The aquaporin-1 (AQP1) water transport protein contains a polymorphism corresponding to the Colton red blood cell antigens. To define the fraction of membrane water permeability mediated by AQP1, red cells were obtained from human kindreds with the rare Colton-null phenotype. Homozygosity or heterozygosity for deletion of exon I in AQP1 correlated with total or partial deficiency of AQP1 protein. Homozygote red cell morphology appeared normal, but clinical laboratory studies revealed slightly reduced red cell life span in vivo; deformability studies revealed a slight reduction in membrane surface area. Diffusional water permeability (Pd) was measured under isotonic conditions by pulsed field gradient NMR. Osmotic water permeability (Pf) was measured by changes in light scattering after rapid exposure of red cells to increased extracellular osmolality. AQP1 contributes −64% (Pf = 1.5 × 10⁻³ cm/s) of the total diffusional water permeability pathway, and lipid permeation apparently comprises −23%. In contrast, AQP1 contributes >85% (Pf = 19 × 10⁻³ cm/s) of the total osmotic water permeability pathway, and lipid permeation apparently comprises only −10%. The ratio of AQP1-mediated Pf to Pd predicts the length of the aqueous pore to be 36 Å.

It has long been argued whether the fundamental process of membrane water permeability results from diffusion of water through the lipid bilayer, transit of water through protein pores, or the sum of both processes (reviewed by Finkelstein (1987)). Diffusional water permeability (Pd) represents transmembrane flow of water in the absence of an osmotic gradient; human red cells exhibit Pd = 3 × 10⁻³ cm/s at 25 °C (Brahm, 1982). Osmotic water permeability (Pf) represents transmembrane flow of water driven by an osmotic gradient; human red cells exhibit Pf = 20 × 10⁻³ cm/s at 25 °C (Moura et al., 1984). Recognition that red cell water permeability is inhibited by mercurials was taken as evidence that protein water pores must exist (Macey and Farmer, 1970), but it remains uncertain how much membrane water permeability is due to lipid and how much is due to protein pores.

Discovery of the water transporter AQP1 (CHIP28) in red cells and renal tubules (Denker et al., 1988; Smith and Agrin, 1991; Preston and Agrin, 1991) led to the identification of the aquaporin family of water transporters (reviewed by Knepper (1994); Chriseps and Agrin, 1994). Analysis of AQP1 cDNA (Preston et al., 1992) and highly purified AQP1 protein (Zeidel et al., 1992b, 1994) permitted molecular characterization of water transport. The structure of aquaporins has been resolved by site-directed mutagenesis (Preston et al., 1993, 1994a; Shi et al., 1994; Jung et al., 1994) and by two-dimensional (Walz et al., 1994a, 1995; Mitra et al., 1994, 1995; Jap and Li, 1995) and three-dimensional electron crystallography (Walz et al., 1994b).

The physiological importance of the collecting duct aquaporin homolog became apparent when mutations in the AQP2 gene were found in some patients with nephrogenic diabetes insipidus (Deen et al., 1994). The Colton blood group antigens (Co⁺ and Co⁻) represent a surface polymorphism in the AQP1 molecule (Smith et al., 1994), and extremely rare individuals (Colton-null) became sensitized to Co⁺ and Co⁻ fetal red cells during pregnancy (Lacey et al., 1987). The physiological importance of AQP1 was shown in question when all three unrelated individuals with the Colton-null phenotype were found to be homozygous for disruptions in the AQP1 gene, yet none suffered an obvious clinical defect (Preston et al., 1994b).

Detailed biochemical and biophysical studies of red cells from homozygous Colton-null individuals and their heterozygous relatives have not previously been performed. Thus, it is not certain if they are entirely normal clinically or how they may compensate for absence of AQP1, the major red cell water transporter. Existence of red cells with a specific deficiency of AQP1 protein should provide the purest system for determining the fractions of diffusional (Pd) and osmotic (Pf) water permeabilities mediated by AQP1 and will permit refined calculation of the length of the aqueous pathway.

Experimental Procedures

Materials—Polyclonal, affinity-purified rabbit antibodies were described (Smith and Agrin, 1991). Anti-rabbit IgG was from Boehringer Mannheim; enhanced chemiluminescence reagents were from Amer sham Corp.; electrophoresis reagents were from Bio-Rad.

Blood Preparations—Human blood was obtained by institutionally approved venipuncture. Red cells were washed in 3 volumes of phosphate-buffered saline (7.5 mM sodium phosphate, pH 7.4, 150 mM NaCl) at 1000 × g for 10 min and resuspended to the original volume just before analyses. Red cell membranes were prepared by hypotonic lysis with chilled 7.5 mM sodium phosphate, pH 7.4, 1 mM Na₂EDTA, 0.2 mM phenylmethylsulfonyl fluoride (Bennett, 1983). inhibition studies were performed on red cells after a 30-min incubation period at 37 °C in 1 mM PCMB5. SDS-PAGE was performed with 11% acrylamide slabs (Laemmli, 1970). Immunobots were prepared with enhanced chemilu-
Aquaporin-1 Deficient Red Cells

Southern Blot—Leukocyte genomic DNA was isolated by QiAamp (QiAGEN), digested with PstI, electrophoresed into 1% agarose gels, and transferred to nylon membranes (GeneScreen Plus, DuPont NEN). Blots were hybridized with a 32P-labeled human AQP1 cDNA (106 dpm/ml) corresponding to nucleotides 15–222 (Moon et al., 1993). After 2-4 h washes at 65°C in 0.1 SSC, 0.1% SDS, blots were exposed to Kodak XAR-5 film for 4 days.

Cellular Deformability—Osmotic gradient ektacytometry was employed to continuously assess whole cell deformability over a range of osmolarities (Clark et al., 1983). Osmality at the deformability minimum in the hypotonic region reflects the surface to volume ratio for the whole population of cells. A deformability maximum at 290 mosM reflected membrane surface area. Red cells were exposed to osmolarities for 45 s prior to measuring osmotic deformability profiles over 8 min.

Diffusional Water Permeability (Pd)—Water permeability in the absence of an osmotic gradient was measured by pulsed field gradient NMR (Andrasko, 1976; Kärger et al., 1988). By applying a pair of pulsed field gradients to a stimulated echo sequence, water resonance peak intensity can be sensitized to molecular diffusion. In a system consisting of two compartments (A (internal) and B (external)) with different water diffusivity (DA and DB), the signal intensity (S/A) obeys Equations 1–4:

\[
S/A = p_B e^{-k_B \cdot D_A \cdot t} + p_A e^{-k_A \cdot D_B \cdot t}
\]

where
\[
D_{A,B} = \frac{1}{2} (D_A + D_B + \frac{1}{k} (k_A + k_B)) \pm \left( \left[ (D_A + D_B + \frac{1}{k} (k_A + k_B))^2 - 4 k A k_B \right]^{1/2} \right) \quad (Eq. 1)
\]

\[
p_\lambda = \frac{1}{D_1 - D_2} (p_D A + p_A D_B - D_2)
\]

\[
p_\sigma = 1 - p_\lambda
\]

S and S/A are water signal intensities in the presence and absence of gradient, k_A and k_B are forward and back rate constants, and p_A and p_B are the mole fraction of spins in each compartment; in K = γg, γ is the nuclear gyromagnetic ratio, and g and ð denote gradient strength and length; Δ is the separation between two gradients.

Experimentally, the gradient strength g was changed from 3–55 G/cm, and the signal decay (S/A) recorded with at least two values of Δ (50 and 100 ms) and simultaneously fitted to Equations 1–4 to obtain four unknowns (D_A, D_B, k_A, and k_B). Fitting was by Powell function (Press et al., 1992). Permeability in cm/s was obtained by multiplying the forward rate constant k_B by volume to surface ratio (4.57 × 106 cm). Diffusion was measured in a General Electric Omega 400 NMR Spectrometer equipped with a triple axis gradient unit (up to 130 G/cm); 5-mm sample tubes were analyzed at 20°C.

Osmotic Water Permeability (P_f)—Osmotic water permeability was measured at 20°C (Zeidler et al., 1992b) by abruptly doubling the external osmolality of intact red cells with an equal volume of phosphate-buffered saline-surrogate in a stopped flow apparatus, 0.9 ms dead time (SF17MV, Applied Photophysics, Leatherhead, UK). Red cell volumes were monitored by light scatter (excitation wavelength 600 ± 15 nm, generated with a 150-watt mercury-xenon arc and monochromator, F3.4 grating (Applied Photophysics)); emission wavelength >515 nm was measured through a cut-on filter (Oriel Corp., Stratford, CT). Averaged data from 8 to 16 determinations were fitted to single exponential curves. The P_f was calculated by iteratively solving the water permeability equation using MCAD software (MathSoft, Cambridge, MA).

dV/dt = (-P_f) × (SAV × (MVW × [(C_{osm} - C_{in})] × C_{osm}))

where V(t) is relative red cell volume as a function of time, P_f is in cm/s, SAV is the vesicle surface area to volume ratio, MVW is the molar volume of water (18 m3/mol), and C_{osm} and C_{in} are initial concentrations of total intracellular and extracellular solute. Red cell radii were calculated from cell volume.

RESULTS

Clinical Laboratory Analysis of AQP1 Deficiency—Proband from three kindreds with the Colton-null phenotype were recently found to be homozygous for disruptions of their AQP1 genes: deletion of exon I in kindred 1, frameshift mutation in kindred 2, and missense mutation in kindred 3 (Preston et al., 1994b). Red cells from three generations of kindred 1 (Fig. 1 A) and probands from kindred 2 and 3 were evaluated for abundance of the Coa(C antigen by agglutination with specific antisera; all three probands lacked Coa, and presumed heterozygotes from kindred 1 had reduced levels of Coa (Table I). Hematologic consequences of total AQP1 deficiency are not severe, since red cell morphology, hematocrit, and hemoglobin levels were all normal (Fig. 1B, Table I). Nevertheless, evidence for subtle hemolysis was noted in two probands who had below-normal haptoglobin levels and minimal elevations in reticulocyte count. Zygosity for members of kindred 1 was confirmed by genomic Southern blot of PstI-digested DNA (Fig. 1C, which showed total absence of exon I in the proband sample, subject IIa (–/–), and partial deficiency of the exon I fragment in the DNA from a presumed heterozygote, subject IIIa (+/–).

Biochemical Analysis of Red Cell Membranes—Hypotonically lysed red cell membranes from kindred 1 were studied by SDS-PAGE and immunoblotting. Red cell membranes from unrelated control (+/+), homozygote (–/–), and heterozygote (+/–) appeared equivalent when stained with Coomasie (Fig. 2). Abundance and mobility of spectrin, anion exchanger/band 3 (AE1), glucose transporter (GLUT1), and red cell urea transporter (UT) were equivalent when assessed by immunoblot. In contrast, AQP1 was undetectable in membranes of the homozygote (–/–), and membranes from the heterozygote (+/–) were ~50% deficient in the protein, although its mobility was not altered (Fig. 2).

Cellular Deformability—Ektacytometry of red cells exposed to a continuously changing osmotic gradient will reveal abnormalities in membrane deformability, surface area, and the ratio of surface-to-volume (Clark et al., 1983). Since osmotic gradient ektacytometry is dependent upon transmembrane water movement, the technique was utilized to study AQP1-deficient red cells. When peripheral red cells from a totally AQP1-deficient homozygote (–/–) were compared to red cells from a normal unrelated control (+/+), the deformability maximum at
290 mosM/kg was slightly reduced, consistent with a small reduction in membrane surface area (Fig. 3). Also, the deformability minimum in the hypotonic area of the profile was shifted slightly to higher osmolality values, consistent with a modest reduction in surface area to volume. In none of the studies was a major alteration of the profile noted, indicating that the anticipated reductions in water permeability for AQP1-deficient red cells is obscured by the relatively long time frame of this technique. The small reduction in surface area and a small decrease in surface-to-volume ratio, the Colton-null red cells exhibit a minor reduction in maximum deformability (at ~290 mosM/kg) and a small shift in the osmolality value at which red cells exhibit minimum deformability in hypotonic medium (~140 mosM/kg).

2.36 × 10⁻³ cm/s) consistent with the value determined by tracer efflux studies (Brahm, 1982). Compared to the control, the homozygote exhibited a \( P_d \) value 36% as large (0.86 × 10⁻³ cm/s), and the heterozygotes exhibited intermediate values (1.4 × 10⁻³ cm/s). Although relatively small, the \( P_d \) of red cells totally deficient in AQP1 is still significant and appears to reflect the permeability of two pathways (Fig. 4B): (i) one pathway is insensitive to PCMBS (\( P_d = 0.55 \times 10^{-3}, -23\% \) of total \( P_d \) of control) and (ii) the other pathway is inhibited by PCMBS (0.86 × 10⁻³ – 0.55 × 10⁻³ = 0.31 × 10⁻³, -13\% of total \( P_d \) of control).

**Osmotic Water Permeability (\( P_w \))**—When rapidly exposed to a doubling of external osmolality, intact normal red cells shrank to equilibrium in <1 s. Red cells totally deficient in AQP1 exhibited a long time constant, and red cells partially deficient in AQP1 exhibited an intermediate value (Fig. 3A). The osmotic water permeability for control red cells (\( P_w = 22.8 \times 10^{-3} \) cm/s) is similar to that previously established (Moura et al., 1984). The \( P_w \) measured for the homozygote was significantly lower (3.0 × 10⁻³ cm/s), while the heterozygote value was intermediate (7.1 × 10⁻³ cm/s). Addition of PCMBS to all of the red cell samples decreased the \( P_w \) values significantly (Fig. 3B).

**Temperature Dependence of \( P_w \) and \( P_d \)**—The Arrhenius activation energy measured for normal control red cells (Eₐ = 5 kcal/mol, Table II) was similar to the activation energy for diffusion of water in absence of any barrier (4.8 kcal/mol) (Wang, 1965). The activation energy for red cells totally deficient in AQP1 (10–11 kcal/mol, Table II) was close to the value measured for water crossing simple lipid bilayers (12–14 kcal/mol).
mol) (Redwood and Haydon, 1969; Price and Thompson, 1969). Activation energies measured for red cells with partial AQP1 deficiency exhibited an intermediate value (6–7 kcal/mol). Water exists mostly as three-dimensional hydrogen-bonded network, and the energy required to break a hydrogen bond is ≈ 5 kcal/mol (Stillenger, 1980). The low activation energy for water permeation through AQP1 suggests that the water molecules move through the pore without significant interactions with the walls of the pore.

DISCUSSION

These studies have further defined the biophysical behavior of AQP1-mediated water permeability in red cells. Several years before identification of the aquaporins, indirect studies using mercurial inhibitors suggested that ~90% of the red cell osmotic water permeability and ~50% of diffusional permeability results from transit of water through hypothetical pores in the membrane, while the remainder is due to passage of water through the lipid bilayer (reviewed by Finkelstein, 1980). The low activation energy for water permeation through AQP1 suggests that the water molecules move through the pore without significant interactions with the walls of the pore.

TABLE II

<table>
<thead>
<tr>
<th>Aquaporin-1 Zygosity</th>
<th>Osmostic permeability $E_a$ (kcal/mol)</th>
<th>Diffusional permeability $E_a$ (kcal/mol)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (+/+), IIa</td>
<td>4.6</td>
<td>5.6</td>
</tr>
<tr>
<td>Heterozygote Ia (+/-), IIa</td>
<td>6.2</td>
<td>6.8</td>
</tr>
<tr>
<td>Homozygote IIa (-/-)</td>
<td>10.2</td>
<td>10.8</td>
</tr>
</tbody>
</table>

**Fig. 4.** Diffusional water permeability ($P_d$) of red cells measured by pulsed field gradient NMR spectroscopy. A, Water signal intensity versus $K^2\Delta$ values for a series of red blood cell suspensions. B, coefficient of diffusional permeability values computed from measurements in absence (black bars) and presence of 1 mM PCMBS (stippled bars). Shown are mean values ± S.D. (n = 6 measurements on different control individuals and subject IIa; n = 4 measurements of subjects Ia and IIa).

**Fig. 5.** Osmotic water permeability ($P_f$) of red blood cells. A, representative tracings of red cells abruptly exposed to twice the external osmolality with time course of water efflux monitored in a stopped flow spectrophotometer. B, coefficients of osmotic water permeability in the absence (black bars) and presence of 1 mM PCMBS (stippled bars). Shown are mean values ± S.D. (n = 6 measurements of different control individuals; n = 4 measurements of subject Ia; n = 2 measurements of subjects Ia and IIa). Note that tracings in panel A are exponential fits.

**Fig. 6.** The structure of AQP1 is being investigated by membrane crystallography of function-
Fig. 6. Schematic of single file diffusion of water through a pore. The equivalent length of the pore (L) is 36 Å (N, the number of water molecules: $\times 2.72$ Å, the molecular diameter of water). The assumed width of the bilayer is $50$ Å.

\[ \frac{P_f}{P_d} = N = 9.5 \]

\[ \Delta P_f = \frac{P_f (AQP1 - AQP1)}{P_d (AQP1 - AQP1)} = 13.2 \]

way in addition to the PCMBs-resistant pathway, and their composite actions exhibit a high activation energy indicating that they are not aqueous pores. While the identities of these two minor water permeation pathways are unknown, it may be speculated that the PCMBs-inhibitable pathway is a protein, and the glucose transporter has been shown to transport water at a very low rate (Fischbarg et al., 1990; Zeidel et al., 1992a). The PCMBs-resistant pathway may represent simple diffusion through the lipid bilayer. Thus, the movement of water across the red cell membrane may reflect the complex behaviors of multiple membrane components in addition to AQP1.

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