluded that CFTR is an ATPase, but not an adenylate kinase. That study raised questions of whether or not a membrane-embedded CFTR could function as an adenylate kinase. That study suggested that CFTR is an ATPase, but not an adenylate kinase. CFTR Exhibits Adenylate Kinase Activity

Expression of CFTR in HeLa Cells and Preparation of Membranes—Wild-type and mutant CFTR were transiently expressed in HeLa cells using a vaccinia virus/17 hybrid expression system (25). Cell membranes were prepared following methods described by Travis et al. (26) in the presence of a proteinase inhibitor mixture of 125 μg/ml benzamidine, 4 μg/ml aprotinin, 2 μg/ml leupeptin, 100 μg/ml Pefabloc, and 7 μg/ml trans-epoxy succinyl-1-leucylamido-(4-guanidino)butane (E-64). A high-speed membrane pellet (70,000 × g, 40 min, 4 °C) was resuspended in 20 mM Heps (pH 7.5), 50 mM NaCl, 3 mM MgCl₂, 2 μg/ml leupeptin, 100 μg/ml Pefabloc, and 7 μg/ml E-64.

CFTR Adenylate Kinase Assay—Membranes containing either 30 μg of protein (from cells expressing wild-type CFTR) or 90 μg of protein (from cells expressing S1248F CFTR) were incubated gently shaking with nonradioactive 8- or 2-N₃-AMP (at concentrations given in the figure legends), radioactive [γ-³²P]GTP (30 μCi, 6000 Ci/mmol), 20 mM Heps (pH 7.5), 50 mM NaCl, 3 mM MgCl₂, and 1 mM Tricine (pH 7.6) for 5 min at 37 °C in a total volume of 30 μl followed by UV irradiation for 30 s (302 nm, 8-watt lamp) at a distance of 5 cm. Immediately after exposure to UV light, first 20 μl of Stop buffer (25 mM dithiothreitol, 4% SDS, 20 mM Heps (pH 7.5), 50 mM NaCl, 125 μg/ml benzamidine, 4 μg/ml aprotinin, 2 μg/ml leupeptin, 100 μg/ml Pefabloc, 7 μg/ml E-64) and then 875 μl of 1% Triton X-100 in 20 mM Heps (pH 7.5), 50 mM NaCl, 125 μg/ml benzamidine, 4 μg/ml aprotinin, 2 μg/ml leupeptin, 100 μg/ml Pefabloc, and 7 μg/ml E-64 were added. Samples were stored at −80 °C overnight and thawed on ice before adding CFTR antibodies for immunoprecipitation. CFTR was immunoprecipitated by adding monoclonal CFTR antibodies to its regulatory (R) domain (13-1, 0.2 μg/sample) (R&D Systems, Inc., Minneapolis, MN) (27) and NBD2 (M3A7, 1 μg/sample) (EMD Millipore, Billerica, MA) (28). Immunocomplexes were fractionated on 6% SDS-polyacrylamide gels. After electrophoresis, either the gels were dried or the fractionated proteins were transferred onto a PVDF membrane (Immobilon®-FL transfer membrane, EMD Millipore) for Western blotting. The dried gels or the PVDF membranes were then subjected to digital autoradiography using a FLA-7000 imaging system (Fuji Photo Film Co., Ltd., Tokyo, Japan).

Western Blotting—PVDF membranes blocked in 0.01% casein were incubated for 2 h with the monoclonal anti-human CFTR antibody indicated for each experiment in the figures, diluted 1:1,000 in TTBS buffer (137 mM NaCl, 2.7 mM KCl, 25 mM Tris-Cl (pH 8.0), 0.05% Tween 20). Membranes were washed twice in TTBS buffer and then incubated for 1 h with donkey anti-mouse IRDye (0.1 μg/ml, in TTBS plus 0.01% casein, 0.01% SDS) (LI-COR Biosciences, Lincoln, NE) as secondary antibody. Immunoreactive proteins were visualized with the Odyssey Infrared Imaging System (LI-COR Biosciences).

Data Presentation and Statistics—Data are presented as means ± S.E. p values <0.05 were considered statistically sig-
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RESULTS

To test the hypothesis that full-length CFTR displays adenylate kinase activity, we developed the strategy illustrated in Fig. 1. CFTR has two ATP-binding sites formed in the NBD head-to-tail dimer interface. In other ABC proteins, the three ATP phosphates are bound to the phosphate-binding loop or Walker A motif (29) of one NBD and the ABC signature motif of the other NBD. In ATP-binding site 1, this is the Walker A motif of NBD1 and the signature motif of NBD2. In ATP-binding site 2, it is the Walker A motif of NBD2 and the signature motif of NBD1. Previous patch clamp studies indicated the existence of a separate binding site for AMP (18). These studies together with structural studies on other ABC protein NBDs provided three lines of evidence indicating that the AMP-binding site is distinct from the two ATP-binding sites. 1) AMP induced positive cooperativity for ATP in the relationship between ATP concentration and CFTR current (18). This finding indicates that in the presence of AMP, two ATP molecules interact simultaneously with CFTR. Therefore, AMP must interact with a different site. 2) ATP- and AMP-binding sites showed different nucleotide base specificities; the ATP-binding sites accept both ATP and GTP (guanosine 5'-triphosphate) (18, 26, 30, 31). In contrast, the AMP-binding site showed high specificity for the adenine base; i.e. GMP (guanosine 5'-monophosphate) did not mimic the effects of AMP on current. This discrimination was also revealed by the effect of agents that interact with both an ATP-binding site and an AMP-binding site to inhibit adenylate kinase activity; ApG and GpG inhibited CFTR Cl− current, whereas GpG did not (18). 3) In ApG, bound to an adenylate kinase, the ribose oxygens are ~16 Å apart (23). Crystal structures of other ABC protein NBDs in the dimeric state with bound ATP showed the ribose oxygens of the two ATPs ~34–37 Å apart (5, 6). Therefore, a similar dimeric structure in CFTR would not permit ApG binding simultaneously to the two ATP-binding sites. The recently solved crystal structure of the ABC-NBD of an SMC protein in complex with ApG confirmed a binding site for one ApG adenosine that is distinct from the two ATP-binding sites (21).

We predicted that when membranes containing CFTR are incubated with radioactive [γ-32P]GTP and nonradioactive, photoactivatable azido (N3)-AMP, CFTR adenylate kinase activity would catalyze transfer of the radioactive γ-phosphate of [γ-32P]GTP onto N3-AMP, forming radioactive N3-[β-33P]ADP. Subsequent exposure to UV light would mediate cross-linking of N3-[β-33P]ADP to the CFTR protein. The N3-group absorbs UV light, which results in photolysis and formation of a reactive intermediate that reacts with nearby amino acid residues to become covalently attached (32, 33). Thus, CFTR would become radioactively labeled. We chose to use [γ-32P]GTP rather than [γ-32P]ATP because in preliminary experiments, we found that incubating native membranes containing CFTR with [γ-32P]ATP at 37°C resulted in some radioactive labeling of CFTR even in the absence of UV light. This result suggested that the radioactive phosphate group was incorporated into CFTR in a different way than via a cross-linked N3-[β-32P]ADP, e.g. perhaps by direct phosphorylation. In contrast to ATP, GTP is not a substrate of the major protein kinases known to phosphorylate CFTR in the cell membrane (34–37).

We expressed CFTR in HeLa cells using a double vaccinia virus/T7 RNA polymerase system (25) and collected cell membranes. Western blotting confirmed the presence of CFTR (Fig. 2A). The majority of CFTR migrated as the highly glycosylated band C (27, 38). No CFTR could be detected in membranes from HeLa cells not infected with the recombinant vaccinia virus encoding CFTR. To test for adenylate kinase activity, we incubated membranes containing CFTR with [γ-32P]GTP and nonradioactive N3-AMP followed by UV irradiation (Fig. 1). This procedure radioactively labeled CFTR (Fig. 2B, lane 3), indicating phosphor group transfer activity between [γ-32P]GTP and N3-AMP, i.e. adenylate kinase activity.

Labeling was greater when we used azido-AMP with the N3-group substituted at the C-2 position of the adenine ring.
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(2-N\textsubscript{3}-AMP) versus at the C-8 position (8-N\textsubscript{3}-AMP) (Fig. 2C). There are at least two explanations for this difference. The photoactivated reaction of the N\textsubscript{3}-group with nearby amino acid residues (32, 33) might be sterically favored if the N\textsubscript{3}-group is substituted in the C-2 position versus the C-8 position of the adenine ring. Alternatively, the affinity of 8-N\textsubscript{3}-AMP for the AMP-binding site might be less than that of 2-N\textsubscript{3}-AMP due to conformational differences between these two analogs. Studies in other adenylate kinases support this possibility. The torsional angle between the base and the ribose of AMP can be syn or anti (39). At physiologic pH, AMP preferentially adopts the anti conformation (40). An N\textsubscript{3}-group at the adenine C-8 position likely shifts the conformation of the nucleotide toward a syn angle, whereas substitution at the C-2 position allows for an anti conformation (41). NMR studies with rabbit muscle adenylate kinase (42) and the crystal structure of Escherichia coli adenylate kinase in complex with AMPPPNP and AMP show AMP bound in an anti conformation (43). Moreover, in chicken muscle adenylate kinase, when compared with 8-N\textsubscript{3}-AMP, 2-N\textsubscript{3}-AMP supports greater phosphoryl group transfer activity, and the AMP-binding site is preferentially photolabeled with 2-N\textsubscript{3}- versus 8-N\textsubscript{3}-nucleotide analogs (44). Our findings suggest a similar requirement for AMP in CFTR. Consequently, 2-N\textsubscript{3}-AMP was employed in all subsequent experiments.

We did several studies to test whether radioactive labeling was due to CFTR adenylate kinase activity. 1) We predicted that if labeling required phosphoryl group transfer activity between [\(\gamma\textsuperscript{32P}\)]GTP and N\textsubscript{3}-AMP (adenylate kinase activity) as illustrated in Fig. 1, it should decrease in the presence of the adenylate kinase inhibitor Ap\textsubscript{5}A. Labeling should also decrease if nonradioactive ATP was added to compete with [\(\gamma\textsuperscript{32P}\)]GTP or if AMP was added to compete with N\textsubscript{3}-AMP. Experimental testing showed that excess ATP, AMP, and Ap\textsubscript{5}A indeed reduced labeling (Fig. 3). 2) If radioactive labeling depended on UV light-induced cross-linking of N\textsubscript{3}-[\(\beta\textsuperscript{32P}\)]ADP to CFTR after phosphoryl group transfer, labeling should not occur in the absence of either N\textsubscript{3}-AMP or UV irradiation. Experimental testing confirmed that both were true (Figs. 2B and 4A). Thus, \textsuperscript{32P} was not incorporated into CFTR by means other than the cross-linked N\textsubscript{3}-nucleotide, e.g., not by a protein kinase present in the membrane preparation. 3) We considered the possibility that an adenylate kinase other than CFTR might form N\textsubscript{3}-[\(\beta\textsuperscript{32P}\)]ADP, which could then bind and label CFTR during UV irradiation. To test this possibility, we incubated nontransfected HeLa cell membranes with [\(\gamma\textsuperscript{32P}\)]GTP and N\textsubscript{3}-AMP at 37 °C. We then added membranes containing CFTR on ice and irradiated with UV light. Lack of radioactive CFTR (Fig. 4A, lane 2) suggests that it was adenylate kinase activity intrinsic to CFTR rather than another adenylate kinase that generated the N\textsubscript{3}-[\(\beta\textsuperscript{32P}\)]ADP that labeled CFTR.

To further test that the observed adenylate kinase activity was intrinsic to CFTR, we asked whether it could be eliminated by a CFTR mutation. We chose a phenylalanine substitution for serine at position 1248 (S1248F) in the phosphate-binding loop of ATP-binding site 2. A previous study showed that this mutation abolished nucleotide interaction with ATP-binding site 2 (45). However, this mutation did not interfere with intracellular processing of CFTR to the highly glycosylated form migrating.
as band C (Fig. 4C). When we incubated membranes containing S1248F CFTR with [γ-32P]GTP and nonradioactive N3-AMP, followed by UV irradiation, we found very little labeling (Fig. 4A, lane 6). Western blotting confirmed that the mutant CFTR was present in an amount similar to that of wild-type CFTR (Fig. 4C). We could not assess the effect of the homologous mutation in ATP-binding site 1 (A462F mutation) on adenylate kinase activity because that mutation affected intracellular CFTR processing to an extent that we were unable to detect the mutant CFTR protein in our membrane preparations by Western blot.

DISCUSSION

In this study, we developed a biochemical assay that radioactively labeled CFTR as a consequence of phosphoryl group transfer activity between GTP and a photoactivatable AMP analog (adenylate kinase activity). Our results show that when N3-AMP was added, membrane-bound CFTR displayed adenylate kinase activity. The findings further suggest that the interaction of nucleotide triphosphate with CFTR at ATP-binding site 2 is required for CFTR adenylate kinase activity.

Our data complement previous electrophysiological data indicating that CFTR channel activity is coupled to adenylate kinase activity. Patch clamp studies with excited inside-out membrane patches containing CFTR showed that the adenylate kinase inhibitor Ap5A inhibited CFTR current. Inhibition was attenuated by increasing the ATP concentration or by adding AMP, suggesting a similar mechanism of inhibition as seen in other adenylate kinases, i.e. binding to an ATP site and an AMP site. Furthermore, AMP noncompetitively altered the response of current to different ATP concentrations. However, an AMP analog that cannot act as a phosphoryl group acceptor, AMP-NH3, did not mimic the effects of AMP. Instead, AMP-NH3 inhibited current partially and noncompetitively with ATP by reducing the channel opening rate. The addition of AMP reversed AMP-NH3 inhibition (18). Patch clamp studies also suggested that physiological intracellular AMP concentrations could support the adenylate kinase activity (18). Our biochemical results are consistent with that interpretation.

A previous study failed to detect adenylate kinase activity after solubilization of recombinant CFTR from membranes (24). Because we used membrane-bound CFTR that had not been detergent-solubilized, the difference in results emphasizes the importance of the native, membrane-embedded conformation for CFTR adenylate kinase activity.

Substituting a phenylalanine into the phosphate-binding loop of NBD2 (the S1248F mutation) interfered with labeling. Possible explanations include disruption of adenylate kinase activity by the mutation and interference with UV light-dependent photolabeling. Previous observations support the interpretation that the S1248F mutation disrupted adenylate kinase activity. 1) A study characterizing the gating characteristics and the interaction of ATP with S1248F CFTR found that this mutation interfered with the interaction of nucleotides at ATP-binding site 2. It did not abolish photolabeling of ATP-binding site 1 (45). 2) Patch clamp studies showed that mutations K1250A and D1370N, located within conserved motifs of ATP-binding site 2, abolished the effects of Ap5A and AMP on CFTR current. The homologous mutations in ATP-binding site 1, however, did not (18). Our findings plus those previous observations suggest that the interaction of nucleotide triphosphate with CFTR at ATP-binding site 2 is required for adenylate kinase activity. It may be that the phosphoryl group donor nucleotide triphosphate interacts with ATP-binding site 2, the same site at which ATP is hydrolyzed in the absence of AMP (45, 46). Alternatively, the mutation may also interfere with the interaction of AMP with CFTR. Of note, mutations within the ATP-binding site of other adenylate kinases also affect the interaction with AMP (23).

These biochemical data complement earlier biophysical studies of CFTR and further establish that CFTR can function as an adenylate kinase when embedded in the membrane. The approach employed in this study may also be useful to test whether cystic fibrosis-associated mutations interfere with adenylate kinase activity and whether the effects of such mutations can be counteracted by small molecules. The methods used here may also allow investigations into whether other ABC transporters have intrinsic adenylate kinase activity.

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