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Energy transduction in ATP synthase

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Mitochondria, bacteria and chloroplasts use the free energy stored in transmembrane ion gradients to manufacture ATP by the action of ATP synthase. This enzyme consists of two principal domains. The asymmetric membrane-spanning F_o portion contains the proton channel, and the soluble F_1 portion contains three catalytic sites which cooperate in the synthetic reactions[1]. The flow of protons through F_o is thought to generate a torque which is transmitted to F_1 by an asymmetric shaft, the coiled-coil γ-subunit. This acts as a rotating 'cam' within F_1, sequentially releasing ATPs from the three active sites[1–5]. The free-energy difference across the inner membrane of mitochondria and bacteria is sufficient to produce three ATPs per twelve protons passing through the motor. It has been suggested that this protonmotive force biases the rotor's diffusion so that F_o constitutes a rotary motor turning the γ shaft[6]. Here we show that biased diffusion, augmented by electrostatic forces, does indeed generate sufficient torque to account for ATP production. Moreover, the motor's reversibility—supplying torque from ATP hydrolysis in F_1 converts the motor into an efficient proton pump[7]—can also be explained by our model.

Figure 1a shows the molecular geometry of ATP synthase based on the available structural information[5]. Growing evidence indicates that the entire structure of ATPase can be divided into two counter-rotating assemblies (Fig. 1b). We shall call the assembly consisting of a, b, δ and the F_1 hexamer the 'stator', and place our coordinate system on it. The assembly consisting of c, γ and ε is the 'rotor'. Proton flow through the channels at the a–c interface generates torque which drives the rotor and stator in opposite directions. The motor must generate sufficient torque to produce three ATPs per revolution, an amount of work equivalent to $\sim 20\, k_B T$ per ATP molecule (k_B is Boltzmann's constant and T the absolute temperature; at room temperature $1\, k_B T \approx 0.6\,\mathrm{kcal\,mol^{-1}} = 4.1\,\mathrm{pN\,nm}$).

The central proton carrier in F_o is Asp 61, which is found on the c subunit in 9–12 copies[8,9]. Arg 210 is also an essential amino acid, and it resides on the a subunit in a single copy. (His 245 and Glu 219 are also involved, but may not be essential[10].) These residues hold protons in an energy well whose depth is related to their pK_a values by $V/k_B T \approx -2.3\,\mathrm{p}K_a$. The sequence and topological arrangement of the amino acids in the a and c subunits have been determined, although their exact geometric configuration is uncertain[3,5,11]. The charge configuration we show here is the simplest geometry consistent with structural data; however, our mathematical description can accommodate other charge geometries[12,13]. The geometrical relationship of the rotor Asp 61 sites and the stator Arg 210 site is shown in Fig. 2a. The key elements in this structure are: (1) the two half-channels that allow access of protons from the acidic and basic reservoirs to the rotor sites are offset, which confers an asymmetry on the proton flux. The notion of aqueous half-channels was first proposed for the bacterial flagellar motor[14,15]. (2) The location of the positive stator charge between the half-channels is in a position to interact electrostatically with the rotor sites[13].

The pK_a of Arg 210 is high enough that it is always protonated, and so its charge is fixed at +1. The rotor sites, however, have an intermediate pK_a, and so can be either protonated or not. When unprotonated, they cannot rotate out of the rotor–stator interface, for that would entail a large free energy penalty. Thus all rotor sites facing the bilayer must be protonated, and the membrane interface prevents any unprotonated rotor site from moving out the stator.

Arg 210 interacts with the rotor sites according to Coulomb's law in a dielectric and shielding environment typical of a protein interior (Table 1). If a rotor site passes close to the Arg 210 stator charge, the electrostatic interaction can reduce the rotor pK_a allowing the proton to dissociate. (This is because a protonated site is not exactly neutral, but constitutes a dipole whose strength is not sufficient to prevent it rotating into the bilayer but is strong enough to interact with a nearby charge.) The work of reducing a

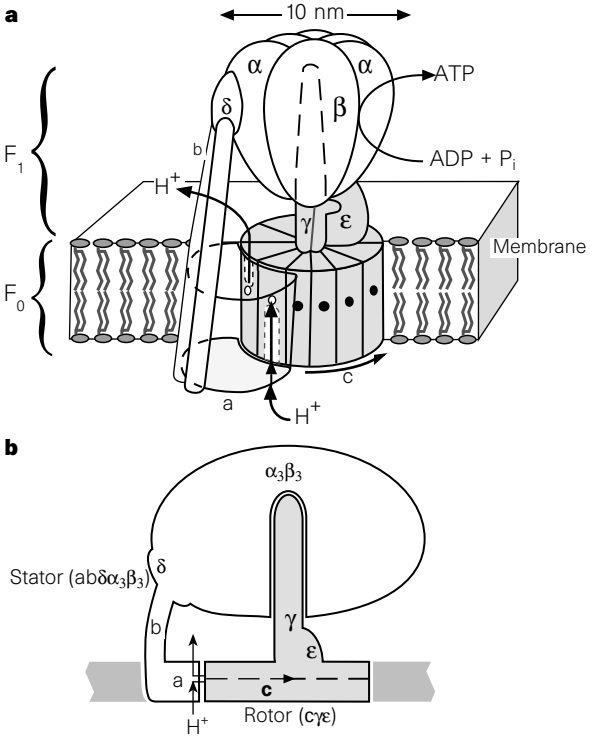

Figure 1 Structure of F_oF_1 ATP synthase[5,6]. **a**, The c subunit consists of 9–12 twin α-helices arranged in a central membrane-spanning array[8]. The a subunit consists of 5–7 membrane-spanning α-helices. The proton channels lie at the interface between the a and c subunits (dashed lines indicate the putative inlet and outlet channels). The a subunit is connected to F_1 by the b and δ subunits. Proton flow through the channels develops torque between the a and c subunits. This torque is transmitted to F_1 via the γ shaft and the ε subunit, where it is used to release ATP sequentially from the three catalytic sites in F_1. (Adapted from refs 4, 5.) **b**, Profile of the F_oF_1 structure showing the two counter-rotating structures. We put our coordinate system on the 'stator', which consists of the a, b, δ subunits and the F_1 hexamer. The 'rotor' is shaded, corresponding to the shaded region in **a**; it comprises the c, γ and ε subunits.

rotor site's pK_a values carries an energetic price: the proximity of a rotor and stator charge creates an electrostatic force between the rotor and stator that impedes its rotation.

The stator charges involved in proton transport are located on adjacent α-helices in the a subunit. Therefore, we shall assume that there are two rotor Asp 61 sites at the rotor/stator interface, as shown in Fig. 2a. We shall also assume that the rotor sites are accessible from the low- and high-pH sides through aqueous channels in the stator[11,14,16]. Protons in the acidic reservoir have access to the right-hand rotor site and protons in the basic reservoir have access to the left-hand rotor site. We place the positively charged Arg 210 stator residue in a position midway between the two aqueous channels, and offset 0.52 nm out of the rotor plane.

Intuitively, the motor works as follows. First consider the situation when the positive stator charge is absent, which has been discussed elsewhere[6]. The two rotor sites within the stator can be protonated or unprotonated. When both sites are unprotonated, the rotor cannot diffuse in either direction, for that would entail moving an Asp 61 site into the bilayer. When the right-hand site is protonated, the rotor can diffuse to the right unimpeded, but is prevented from diffusing to the left by the other unprotonated site. Conversely, when the left site is neutralized by a proton, it can diffuse to the left, but not to the right. When both sites are neutralized, the rotor can diffuse freely in both directions. When the proton electrochemical potential difference across the membrane tends to drive protons upwards with reference to Fig. 2a, the rotor will diffuse preferentially to the right because the right-hand site will be protonated more often than the left-hand site as it faces a higher proton concentration. Thus, on average, protons enter from the acidic reservoir, board the rotor and rotate to the right by one full revolution, then exit to the basic reservoir when they re-enter the stator from the left. However, this is not an efficient motor, for when both sites are occupied, the rotor will be forced backwards by the load torque, allowing protons to leak through to the basic reservoir without performing any work. Indeed, we will show that, without Arg 210, this biased diffusion cannot account for the observed properties of the motor.

Now consider the situation when the stator charge is present. When the right-hand site is protonated, half the time it will diffuse to the right and enter the membrane. This brings a corresponding charge into the stator from the left, where it can exit to the basic reservoir. However, when the rotor diffuses to the left and approaches the stator charge, its pK_a will drop and it will promptly relinquish its proton back to the acidic reservoir. Unprotonated, the bare site is quickly pulled into apposition with the stator charge and held in place against the load torque. However, a thermal fluctuation can carry the site away from the stator charge far enough to reprotonate from the acidic channel, whereupon the site gets another try at diffusing to the right. The same cycle of events takes place at the basic channel, but owing to the proton gradient, the rotor's diffusion is consistently biased to the right. The presence of the positive stator charge prevents back-diffusion of the rotor and couples the proton flux tightly to the rotor motion. This more than compensates for the retarding effect of the electrostatic interaction,

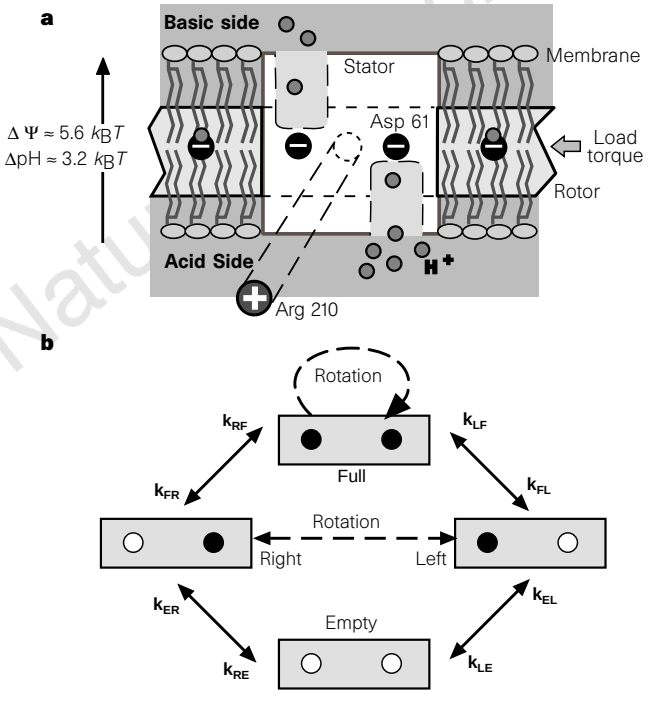

Figure 2 Charge geometry and movement of protons in ATP synthase. **a**, Face-on view showing the relative locations of the stator and rotor charges and the proton channels. The two proton reservoirs are connected by offset 'half-channels' which confer an asymmetry on the assembly[6,14]. Arg 210 is located on the a subunit in a plane 0.52 nm offset from the plane of the rotor. **b**, Markov chain describing the four possible motor states and their transition rates, $k_{i\to j}$. E, empty; F, full; L, left site occupied; R, right site occupied. White circles, unprotonated Asp 61 sites; black circles, protonated sites.

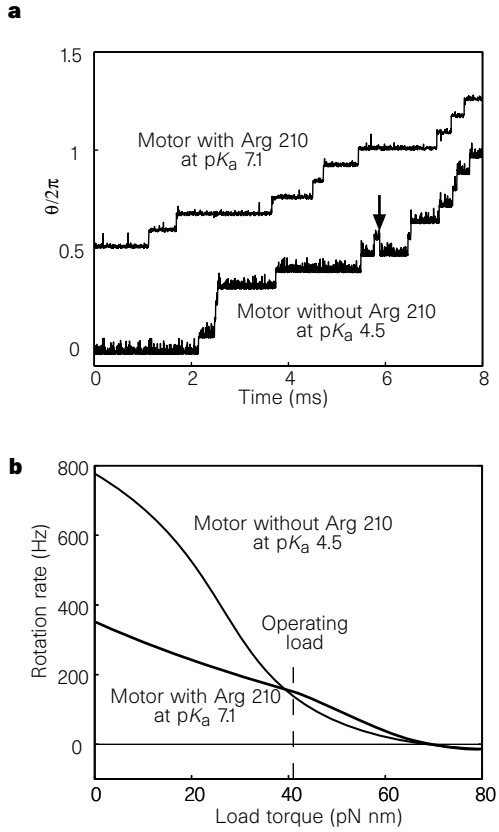

Figure 3 Properties of the ATP synthase rotor. **a**, Stochastic simulation of the rotor motion when a protonmotive force of 220 mV is imposed across the membrane and a load torque of 41 pN nm resists the motion. In the absence of Arg 210, the rotor advances in steps, with occasional reversals (arrow), when protons can leak through the stator without advancing the rotor. When Arg 210 is present, the motor suffers almost no reversals, and the amplitude of its stochastic fluctuation is smaller. **b**, Angular velocity plotted against load torque for the motors with and without Arg 210.

and enables the engine to work more efficiently as both a motor and pump. To justify this qualitative description of the motor's operation, we must write and solve the equations governing the rotor motion. Various aspects of this mechanism have already been discussed qualitatively[4,13,17–19].

Proton motions are much faster than rotation of the rotor. This enables us to model the movements of the protons by transitions between a set of discrete states (that is, a Markov chain[20]). As each site can be protonated or not, there are four possible protonation states of the assembly, denoted by s = R (right), L (left), E (empty), F (full), as in Fig. 2b. Each time a proton hops into or out of the stator, or the rotor moves, the state switches, and in each state the rotor experiences different torques.

We can neglect inertia and describe the rotation of the rotor by a torque balance that includes thermal fluctuations[21]:

$$\underbrace{\zeta 2\pi\Omega(\theta)}_{\text{viscous drag torque}} = \underbrace{F_E(\theta,s)}_{\text{electrostatic torques from the stator}} + \underbrace{F_H(\theta,s)}_{\text{hydrophobic torque from the membrane}} - \underbrace{\tau}_{\text{load torque from } F_1} + \underbrace{f(t)}_{\text{brownian torque}}, s = \mathrm{R, L, E, F} \quad (1)$$

Here $2\pi\Omega = \mathrm{d}\theta(t)/\mathrm{d}t$ is the angular velocity of the rotor, ζ is the drag coefficient of the rotor, τ is the load torque from F_1, and $f(t)$ is the brownian torque from thermal fluctuations. $F_E(\theta,s)$ is the electrostatic torque acting on the rotor from the interaction between rotor charges and Arg 210. The hydrophobic force, F_H, arises from the potential barrier preventing the motion of an unprotonated site into the membrane; this energy barrier is $\sim 45\, k_BT$. To compute the torque generated by the motor, equation (1) must be solved simultaneously with the Markov process governing the hopping of protons on and off of the rotor sites.

The model equations were solved numerically using the parameter values listed in Table 1; the details of all computations are given in Supplementary Information. Figure 3a shows a stochastic simulation of the rotor motion when the proton flow through the stator is driven by a protonmotive force of $\Delta p \sim 220$ mV and the rotor works against a constant load of 41 pN nm, which is equivalent to the torque necessary to produce three ATPs from F_1 per rotation. We see that the motor progresses stepwise, each step corresponding to the passage of one proton through the motor.

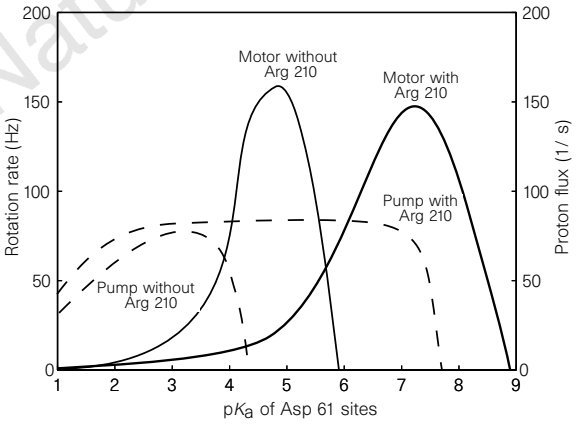

Figure 4 Solid lines show the rotation rate of the motor as a function of the pK_a of the rotor Asp 61 sites with and without the presence of the stator Arg 210 charge when the load torque is fixed at 41 pN nm. The optimum pK_a for the motor operating without Arg 210 is 4.5–5; in the presence of Arg 210, the optimum is 7–7.5. Dashed lines show the reverse proton flux when the motor operates in reverse as a proton pump. $200 k_BT\,s^{-1}$ is supplied by F_1 to rotate the γ-subunit. In the absence of Arg 210, the optimal pK_a is 3–3.5, whereas in the presence of Arg 210, the optimum is 6–7. These plots show that Arg 210 is necessary for F_o to function as both a motor and a pump.

On average, 12 protons pass through the motor per rotation, corresponding to 4 protons per ATP. The rotation is tightly coupled to the proton flux because the presence of Arg 210 prevents leakage of protons by back-rotation. Figure 3b shows a load–velocity curve for the F_o motor. As rotation is tightly coupled with proton flow, the motor efficiency increases roughly in proportion to the load. When rotating against the 'normal' load torque from F_1, the motor is operating at ~60% efficiency. It is likely that the load from F_1 is not constant, so several other load patterns were investigated: our general conclusions were unaltered.

The crucial role of electrostatic forces can be demonstrated quantitatively by computing the motor performance with and without the stator Arg 210 residue. In Fig. 4 we have plotted the rotation rate of the motor as a function of the pK_a of the rotor sites. In the presence of Arg 210, the optimal motor performance is close to the measured pK_a value of 7.1 (ref. 22). In the absence of the stator charge, the motor cannot develop any torque above p$K_a \sim 6$, and is completely decoupled from the proton flux. To work without the stator charge, the rotor pK_a must be lowered to 4.5–5, close to its solution value. In Fig. 3a we have plotted a stochastic simulation of the motor in the absence of Arg 210 at a rotor pK_a of 4.5. It operates quite well, but suffers occasional reversals because it cannot resist the load torque in the doubly occupied F state. Thus without the electrostatic coupling induced by Arg 210, the motor is not as tightly coupled to the proton flux. Moreover, to produce sufficient torque at this low pK_a the entry rate of protons must be at least $10^4\,s^{-1}$, because most protons promptly dissociate back into the acidic reservoir (see Supplementary Information).

There is an additional constraint on the motor's performance. Under anaerobic conditions, the ATP synthase of *Escherichia coli* reverses, using ATP hydrolysis to pump protons against a pH gradient. To investigate the performance of the motor as a pump, we assumed an ATP hydrolysis rate by F_1 of 50 ATP molecules per second[23], an efficiency of 20% in converting this to rotary torque (corresponding to a power input of $2\pi\Omega\tau$), and a gradient of 1 pH unit. The basic reservoir was maintained at a pH of 7.6 as this is the value at which *E. coli* maintains its cytoplasm. Figure 4 shows that, in the absence of Arg 210, the optimal pK_a of the rotor sites is 3–3.5, quite far from the optimal operating region for the motor. Above p$K_a \approx 4.3$, the motor can no longer act as a pump. Thus without Arg 210, the motor is a poor proton pump. However, in the presence of Arg 210, it performs quite well as a proton pump near the optimal pK_a for the motor. Therefore, omitting the electrostatic forces in equation (1) prevents the motor from operating efficiently as both a motor and pump. Moreover, the many protonation–deprotonation

Table 1 Parameter values used in calculations

Parameter	Value
Proton diffusion coefficient (D_p)	9.3×10^9 nm^2 s^{-1}
Rotary diffusion coefficient of the rotor (D_r)	2×10^4 s^{-1}
Dielectric constant of channel (ϵ_c)	10
Dielectric constant of the membrane (ϵ_m)	3
Bilayer viscosity (η)	1 poise
Height of rotor (h)	6 nm
Shielding length of channel charges ($1/\lambda$)	1.1 nm
pH^A (pH of acidic reservoir)	motor, 7; pump, 6.6
pH^B (pH of basic reservoir)	motor, 8.4; pump, 7.6
'Radius' of the proton channel (r)	0.5 nm
Radius of rotor (R)	5 nm
Distance (Δx) between Asp 61 residues, $2\pi R/12$	2.6 nm
pH difference across the rotor (ΔpH)	80 mV $= 3.2 k_BT$
Membrane potential ($\Delta\psi$)	140 mV $= 5.6 k_BT$

events that occur before a successful rotor movement require a high entry rate for protons in order to generate sufficient torque.

The average electrostatic torque felt by the rotor opposes the rotor's motion, so that the field actually works against the motor. However, this energy penalty is more than compensated for by two beneficial effects: (1) the high pK_a of the rotor sites holds protons tightly and prevents futile protonation–deprotonation cycles: this increases the effective proton supply to the stator; (2) by forcing the rotor site to relinquish its proton when passing the stator charge, the stator charge tightly couples the proton flux to the rotor motion. This increases the effectiveness of rectifying the rotor's diffusion, and more than compensates for the additional work done by the protonmotive force against the electric field.

We have presented a mechanism for transducing free energy stored in an ion gradient into a rotary torque. Our analysis delineates the quantitative conditions under which the structure shown in Fig. 1 can actually generate the power required for ATP synthesis. This mechanism has several attractive properties. First, the motor can be reversed to form a proton pump, as in *E. coli* and the V-ATPase proton pumps[24]. Second, the motor works as well when other ions are substituted for protons: for example, the F_oF_1 ATPase of *Progenium modestum*, which is very similar in structure to ATP synthase but operates on sodium ions rather than protons[25]. Finally, the model provides an explanation for the effects of mutations in the crucial rotor and stator amino acids[10]. In addition to elucidating the mechanisms of torque generation, the model provides a framework for integrating the kinetic, thermodynamic and mechanical aspects of protonmotive energy transduction. □

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Supplementary information is available on *Nature*'s World-Wide Web site (http://www.nature.com) or as paper copy from Mary Sheehan at the London editorial office of *Nature*.

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