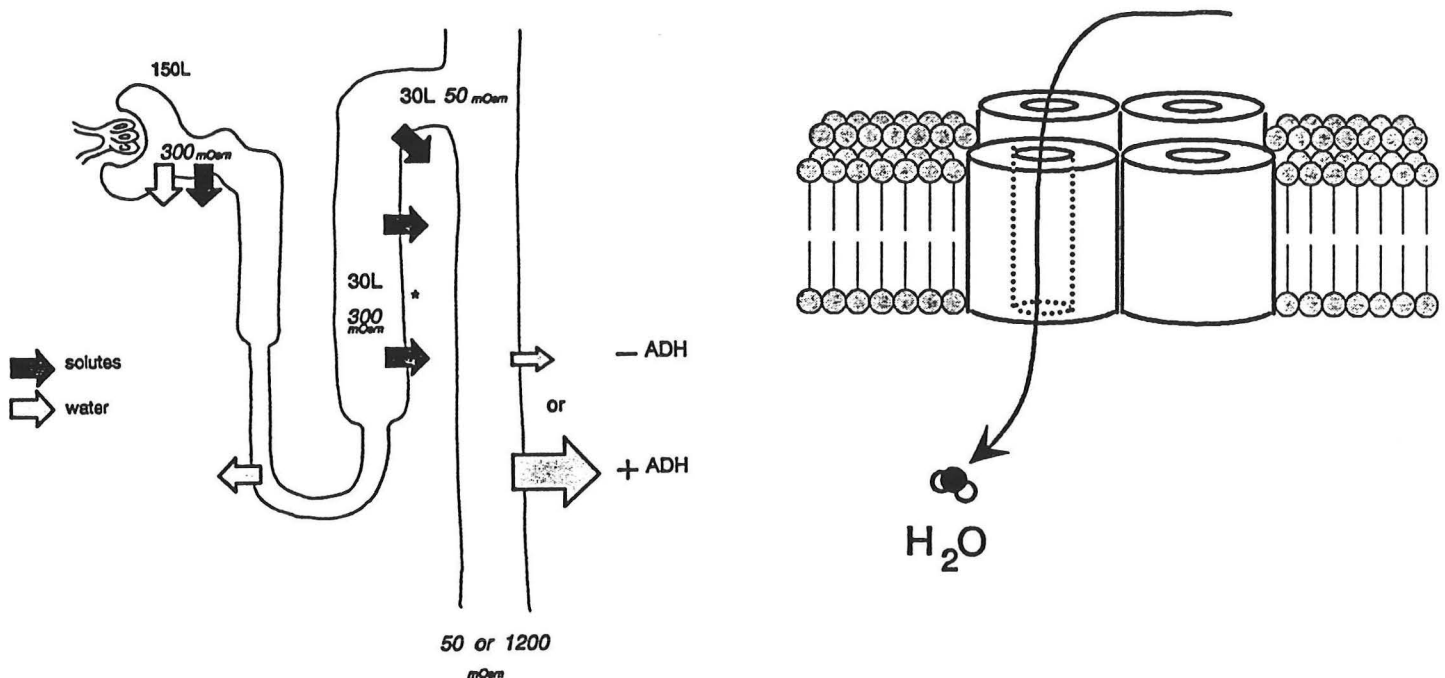


# Understanding Diabetes Insipidus: From Water Clearance to Water Channels

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Orson W. Moe, M.D.

August 21, 1997

Medical Grand Rounds

Department of Internal Medicine

University of Texas Southwestern Medical Center

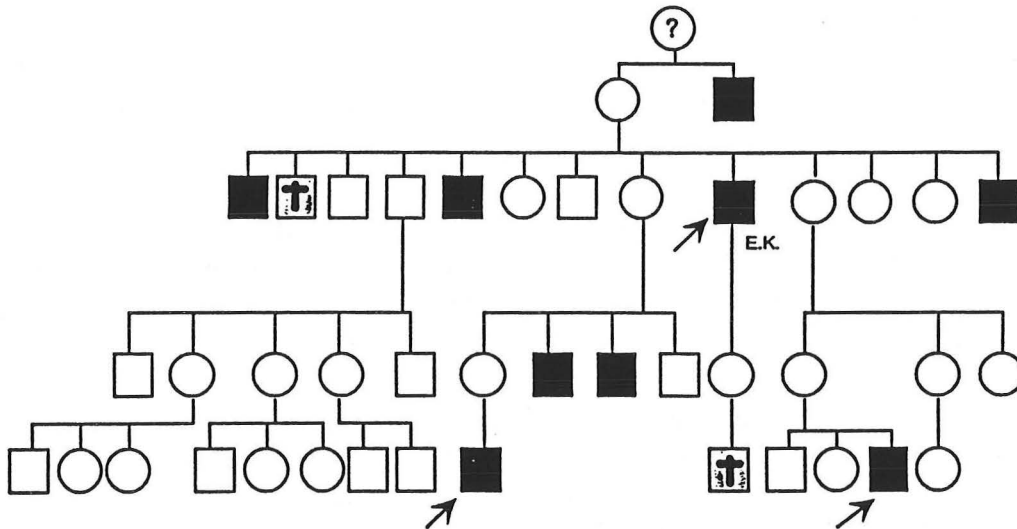
Name: Orson W. Moe, M.D.  
Rank: Assistant Professor  
Division: Nephrology  
Interests: Renal Physiology, Acid-Base and Electrolyte Metabolism, Epithelial Biology.

## HISTORICAL TRIVIA



he first documentation of congenital diabetes insipidus was around the turn of the century based solely on clinical history. A giant German genealogical tree spanning over four generations of patients was compiled by three generations of physicians all within Dr. Weil's family (Weil 1884, Weil 1908, Camerer 1935). These reports stated clearly that congenital diabetes insipidus was inherited as an autosomal dominant trait and such became the axiom in medical textbooks.

The Swedish physician Hans Forssman is believed by many to be the first person to scientifically study the physiology and genetics of congenital diabetes insipidus (Forssman 1942, Forssman 1945). Although he was not quite qualified at the time, Hans Forssman was called upon by the Chief of Medicine during the war to serve as house officer at the University Hospital at Uppsala. One of his first duties was to attend to Mr. E.K, a young man with polyuria. His urine tested positive for sugar and the diagnosis of diabetes mellitus was made. However Forssman noticed that although the diabetes mellitus was of recent onset, the polyuria and polydipsia dated back to childhood. In addition, he noted that despite glycosuria, his urine specific gravity was remarkably low. A revised diagnosis was made of diabetes mellitus superimposed on the background of diabetes insipidus. A careful interview with family members reviewed a classical X-linked recessive inheritance pattern that contradicted the dogma of autosomal dominant inheritance.



*Forssman's first kindred ↗ marks the 3 encounters*

This encounter prompted a lifelong search and study of this disease. Dr. Forssman tracked down families and study patients using the clinical investigative tools available at the time. He came to the

the time, He came to the conclusion that there are two forms of congenital diabetes insipidus. One with autosomal dominant inheritance and one with X-linked recessive with fundamentally distinct underlying pathophysiology and he termed them central vs. nephrogenic diabetes insipidus. Late in Dr. Forssman career, he had two interesting serendipitous encounters (Forssman 1975). On each of these independent episodes, Dr. Forssman heard from his pediatrician colleague, about a challenging case on the ward of an infant with fever of unknown origin. He recognized that they suffered from congenital diabetes insipidus and was requested to serve as consultant. As he traced the family histories on these new patients, he found out that they were related to his first proband Mr. E.K., the first patient he saw with congenital diabetes insipidus.

Contemporaneously in the United States, similar advances were made most likely independent of Forssman by Waring (Waring 1945), Williams (Williams 1947), and Dancis (Dancis 1948). If one looks beyond the medical literature, Dr. Forssman was actually not the first to described the X-linked recessive pattern of the disease. The existence of "water-drinkers" as they were called, was well documented in Scottish folklore dating back to the 17th century; two hundred years before Gregor Mendel described his garden pea experiments and the basic laws of genetics. A modern day translation of an old passage reads as a perfect description of X-linked recessive inheritance (Rogers 1919).

*A gypsy woman and her son were travelling the road and became thirsty. Pausing at a well in front of the next house, the gypsy requested water for her son; the house wife refused, whereupon, the gypsy woman cast upon her a curse. Henceforth, the story goes, the woman's sons would be afflicted with a craving for water. The curse would be passed on by her daughters and revisited upon their sons for generations to come.*

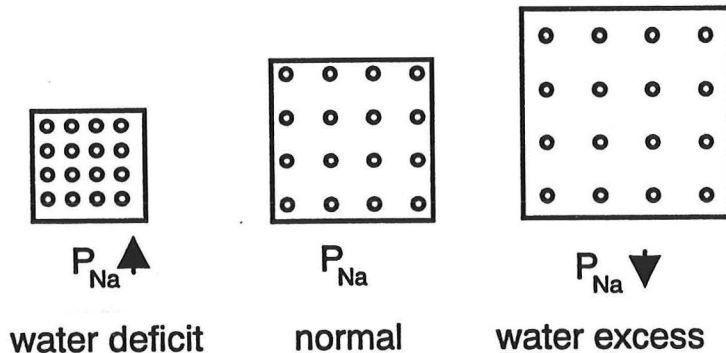
It is fair to ascribe the beginning of scientific study of diabetes insipidus to the early 1940's. In the short span of less than half a century, extraordinary advances were made in the understanding of diabetes insipidus first through well conducted experiments in clinical physiology, and in the last decade through molecular genetics. This manuscript will review the following:

1. The physiology of water homeostasis and the pathophysiology of diabetes insipidus.
2. The genetic lesions of congenital diabetes insipidus tracing the "pituitary-collecting duct axis" from the neurosecretory cells that produce vasopressin to its receptor in the collecting duct, and finally the effector of transepithelial water movement in the kidney.

## PHYSIOLOGY OF WATER HOMEOSTASIS

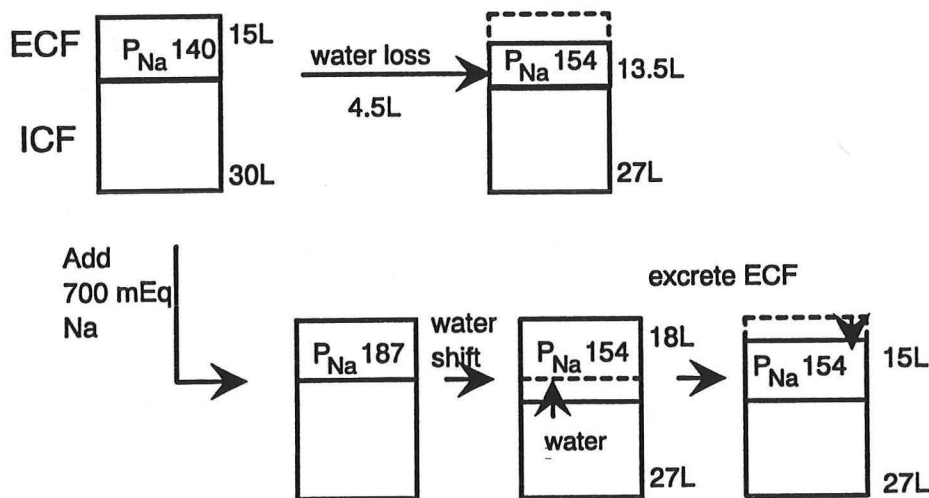
### Plasma Na concentration: a marker for total body water

Body fluid osmolarity can be viewed as the ratio of total solutes to total body water. At equilibrium, intracellular fluid osmolarity must equal extracellular fluid osmolarity; which is approximated by plasma Na concentration. Therefore plasma Na concentration is used as a clinical marker for disturbances of total body water.



Disturbances in plasma osmolarity or plasma [Na] should be viewed as a "denominator disease". Water excess in general leads to low plasma osmolarity and plasma [Na] and conversely, water deficiency in general leads to high plasma osmolarity and plasma [Na].

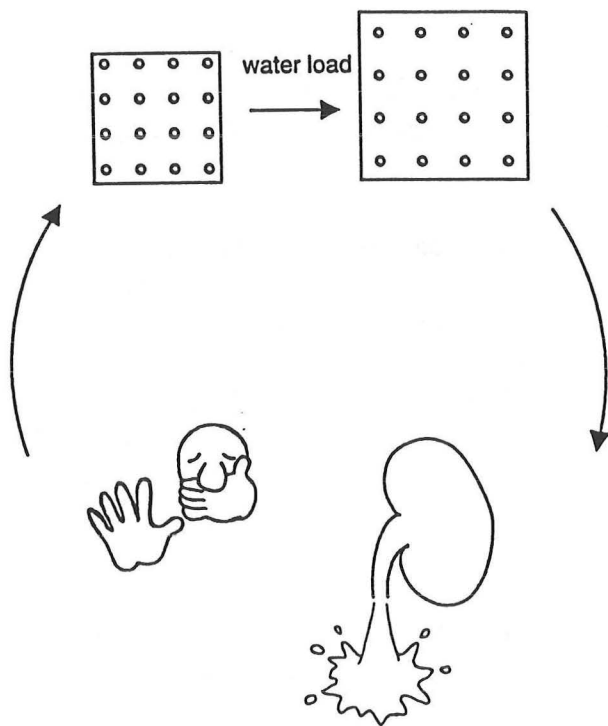
Although the numerator, i.e. Na content in the ECFV can alter plasma [Na]. Changes in plasma [Na] even in that situation still represent a disturbance in total body water. One can consider two examples



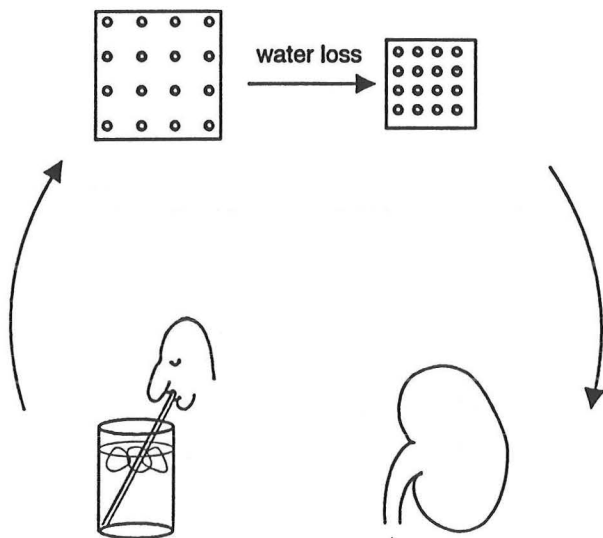
of hypernatremia from either pure NaCl gain or pure water loss. If one loses 4.5 L of water proportionately from the ICF and ECF, plasma [Na] will be increased from 140 to 154 mEq/L. Now consider the same degree of hypernatremia from pure NaCl gain. An acute load of 700 mEq's of NaCl would raise plasma [Na] to 187 mEq/L transiently

followed by rapid movement of water from the ICF to the ECF. This will lead to ECFV expansion from 15 to 18 L's and volume homeostatic mechanisms would return the ECF towards 15 L's. The end result is a plasma [Na] of 154 mEq/L but with a loss of 3L's of water primarily from the ICF.

Terrestrial animals encounter disproportionate gains and losses of solutes and water and are constantly subjected to threats in plasma osmolarity. Maintenance of plasma osmolarity in mammals is achieved within a very narrow range via the partnership of two systems: THIRST and KIDNEY



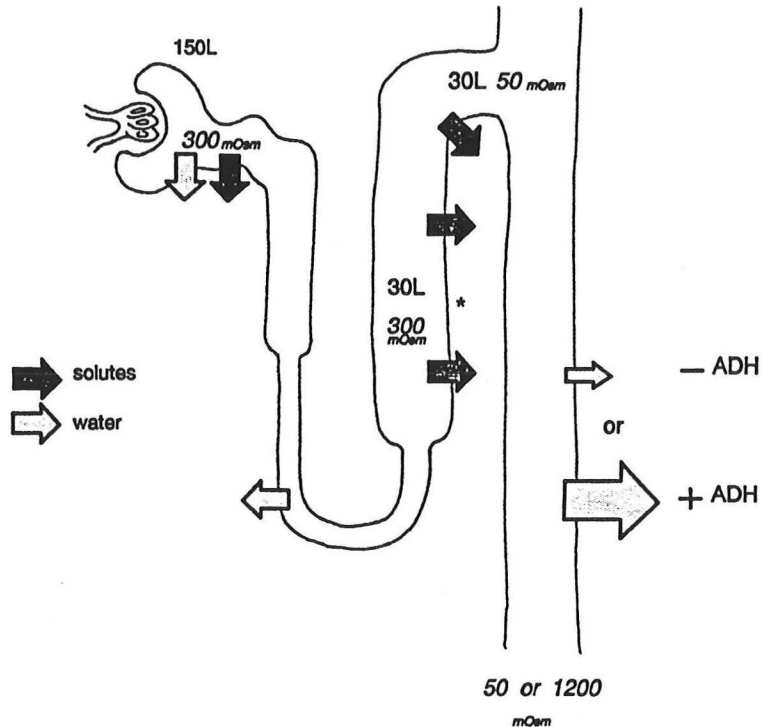
- 1. Cessation of water intake which prevents further aggravation but does not correct the problem.*
- 2. The major player in this defense is the kidney's ability to excrete dilute urine.*



- 1. The elaboration of a scanty and highly concentrated urine to the point where not only there is water conservation but water is actually added to the organism.*
- 2. By far the strongest defense is water drinking.*

## Renal water handling

The mammalian kidney can both excrete or generate water as urine is generated from plasma. This figure shows the amount and the osmolarity of urine from the glomerular filtrate to the renal pelvis.

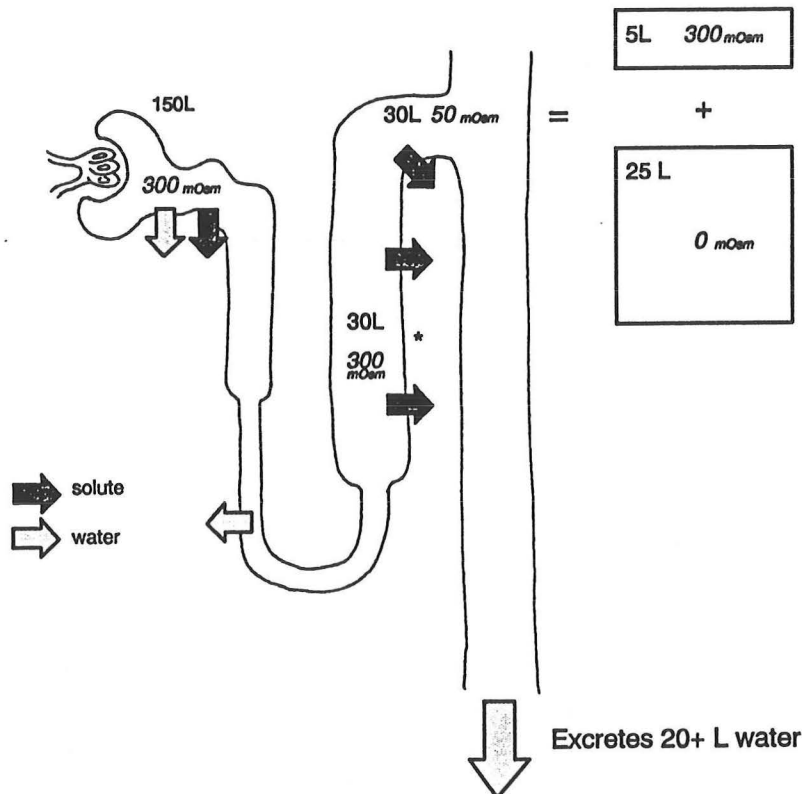


Glomerular filtration and proximal reabsorption are both isotonic therefore no significant net solute-free water exchange results. When urine traverses the loop of Henle, it is concentrated. Upon arrival in the ascending limb, because of solute absorption unaccompanied by water movement, the urine becomes progressively more dilute until some point in the thick ascending limb, it reaches isotonicity (\*). During euolemia, of the 150 L's of water filtered at the glomerulus daily, approximately 30 L's reach this point of isotonicity. An excellent discussion of the quantitative estimate of the fluid delivery to the isotonic point by clearance methods can be found in the monograph by Shuster and Seldin (Shuster 1993). Beyond this point, the tubule becomes impermeable to water and as more solutes are reabsorbed, the urine becomes increasingly more dilute reaching its minimal tonicity at the distal nephron. The osmolarity of the 30 L's of urine that came from the isotonic point (\*) is now down to about 50 mOsm. The thick ascending limb and distal convoluted tubule that absorb solutes without water is termed the diluting segment. From this point on, the fate of the water in the urine depends on the water permeability of the collecting duct. If one desires to rid the body of water, one would render the collecting very impermeable like a lead pipe. The dilute urine will then leave the kidney and water excretion is effected. Conversely, if one wishes to conserve water, one would make the collecting duct very permeable such that as the urine navigates through the hypertonic medulla, water is abstracted back into the systemic circulation. The singular most important regulator of collecting duct water permeability is antidiurectic hormone or

vasopressin (Grantham 1966, Sands 1987). In addition to increasing water permeability of the collecting duct, vasopressin also enhances the medullary tonicity by stimulating solute transport in the medullary thick ascending limb (Hebert 1987) and cortical collecting duct (Tomita 1985).

### Limits of renal water excretion

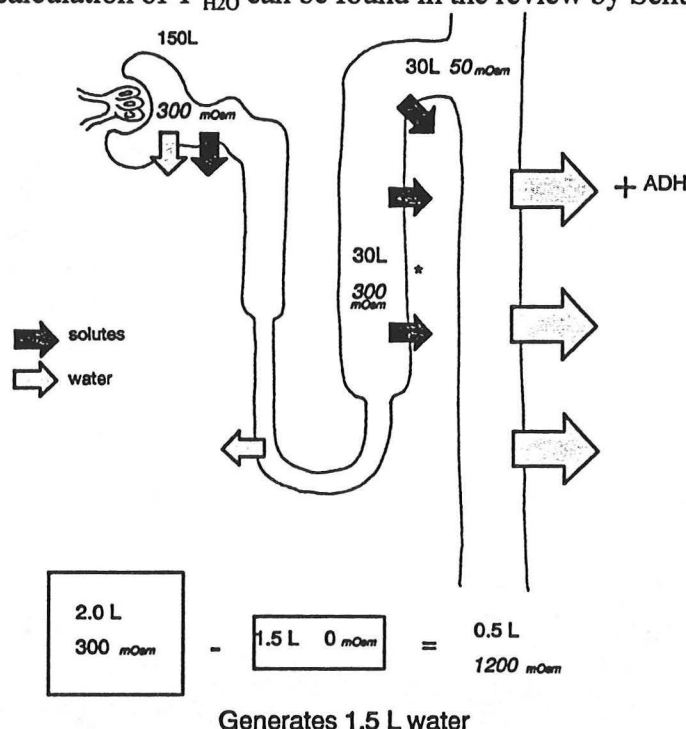
Disturbances in total body water results when water excess or deficit exceeds the homeostatic compensation. To understand disturbances in water one needs to know the limits of this homeostatic system .



Remember that cessation of drinking can only stop further dilution but cannot correct an existing hypotonic state. Defense of water excess therefore depends on water excretion by the kidney. For the sake of this discussion, one can assume that 30 L's of isotonic urine reaches the point of isotonicity in the thick ascending limb. If the diluting segment then renders this urine maximally hypotonic to 50 mOsm, the 30 L's at the end of the diluting segment in essence can be viewed as being partitioned into 5 L's of isotonic fluid and 25 L's of pure water. Although one cannot turn the collecting duct into a real "lead-pipe", one can indeed render this segment relatively impermeable to water. Even in the absence of vasopressin, some finite water permeability remains (Berliner 1957, Jamieson 1971), particularly at the terminal portion of the inner medullary collecting duct (Sands 1987). Nonetheless, if "near-lead pipe" conditions are achievable, one can theoretically excrete some 20+ L's of pure water every day. This is a high capacity system and this is the reason why it is very difficult to cause hyponatremia by polydipsia alone. Solute-free water excretion is called water clearance or  $C_{H_2O}$ . This review will not address the mathematical calculation of  $C_{H_2O}$ . An excellent discussion is found in Schuster and Seldin (Schuster 1993). [See footnote below re:  $C_{H_2O}$ ]

## Limits of renal water generation

In the face of water deprivation, antidiuresis is desired. In this instance, the collecting tubule is highly permeable to water. One elaborates a highly concentrated low volume urine of say 0.5 L of 1200 mOsm. In producing this urine, one has taken 2 L's of 300 mOsm plasma, extracted 1.5 L's of electrolyte-free water from it to remain in the plasma, and excreting 0.5 L of urine of 1200 mOsm. The extraction of electrolyte-free water to remain in plasma is termed free water generation or  $T_{H_2O}^c$ . A discussion of the calculation of  $T_{H_2O}^c$  can be found in the review by Schuster and Seldin (Schuster 1993).



As one can see instantly that the capacity of this system is rather low compared to the 20 L's capacity of water excretion. However, providing the thirst mechanism is intact and water is available, the ability to drink water is virtually limitless so 1.5 L's of free water generation is adequate. The kidney becomes a minor player in the defense against water deficit.

Footnote: Some investigators prefer the use of "effective water clearance" (EWC) rather than free water clearance based on the premise that not all solutes are effective osmoles.

$$C_{H_2O} = V - C_{osm} \quad C_{osm} = U_{osm} \cdot V / P_{osm}$$

$$EWC = V - C_{lytes} \quad C_{lytes} = U_{(Na+K)} \cdot V / P_{(Na+K)}$$

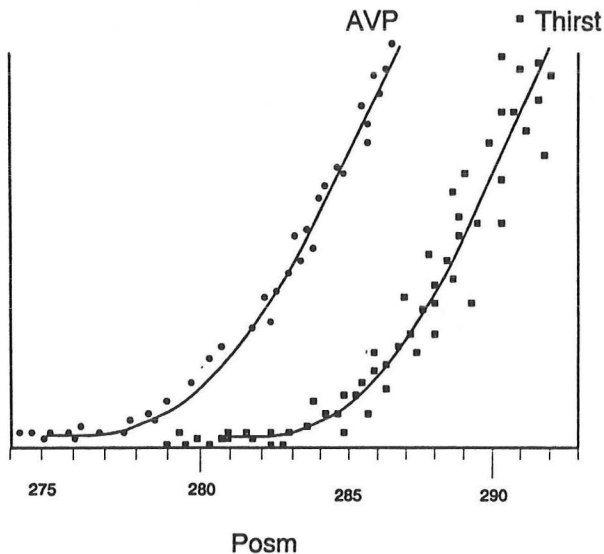
A similar argument can be made for  $T_{H_2O}^c$  to substitute  $C_{osm}$  by  $C_{lytes}$

Bankir L. 1996 Urea and the kidney. In: Brenner and Rector's the kidney Ed BM Brenner 571

Mallie JP, Bichet DG, Halperin ML. 1997. Effective water clearance and tonicity balance: the excretion of water revisited. Clin Invest Med 20:16.

## Thirst and renal water handling: Integrated system

In conjunction, these two systems work to control plasma osmolarity within very tight limits. At hyperosmolar states, AVP is stimulated and thirst is turned on. The kidneys generate solute-free water and the organism drinks. When plasma osmolarity falls towards normal but not quite reached



normal, the organism ceases drinking. At this point, the water that is already in the GI tract will be absorbed and plasma osmolarity will be rectified. In case when too much water is absorbed such as overdrinking or as a deliberate experimental overcorrection, AVP is suppressed to zero and the powerful renal water excretion mechanism comes into play to bring the plasma osmolarity back up to normal. Note that the inflection point or the threshold

of activation of the two curves are about 5-7 mOsm apart. This minimizes overcorrection in either direction.

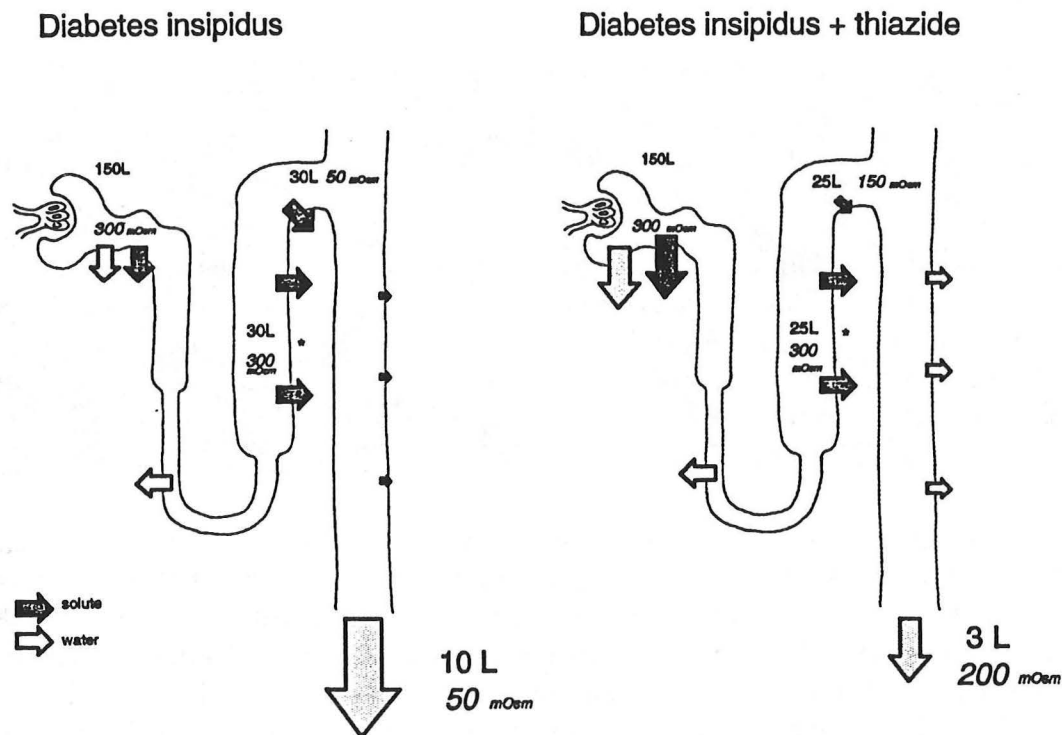
**In summary, the kidney is the major player in correcting water excess while thirst is far more important than the kidney in defending against water deficit.**

## Water handling in diabetes insipidus

In diabetes insipidus, there is a breakdown in the homeostatic loop because the ability to generate water is lost. In fact the kidney is constantly operating in the large capacity water excess mode clearing free water regardless of the plasma osmolarity. This perpetually brings the organism to a water deficient state. One must keep in mind that even when one is relentlessly excreting free water, the capacity for this system although high, does have an upper limit. The thirst mechanism on the other hand is infinite. Therefore, correction of water deficit should always be possible if thirst is intact. For this reason, the awake patient who walks into the office with diabetes insipidus usually presents with a normal or only slightly elevated  $P_{Na}$  and a Hx of polyuria and polydipsia. The slightly elevated  $P_{Na}$  is due to a single (thirst) rather than a dual (thirst and kidney) homeostatic system and that the thirst threshold (Posm) is slightly higher than the AVP threshold. It is only upon withholding water that water deficiency and severe hypernatremia develops.

## Physiologic basis for treating diabetes insipidus with thiazides

This review will not be an inclusive account of the treatment of diabetes insipidus. Excellent reviews are available on this topic (Star 1990, Howard 1992, Star 1993). For central diabetes insipidus, hormonal replacement is no doubt the main therapy. For both central and nephrogenic diabetes insipidus, other measures can be taken to minimize the urinary water loss. While it is true that water drinking alone should suffice, it is desirable to lower the obligatory water requirement. One very effective therapy is the use of thiazide diuretics.



Thiazides are aimed at several targets along the cascade of free water clearance. Consider a patient with diabetes insipidus with a normal diluting segment but absence of water permeability in the collecting duct. This patient is excreting 600 mOsm of solutes with a obligatory water volume of about 12 L's. With adequate volume contraction, compensatory increase in proximal absorption will decrease delivery to the diluting segment; hence less filtrate is available for free water formation. The main action of thiazides is impairment of NaCl transport and urinary dilution in the distal convoluted tubule. This will impair urinary dilution without disturbing urinary concentration. Lastly, as we mentioned before, even in the absence of AVP, the collecting tubule is not entirely impermeable to water; particularly the terminal IMCD. If urinary flow can be slowed as in the case with volume contraction, urinary osmolarity can actually rise significantly (Berliner 1957, Jamison 1971, Valtin 1987). In this patient on thiazides, the 600 mosmoles is excreted with 2 rather than 12 L of water. This patient is therefore a lot less prone to dehydration if water access were limited in any way.

# **AUTOSOMAL DOMINANT CENTRAL DIABETES INSIPIDUS**

## **Clinical and physiologic studies**

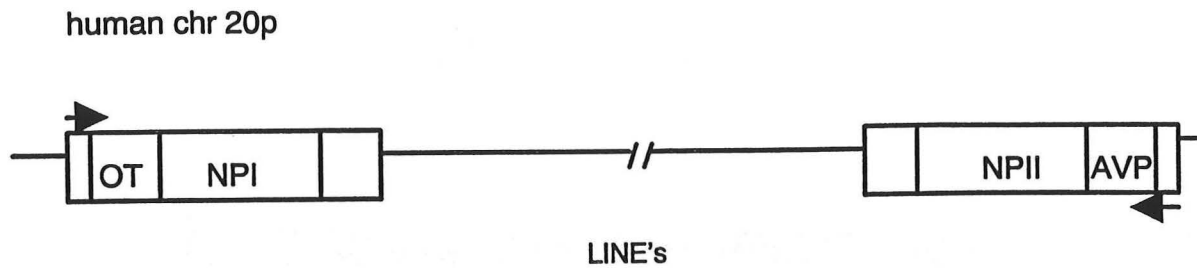
The very first kindred of congenital diabetes insipidus described was of the autosomal dominant variety (Weil 1884, Weil 1908, Camerer 1935). If one were to combine world wide literature to date, this will probably still be the commonest form of congenital diabetes insipidus. A vast number of clinical and laboratory observations were made over about three decades. They can be briefly summarized:

1. Autosomal dominant.
2. Slow onset.
3. Milder and incomplete but progressive.
4. Intact renal response to exogenous administered arginine vasopressin (AVP).
5. Cell death and gliosis limited to the magnocellular neurons in the supraoptic and paraventricular nuclei where AVP is synthesized.
6. In patients with established disease, plasma AVP levels are virtually undetectable.
7. Linkage analysis mapped the locus to 20p: very close to AVP gene.

The patients present more often in later childhood or adolescence rather than in infancy (Pender 1953, Levinger 1955, Kaplowitz 1982). An occasional patient will not receive medical attention till his or her twenties. The disease is often incomplete and the patients retain some ability to concentrate their urine. When AVP analogues such as des-amino-8-D-arginine vasopressin (DDAVP) was administered, these patients concentrated their urine appropriately (Cobb 1978, , Harris 1989). The kidneys are considered to be completely normal. Post mortem findings show a progressive degeneration of the neurons in the supraoptic and paraventricular nuclei where AVP is produced (Braverman 1965). Now we know this form of the disease is due to mutations in the AVP gene leading to defects in AVP secretion by the posterior pituitary.

## **AVP genomic organization**

The AVP gene encodes the prepro form of the enzyme which includes a 19 amino acid leader signal sequence, the 9 amino acid AVP sequence itself followed by a 95 amino acid carrier protein called neurophysin II (NPII). C-terminal to NPII is a 39 amino acid glycoprotein of yet undefined function. In close proximity on chromosome 20 separated by about 10,000 base pairs from the AVP gene is a sister gene oxytocin (OT) (Schmale 1983, Land 1982, Land 1983, Schmitz 1991). Interspersed between OT and AVP is a region of repetitive DNA sequences called Linear Interspersed repetitive Nucleic acid Elements, or LINE's. The function of these sequences are unclear but they appear to hybridize to a poly-A- fraction of cellular RNA that is localized in the nucleus and contains multiple potential reading frames (Schmitz 1991).



The AVP and OT genes are similar in 3 aspects.

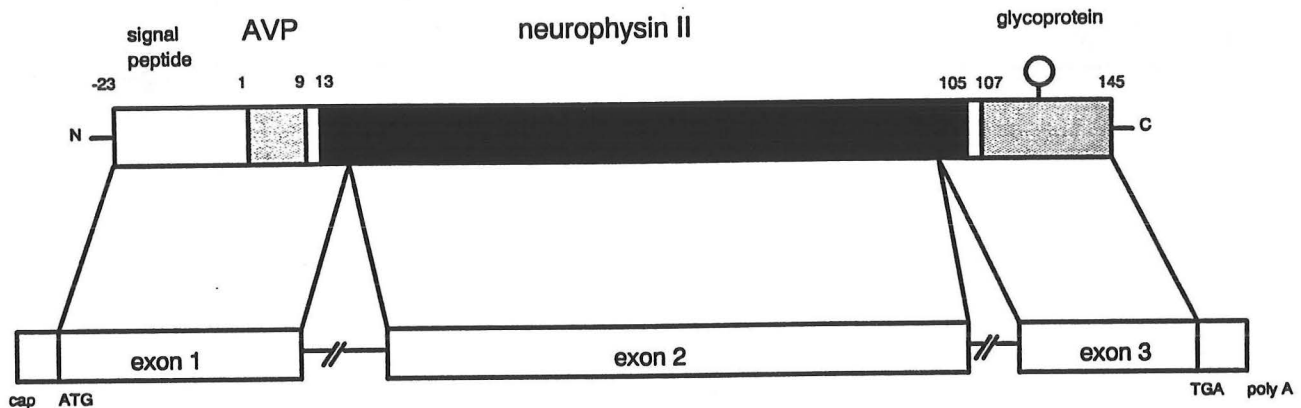
1. OT and AVP peptides are identical to each other in seven out of nine amino acids.
2. In its prepro form, the OT gene has a similar genomic organization as AVP. The carrier protein for OT is neurophysin I (NPI).
3. In addition to the homology between OT and AVP, there are long regions (197 bps to be exact) of NPI and NPII that are identical not only in amino acids but in nucleic acid sequence in several species.

It has been suggested that these genes are the result of recent gene conversion (Rupert 1984, Baltimore 1981). Although a lot of duplicated genes are on the same strand of the DNA (Miller 1983), OT and AVP are actually read off complementary DNA strands (Schmitz 1991). OT and AVP are both synthesized and secreted by the magnocellular neurons of the paraventricular and supraoptic nuclei which are neurosecretory cells in the hypothalamus. It turns out that a given magnocellular neuron secrete either AVP or OT but not both (Mohr 1988, Mohr 1990). Expression of OT is maximally suppressed in AVP-secreting neurons and vice versa. These two peptide hormones serve very different purposes and are regulated by different stimuli (Richter 1988, Mohr 1990). It makes intuitive sense that OT and AVP are transcribed off opposite strands so they can have a 5'-flanking promoter region away from each other and away from the LINE's to secure cell-specific expression and regulation.

## The processing of AVP-NP<sub>II</sub>

The AVP-NP<sub>II</sub> gene is a modular gene. The structure of the polyprotein preprohormone is shown here.

### PreproAVP: A Modular Gene



The mature transcript harbors four polypeptides in a single reading frame. These are the signal peptide, AVP itself, the carrier protein NP<sub>II</sub>, and a glycoprotein of unknown function (Schmale 1983). The three parts of the preprohormone is represented by 3 exons each dedicated to approximately one of the proteins. AVP is synthesized in the magnocellular neurons in the paraventricular and supraoptic nuclei under the control of plasma tonicity (Richter 1988). These neuroendocrine cells send their axons down to the posterior pituitary where AVP is released into the circulation.

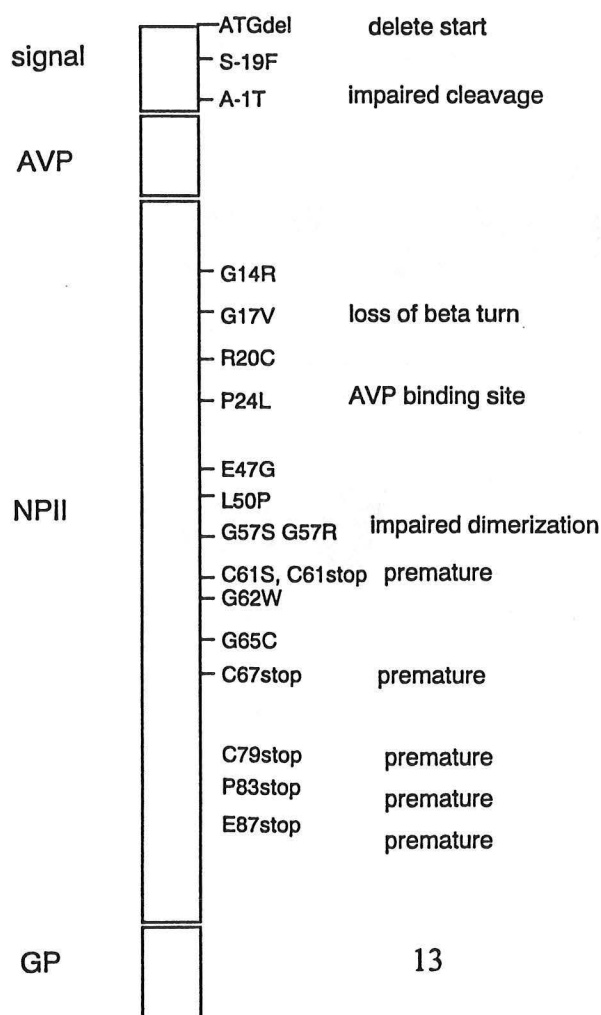
The processing of AVP/NP<sub>II</sub> has been studied in detailed (Gainer 1985, Cohen 1987, Richter 1988). After synthesis as a pre-pro-hormone, AVP/NP<sub>II</sub> is translocated to the ER, targeted to the Golgi where the signal peptide is cleaved off. Within the Golgi, the prohormone is cleaved into AVP and NP<sub>II</sub>. Both proteins undergo extensive disulphide bridge formation and secondary folding. From the Golgi, secretory vesicles are packaged and transported down the axon to the posterior pituitary. Inside these vesicles, AVP and NP<sub>II</sub> is cleaved and are reassembled into a hormone:carrier complex. The crystal structure of these complexes revealed that NP<sub>II</sub> forms dimers. Dimer-dimer contacts then allow formation of NP<sub>II</sub> tetramers. The biochemical studies suggest that each NP<sub>II</sub> tetramer is associated with 4 AVP molecules however crystallographic studies suggest 5 AVP analogues are bound to each NP<sub>II</sub> tetramer (Chen 1991). Four of each are at the major hormone binding site while one straddles one of the monomer-monomer interfaces. NP<sub>II</sub> oligomerization allosterically increases the binding affinity of AVP to NP<sub>II</sub>. In turn, AVP binding to NP<sub>II</sub> also allosterically stabilized oligomerization. The secretory vesicles are transported down the axon to the posterior pituitary, stored in neurosecretory granules. Changes in ambient tonicity as small as 1% causes changes in cell volume of the neurosecretory neuron and activates mechanosensitive cation channels which transduce the mechanical signal to an electrical one (Oliet 1993, Bourque 1994).

Discharge of vesicles is triggered by cell depolarization (Bourque 1994). AVP is released into the circulation dissociated from NPII and the glycoprotein. Although secreted, no specific effects of NPII or the glycoprotein in the periphery has been described.

### Mutations of the AVP gene: more aptly called a disease of neurophysin II

This is a catalogue of the mutations as of a recent search (Ito 1991, Pan 1992, van den Ouweland 1992, Bahnsen 1992, Lolait 1992, Ito 1993, Yuasa 1993, McLeod 1993, Krishnamani 1993, Repaske 1994, Nagasaki 1995). The sequelae of some but not all of these mutations have been worked out. A mutation abolishing the removal of the signal peptide prevents conversion from prepro- to prohormone and trapping of the preprohormone in the ER. *Note that not a single mutation has been described in the AVP sequence itself.* The majority of the mutations reside in the carrier protein NPII. Congenital central diabetes insipidus is really a genetic disease of NPII and not AVP. These mutations perturb NPII structure/function by either gross deletions as premature stop codons, by disruption of the secondary folding, or by impairment of AVP binding.

#### AVP/NPII mutations

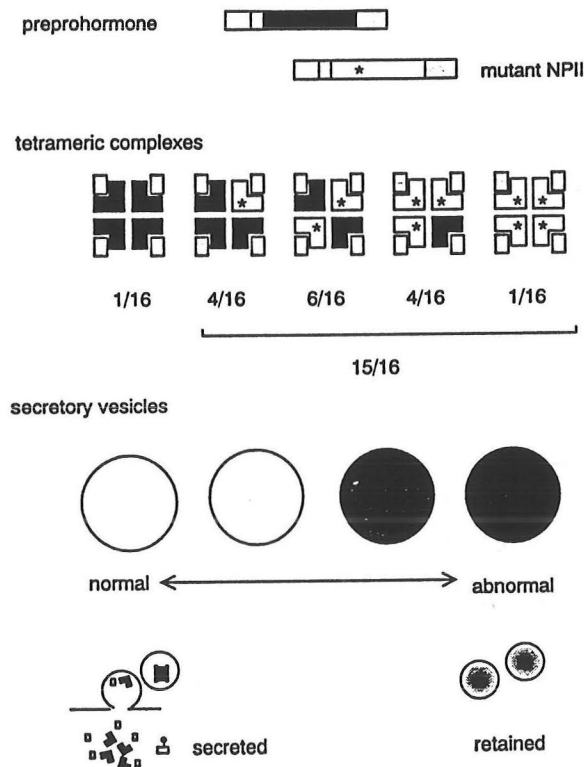


## Genetic basis for the clinical manifestations

A heterozygous mutant alleles of the NPII sequence actually explains most of the clinical findings. Recall the cardinal clinical features of the disease are:

1. Autosomal dominance
2. Late onset of disease
3. Incomplete diabetes insipidus but progressive to complete more severe disease.

In general, there are two reasons why an inherited trait is autosomal dominant. One is bi-allelic dependence. The second is gain-of-function or dominant negative function of the mutant protein. For the AVP/NPII gene, one can envision the following mechanisms at play. First is that since the hormone:carrier complex exist as tetramers, one mutant NPII subunit may ruin the whole complex and impair processing down the axon. A dominant negative effect. However, since there is still one normal allele, there is a  $(1/2)^4 = 1/16$  chance of assembling a completely normal tetramer. In addition, tetramers with only one abnormal NPII may function close enough to normal that it is actually secreted. This explains why early in the disease, the phenotype is that of partial central diabetes insipidus. However, since 15/16 complexes are abnormal, the chronically retained complexes may be toxic to the magnocellular neurons. So a few trapped complexes accumulated over time is sufficient to lead to neuronal degeneration. This explains the progressive nature of the disease and the autosomal dominance pattern.



## X-LINKED RECESSIVE NEPHROGENIC DIABETES INSIPIDUS

### Clinical and physiologic findings

The second commonest form is the X-linked variety. Recall that in certain communities in Eastern Canada, this is not considered a rare disease (Bode 1969). There is a large body of data on the clinical features and pathophysiology of this disease (reviewed in Reeves 1989, Howard 1992, Bichet 1994). A brief summary is presented.

1. Onset in infancy.
2. Resistance to AVP.
3. Locus mapped to Xq28

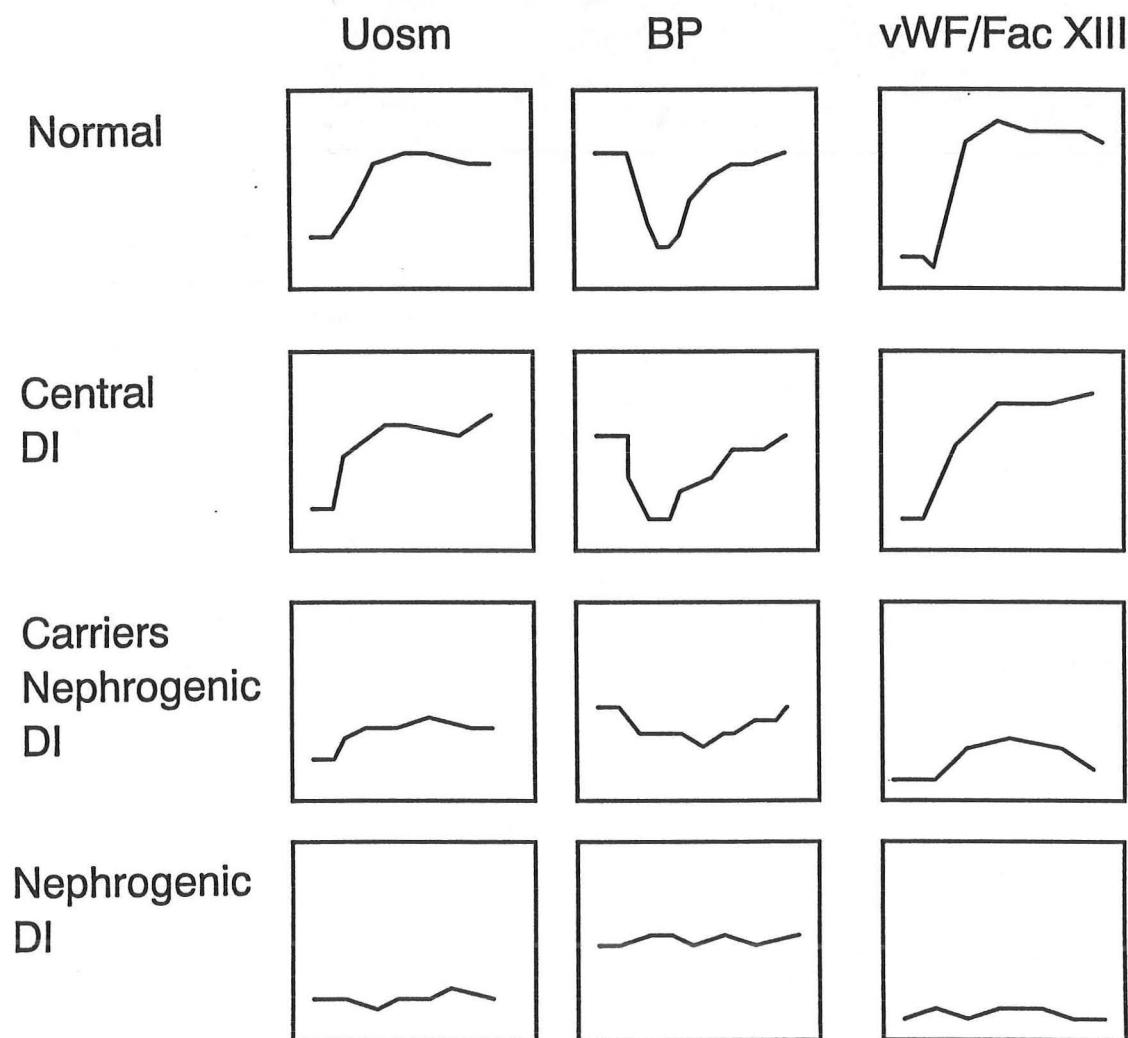
Unlike the autosomal dominant variety, this is truly a neonatal disease. The infants are irritable, eager to feed but will vomit milk unless adequate water is given. Constipation and fever of unknown origin is common. Neonatal mortality is extremely high unless ample water is given. Failure to thrive is common. Because of frequent repeated bouts of hypertonicity causing cerebral dehydration, mental retardation is extremely common if the child survives infancy (Reeves 1989). At one point in the 1950's, one out of ten males in institutions for the mentally retarded in Nova Scotia were believed to be suffering from this disease.

Before the vasopressin receptors were even cloned, the implication of the V2R as a candidate gene for this disease was extremely strong based entirely on clinical physiology (Bichet 1988, Bichet 1989, Bichet 1991, Bichet 1991). AVP receptors were classified according to their pharmacologic characteristics before the cDNA's were obtained (Jard 1988).

	Signalling coupling:	Predominant tissue:	Functional role:
V1a	PLC/Ca <sup>2+</sup>	Vascular	Vasoconstriction
V1b	PLC/Ca <sup>2+</sup>	Pituitary	Regulation of ACTH release
V2	Aden Cyclase	Renal Extrarenal	Regulation of water permeability of collecting duct Vasorelaxation Release of endothelial procoagulants

One seminal paper by Bichet and coworkers in Montreal illustrates the power of clinical physiology (Bichet 1988). They examined the renal and extrarenal effects of V2R agonism in 4 groups of patients: Normal controls, patients with central diabetes insipidus, obligatory carriers, i.e. mothers of affect males, and patients with X-linked nephrogenic diabetes insipidus. The AVP analogue DDAVP which has a 4000-fold higher affinity for the V2R compared to V1R was used.

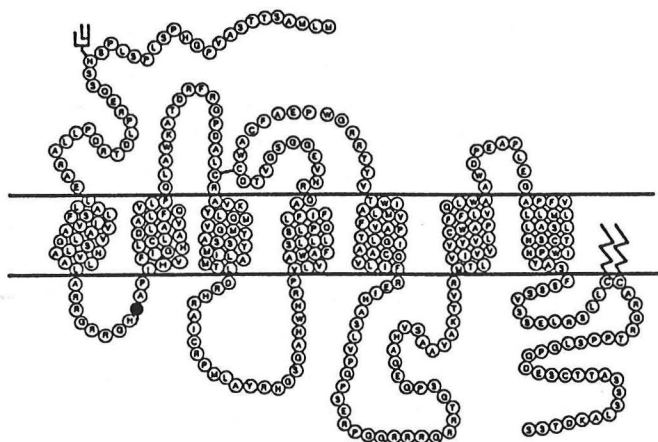
The renal effect of increasing urinary and antidiuresis (urinary concentration) was normal in controls and patients with central diabetes insipidus, completely absent in nephrogenic diabetes insipidus. It is interesting that an intermediate response was noted in obligatory carriers; an effect compatible with X chromosome inactivation. V2R stimulation is known to cause slight hypotension and is also a potent stimulator for Factor and VIII and vWF release via V2R in the endothelium. Both of these extra-renal effects showed absence of response in affected males and an intermediate response in the carriers, an identical pattern to the renal effects of V2R agonism. These results are graphically depicted below.



The clinical evidence was overwhelmingly strong in supporting the V2R as the candidate gene for X-linked nephrogenic diabetes insipidus. When the V2R gene was cloned and mapped to Xq28 (Birnmaumer 1992, Siebold 1992, van Den Ouweland 1992 ), it was not surprising that V2R mutations was uniformly found in all patients tested and cosegregated with the nephrogenic diabetes insipidus phenotype (Bichet 1996).

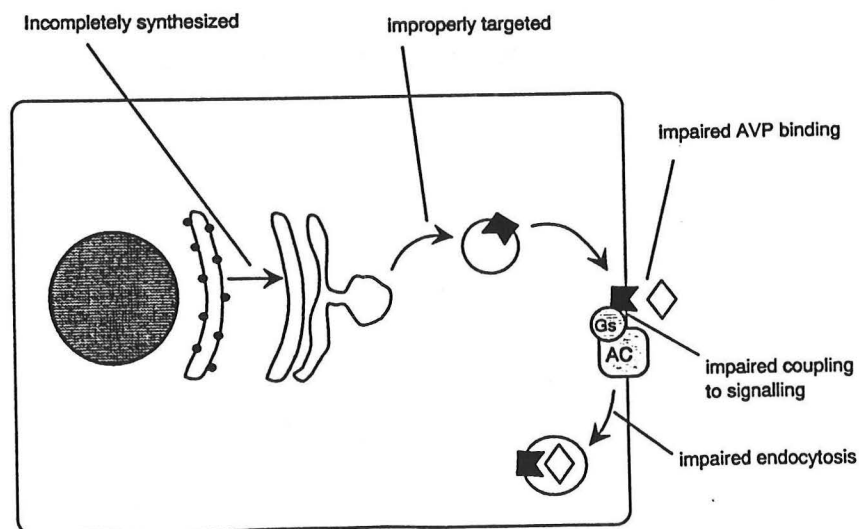
### V2R structure and mutations

The V2R is a typical G-protein coupled receptor of 371 amino acids with 7 transmembrane domains. To date, 87 mutations has been described in 116 families (partially reviewed in Bichet 1996). These mutations involve missense, nonsense, frameshift, small (<20 bps), and large deletions.



These families were gathered from extremely diverse ethnic groups originated from Northern European, Mediterranean, Middle Eastern, South Pacific, Asian, and African ancestry. This unequivocally disproved the Hopewell hypothesis

(Bode 1969) of a single founder bringing this disease to North American on board the ship Hopewell. The famous Hopewell mutation is in amino acid 71 where a tryptophan is mutated to a stop codon resulting in a truncation of the protein. W71X is still one of the more common mutation in North America. The study of the function of these mutant receptors turned out to be extremely educational in understanding the biology of V2R itself. Multiple functional defects of the V2R has been described:



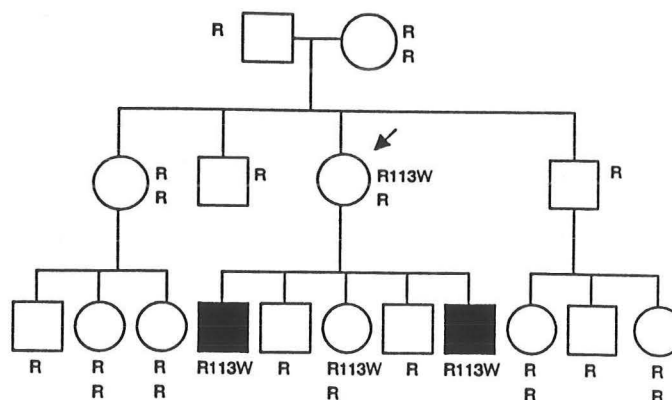
## V2R mutations appear to be in genetic equilibrium

In selected communities in Nova Scotia, the incidence of the disease can be as high as 24 in 1,000 males. Most of the patients with the original Hopewell mutation resided within 2 villages in Colchester county in Nova Scotia. It is difficult to assess the stability of the allele frequency with any accuracy in such small communities since minor migration changes will have significant impact on the results. However, in the province of Quebec with a much larger population and relatively slow migration patterns, the prevalence of the disease has been very constant at 4 in 1,000,000 males for decades (Bichet 1992).

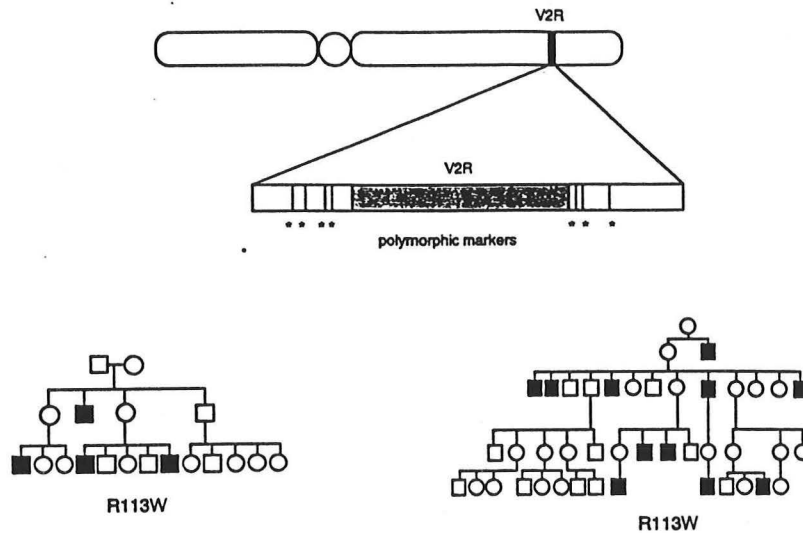
Up until recently, this disease was often lethal for affected males. Even males who survived into reproductive age had a very high incidence of mental retardation (Bode 1969). A great majority of these individuals were confined to institutions and were thus deprived of opportunities to bear offsprings. For these mutations to evade gradual unavoidable attrition, one of two things have to occur. First is a remarkably strong survival and/or reproductive advantage for the female heterozygous carrier. There is no reason to believe that to be true. In fact, the heterozygous females exhibit variable degrees of impaired urinary concentration due to skewed X chromosome inactivation. An alternative explanation appears more likely. The loss of mutant alleles are constantly balanced by a high spontaneous mutation rate thereby maintaining genetic equilibrium. In fact, if one assumes no males reproduce and mutation rates are the same in males and females, one-third of new cases should be due to new mutations. If this true, the recent advances in prenatal and perinatal diagnoses along with aggressive water replacement may unmask the high mutation rate and one should witness an escalating prevalence of X-linked nephrogenic diabetes insipidus. This data is not currently available.

De novo mutations have been shown in two ways. First way is to actually document within a given kindred that the mutation was absent in the grandmother's but present in the mother's somatic cells implying a germ line mutation has occurred in the grandmother. This type of documentation is not commonly available.

De novo mutation in V2R within a pedigree



A more indirect approach is often used. It is not uncommon to encounter the exact identical mutation in seemingly unrelated families. These likely represent independent de novo mutations in "hot spots" if the families are indeed unrelated. To rule out the possibility of distant unrecognized relations, closely linked highly polymorphic markers flanking the V2R gene were examined. If the common mutation in the families were genuinely identical by descent from a common ancestor, then they most likely will share identical alleles in the flanking polymorphic markers.



Using this method, Bichet and coworkers have demonstrated a number of de novo mutations in 18 families to date (Bichet 1994, Bichet 1996). What is the reason for the high susceptibility to spontaneous mutations?

### Molecular basis for high mutation rate in V2R

The predisposing factors lie within the nucleic acid sequence of the V2R gene. There were a total of 9 mutations described at CpG dinucleotides in the V2R gene. Of these, 7 have been documented to be de novo mutations (Bichet 1994, Bichet 1996). These 7 point mutations are shown below.

Amino acid change	Nucleotide change	
V88M	CGTG ⇒	CATG
R113W	CGG ⇒	TGG
R137H	CGC ⇒	CAC
S167L	TCG ⇒	TTG
R181C	CGT ⇒	TGT
R202C	CGT ⇒	TGT

Note that all of these point mutations are either G-to-A or C-to-T changes in the context of CpG dinucleotides. The V2R gene contains 58 CpG's (~5% of dinucleotides) compared to a predicted number of 12-14 CpG's in 1113 bp's of coding sequence. CpG's have long been recognized to be mutational hotspots since an excessive frequency of C-to-T mutations were

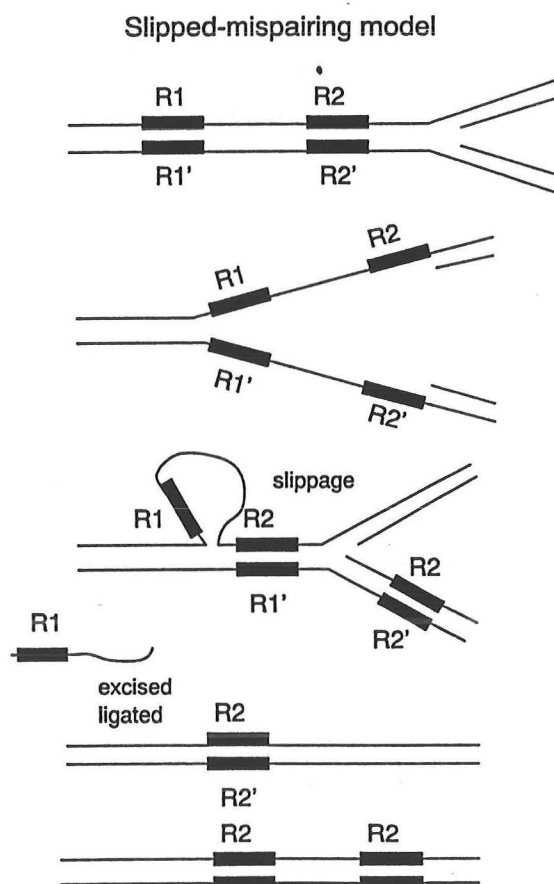
first reported in hemoglobin variants in humans (Vogel 1965, Vogel 1977). The cytosine in CpG in the vertebrate genome often exist as 5-methylcytosine(5mC) which can be deaminated to a thymidine; hence the C-to-T transition. The G-to-A transition occurs from a 5mC-to-T transition on the antisense strand followed by a miscorrection of G to A on the sense strand. As pointed out by Cooper and Krawczak (Cooper 1990 ), CG to TG or CA substitutions are 18 times more frequent than any other mutations at CpG dinucleotides.

Another group of mutations of the V2R that are known hot spots are the small deletions. Of the 18 small deletions, 13 involved direct or complementary repeats (2-9 bps) or strings of 4-6 nucleotides that are either direct repeats or palindromic repeats (Bichet 1994). These sequences carry their own inherent mechanism for mutability (Krawczak 1991, Sinden 1992). Of the 13 small deletions based on this mechanism, 2 are shown here to illustrate the mutation mechanism. First one involves 2 direct repeats.

5'....GCCTTCCTGGGGCTGGTCCTGGGAGCCA...

-----  
12 bp's deleted  
including one repeat

Two replication-based models can be used to explain these deletions (Cooper 1990, Krawczak 1991). First is the *slipped mispairing* model. During replication of a DNA strand containing R1 and R2 direct repeats, the duplex becomes single-stranded at the replication fork. If R2 "slips" and pairs with R1' instead of R2', a single stranded loop containing R1 is transiently created. The error can be corrected if R2 dissociate with R1' and pairs with R2'. However, the loop may exist long enough for DNA repair enzymes to excise and ligate the loop. If this comes to pass, one replicated daughter strand will be missing

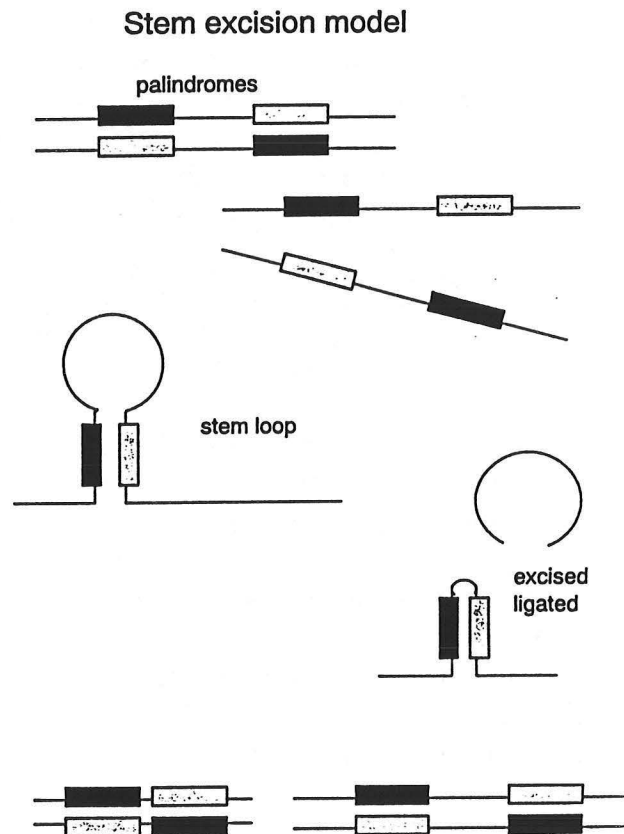


The second model explains palindromic repeats such as this sequence.

5'...GCGGCCCTAGCTCGGCGGGGCCGCGGGG...

-----  
10 bp's deleted  
between two repeats

In this second model, when DNA strands separate during replication. One strand pairs with itself on account of the inverted repeats or palindromes and create a stem loop structure. The single stranded loop is then excised and ligated. When the stem releases itself to resume DNA replication, one daughter strand will have a deletion of the sequence between the two inverted repeats.



# AUTOSOMAL RECESSIVE NEPHROGENIC DIABETES INSIPIDUS

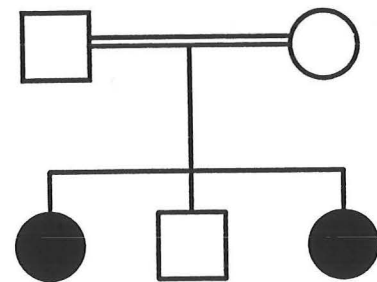
## Identification of another form of nephrogenic diabetes insipidus

The third genetic form of the disease, which is the rarest form documented to date, is the autosomal recessive variety. In certain families suffering from nephrogenic D.I. Two discrepancies were repeatedly observed. First, some families did not exhibit classical X-linked inheritance. Second, some patients have near normal or completely normal urinary cAMP and/or plasma vWF in response to exogenous AVP (Zimmerman 1975, Monn 1976, Ohzeki 1984, Brenner 1988, Moses 1988, Knoers 1991). This suggested that the V2R is normal in these patients yet, AVP failed to elicit antidiuresis in any of these patients. Lacking a pathophysiologic explanation, these patients were labeled to have "type II" nephrogenic diabetes insipidus.

1. Autosomal recessive
2. Normal extrarenal response to exogenous AVP
3. Renal response to AVP:  
     Urinary cAMP- normal  
     Urinary concentration- none

The first definitive genetic evidence of a disease distinct from the V2R mutations was a case that came from Sick Children's Hospital in Toronto (Langley 1991). This report actually predated the identification of the V2R genes as the cause for X-linked nephrogenic diabetes insipidus. Two

girls born of a consanguineous marriage had clinical diabetes insipidus but not their brother. Simple genotyping using a marker (DXS52) that was known to be tightly linked to the Xq28 nephrogenic diabetes insipidus locus provided definitive proof. If these sisters had the X-linked form of disease, then they should both inherit the same DXS52 allele since DXS52 cosegregates very tightly with the disease. This was not true. The sisters did not share a particular RFLP fragment of DXS52. The boy who has the same marker allele as one of the affected sisters did not inherit the disease. This dissociation between phenotype



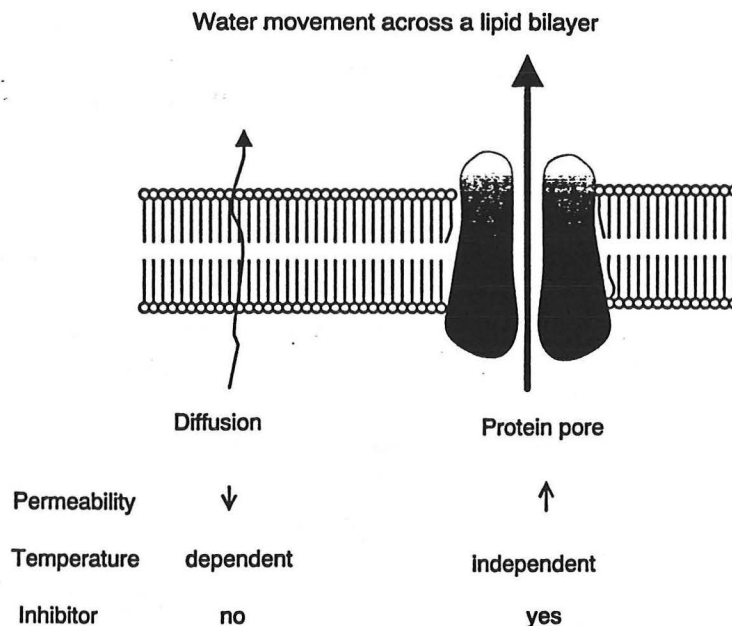
SG	1.000	1.025	1.000
DX352	-	+	+
4.3 kb			
RFLP			

and genotype unequivocally proved that the disease locus was not on Xq28. In conjunction with the physiologic data, particularly the normal urinary cAMP response to DDAVP, a lesion downstream from the V2R seemed inevitable. We now know that this is an autosomal recessive genetic disease of one of the water channels or the aquaporins (van Lieburg 1994, Deen 1994, Oksche 1996).

## Water channels in mammalian cells

Cells are composed primarily of water and are bathed in water. Movement of water in and out of cells is fundamental to all cell function. The search for water channel dates back to the early 1950's (Paganelli 1957, Sidel 1957, Solomon 1983, Solomon 1989 ) when pure biophysical approaches were used. These studies and the models proposed were incredibly accurate even by today's standards in predicting the existence of water channels. However, the actual biological water channel molecules underlying these descriptions remained elusive for decades. Since the purification and cloning of the first water channel, the understanding of water movement through biologic membranes have taken an exponential expansion.

Since the 1950's, biologist have recognized that water can move through lipid bilayers in one of two ways.



Water molecules can indeed enter into the lipid bilayer although the partition coefficient is about  $10^{-6}$ . Given the molar concentration of water being  $>50$  M in the physiologic aqueous phase, there is a small but finite amount of water in the micromolar range within the lipid membrane. This small amount of water is adequate for diffusion across the bilayer. The permeability based on this mode of water transport ( $P_d$ ) is small in magnitude. This permeability is highly temperature dependent with a relatively high Arrhenius activation energy ( $>10$  kcal/mol). As the lipid fluidity decreases with temperature, water movement becomes progressively more restricted. Third, it is independent of covalent pharmacologic modifications as no proteins are involved.

A second mode of transport as predicted by decades of biophysical measurement is through a protein pore. The notion of a water pore and the supportive experimental data of aqueous pores in RBC membranes emerged mostly from the seminal biophysical studies from Solomon and coworkers (Paganelli 1957, Sidel 1957). This water movement is strongly driven by osmotic

gradients and the permeability (Pf) is several times or an order of magnitude larger than that of diffusional water movement (Pd). In fact, the flux of water is so fast that net fluid absorption appeared completely isotonic such as in the RBC and the proximal tubule. In addition, these putative pores are minimally affected by sub-physiologic temperatures with relatively low Arrhenius activation energies (<5 kcal/mol). They are in general sensitive to inhibition by mercurial suhydryl compounds. Therefore for decades, epithelial biologists would measure the Pf/Pd ratio in a membrane, the Arrhenius activation energy for water movement, and sensitivity to mercurial derivatives and be equipped to conclude whether there is an aqueous pore in a membrane.

The kidney is an ideal organ for studying water transport as all aspects of water transport are present.

<i>Water permeability</i>	<i>Segment</i>
Exceedingly high	Proximal tubule and the thin descending limb
Extremely low	Apical membrane of the thick ascending limb
Hormone-dependent	Collecting duct, water permeability can switch from diffusional to osmotic.

### **Cloning of the first water channel... by happenstance**

By the late 1980's, there was little doubt that water channels exist despite an elusive unfruitful search for three decades. Several other membrane transporters such as the band-3 Cl/HCO<sub>3</sub> exchanger (Solomon 1983), the urea transporter (Macey 1984), the facilitative glucose carrier GLUT-1 (Fishbarg 1989, 1990), the vacuolar H pump (Harvey 1991), and the cystic fibrosis transmembrane regulator CFTR (Hasegawa 1992) were all touted as contenders but were all eventually proven to be incorrect. *Xenopus* oocyte expression cloning (Zhang 1990, Tsai 1991) and direct purification out of vasopressin-treated toad bladder epithelium (Harris 1992) failed to yield the desired cDNA. Out of the blue came a classic series of papers by Agre and coworkers who serendipitously encountered the ubiquitous water channel during a search for something completely different (Agre 1987, Saboori 1988, Denker 1988, Smith 1991, Preston 1991). A concise summary of this quest is presented. While purifying the Rhesus (Rh) 32 kD protein from human red cells, they repeatedly encountered what they thought was a 28 kD proteolytic product of the 32 kD Rh polypeptide. Isolation was hampered by a stubborn insolubility of this protein in Triton X-100 suggestive of cytoskeletal association and a peculiar lack of affinity for Coomassie blue staining. Despite these set-backs, their curiosity and motivation soon intensified mainly because this protein has about 150,000 copies per RBC comprising 2.4% of its membrane protein mass. The purification was greatly facilitated by its abundance and a very unusual solubility of this protein in sarcosyl that permitted a one step purification of the protein which can then be easily identified with silver staining rather than Coomassie blue. Cloning using conventional  $\lambda$ -phage expression library screening was unsuccessful as the antisera did not recognize the phage-expressed epitopes. Finally with amino acid microsequence-derived degenerate oligonucleotides, they obtained cDNA's with PCR; from which they use non-degenerate oligo's to screen and clone the full length cDNA. The current nomenclature for this family of proteins is aquaporin (AQP).

## Structure of aquaporins

Hydrophobicity analysis predicts six transmembrane segments separated by five connecting loops. This topology of all AQP's and all known plant and bacterial homologues are very similar (Agre 1993, Chrispeels 1994, Agre 1995). The amino acids are 20-40% identical when the N-termini are aligned. The structure of AQP's have been intensively investigated. A few topologic landmarks will be highlighted here. Extensive reviews are available (Agre 1993, van Os 1994, King 1995, Nielsen 1995, Verkman 1995, Agre 1995, Agre 1996)

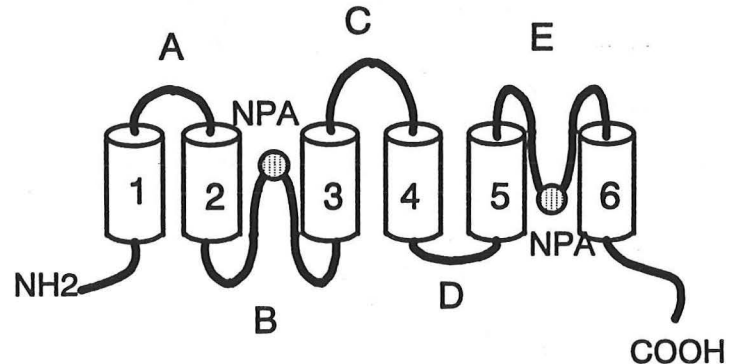
❑ An internal homology between the N- and C-terminal halves of the protein.

❑ Glycosylation sites are present in one of the extracellular loops.

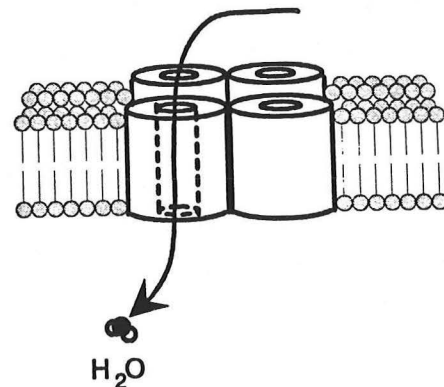
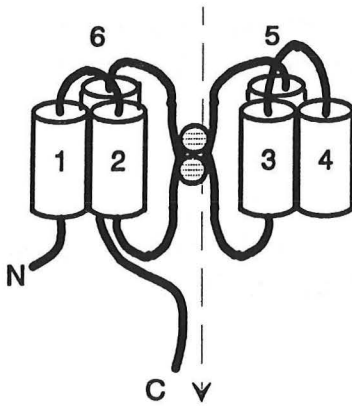
❑ The putative mercurial inhibition site (Cys189) in loop E.

❑ The Colton blood group antigen in loop A.

❑ A highly conserved Asn-Pro-Ala motif in both loops B and E.

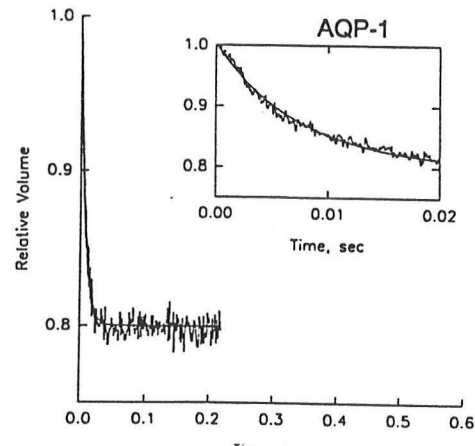
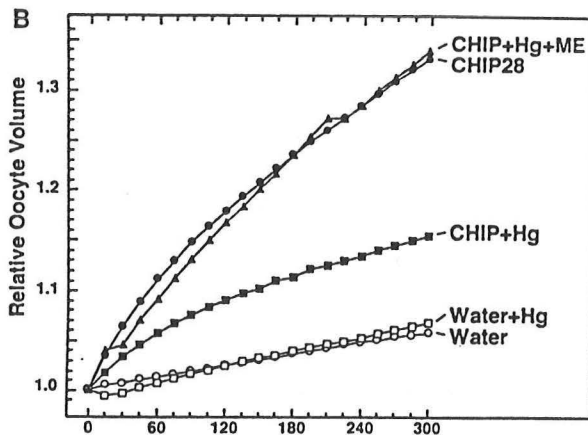
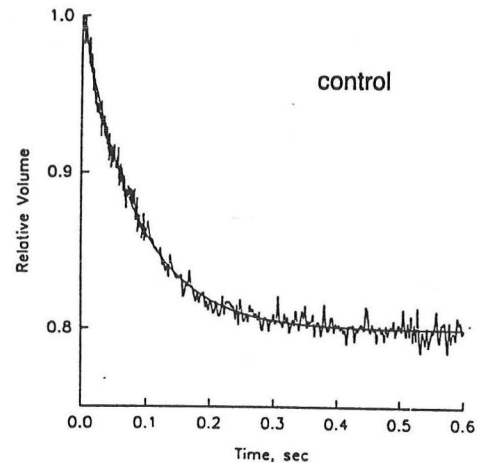
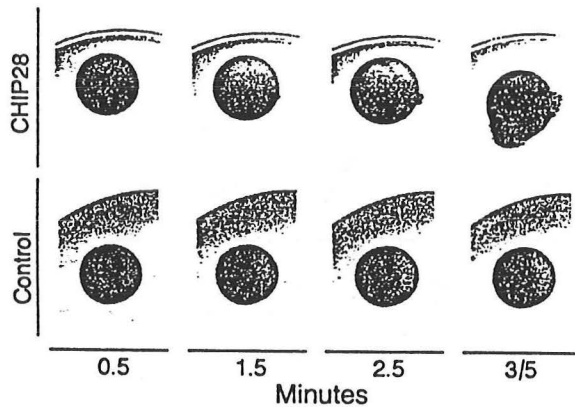


The current consensus appears to be an hourglass model for the protein where loops B and E are imbedded in the membrane from opposite ends of the protein in close proximity creating a critical narrowing through the lipid membrane (Jung 1994). This model places the mercurial covalent site at the critical entry point of the pore. It has also been shown that 4 monomers assemble as homotetramers which results in a characteristic uniform set of intramembrane particles. It appears that each monomeric subunit carries its own functional water channel quite independently of the others.



## Function of AQP-1 as a water channel

AQP as a water channel was shown in two systems. Expression in *Xenopus* oocytes (Preston 1992) and in reconstituted proteoliposomes (Zeidel 1992). In both of these systems, AQP expression dramatically increased water permeability.



□ Oocytes expressing AQP1 swell until they burst when challenged with a hypotonic stimulus.

□ Proteoliposomes containing AQP1 shrinks a lot faster when presented with a hypertonic stress.

In addition, when osmotic permeabilities ( $P_f$ ), Arrhenius activation energies ( $E_a$ ), and sensitivity to mercurial compounds were examined, they were comparable to native highly water permeable membranes. These studies prove that AQP1 is indeed the water channel that has eluded identification for 3 decades.

## Gene family of AQP

Since the cloning of the first cDNA, additional cDNA's have now been cloned. A summary of the isoforms to date is tabulated.

<i>Isoform</i>	<i>Synonyms</i>	<i>Main distribution</i>	<i>Features</i>
<b>AQP0</b>	MIP26	Lens fibre cells	Lower water permeability Murine mutation-congenital cataract
<b>AQP1</b>	CHIP28 DER2	Ubiquitous Erythrocyte <b>Prox tubule</b> <b>Thin des limb</b> <b>Apical and basolateral</b> <b>Vasa recta endothelium</b>	Constitutively active high permeability Epitope for Colton Ag Human mutation- subclinical (?)
<b>AQP2</b>	WCH-CD AQP-CD WCH2	<b>Collecting duct</b> <b>apical membrane</b> <b>subapical vesicles</b> <b>principal cells</b>	AVP-regulated water transport Human mutation- nephrogenic D.I.
<b>AQP3</b>	GLIP BLIP	<b>Collecting duct</b> <b>lateral memb</b> <b>principal cells</b>	Constitutive basolateral exit step No mutations identified
<b>AQP4</b>	MIWC	Ependymal cells Paraventricular Supraoptic nuclei <b>Collecting duct</b> <b>basolateral memb</b> <b>principal cells</b>	Spinal fluid resorption Osmoreception  Constitutive basolateral exit step No mutations identified
<b>AQP5</b>		Salivary & lacrimal glands Cornea Lung	Tears, saliva, sputum

A tremendous amount of data exist for all of these isoforms (reviewed by Os 1994, Agre 1995, Agre 1996). Only a few salient features will be highlighted here.

❑ The current accepted nomenclature enumerates the AQP's according to the order of their identification. AQP0 is named as such because it was recognized only in retrospect to be a water channel when it was cloned. The synonyms represent a haphazard nomenclature that is typical in the early stages of uncovering a gene family. Their use should be discouraged.

❑ AQP0 is major protein that controls fluid balance in the lens. A murine mutation causes congenital cataracts (Muggleton-Harris 1987, Shiels 1993). No human mutations are identified but human AQP0 may play a role in the pathogenesis of senile cataracts in humans.

❑ AQP1 is quite ubiquitous. All the high flux isotonic water movement in the proximal nephron is mediated by AQP1 on both the apical and basolateral membranes (Agre 1995, Agre 1996). Because of its ubiquitous distribution and its abundance in erythrocytes and proximal tubule, one would expect its deletion to be lethal. Worldwide blood group referencing has led to the identification of 5 kindreds whose red cells do not express the Colton antigen (Preston 1994). Analysis of 3 of these individual showed complete or near-complete absence of antigenic and functional AQP1 from homozygous mutations of AQP1. Quite surprisingly, the patient not have any hematologic or renal problems (Preston 1994, Mathai 1995). These five kindreds were found after searching tens of millions of donors and recipients so they are indeed very rare. One possible explanation may be that AQP1 mutations are indeed lethal and these kindreds represent a few rare instances where extraordinary compensatory redundancy exist within the system.

❑ As we will elaborate further, AQP2 is the one responsible for regulated water transport in the collecting duct (Agre 1996, Nielsen 1996) and AQP2 mutations are responsible for autosomal recessive diabetes insipidus.

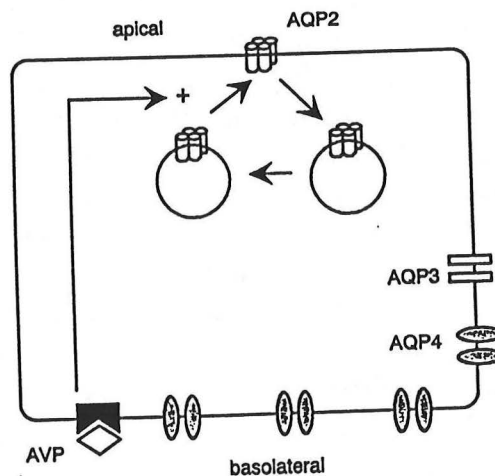
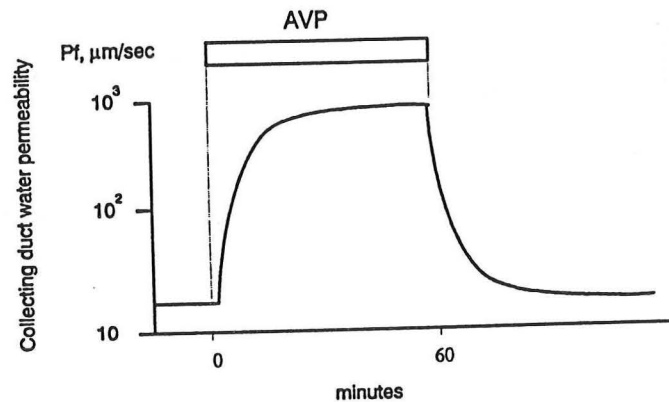
❑ AQP3 is present mostly in the lateral membranes of the collecting duct (OMCDi & outer portion IMCD) that provides the constitutive exit step for water during urinary concentration. It is sensitive to mercurials even though the conserved cysteine is missing. It appears to also transport glycerol and urea to some extent (Echevarria 1994, Ishibashi 1994, Ma 1994). AQP3 may not be entirely constitutive as its expression can be induced by long term administration of AVP (Terris 1996).

❑ AQP4 is only isoform thus far this is insensitive to mercurials. Its mercurial insensitivity is an enigma because introduction of cys189 does not confer mercurial sensitivity. In the kidney, it is diffusely present in the basolateral membrane throughout the collecting duct and likely mediates the constitutive basolateral exit step in urinary concentration. AQP4 is also abundant in the brain. It has been localized to the magnocellular neurons in the supraoptic and paraventricular nuclei and likely represents the channel that allows magnocellular neurons to response to changes in ambient tonicity (Bourque 1994, Oliet 1993, Jung 1994).

❑ AQP5 is the most recent isoform cloned. The "ubiquitous" AQP1 is absent in most glandular tissues suggesting other water channels are probably functional. AQP5 is mostly epithelial in distribution and likely mediates sweat, tears and lung water homeostasis.

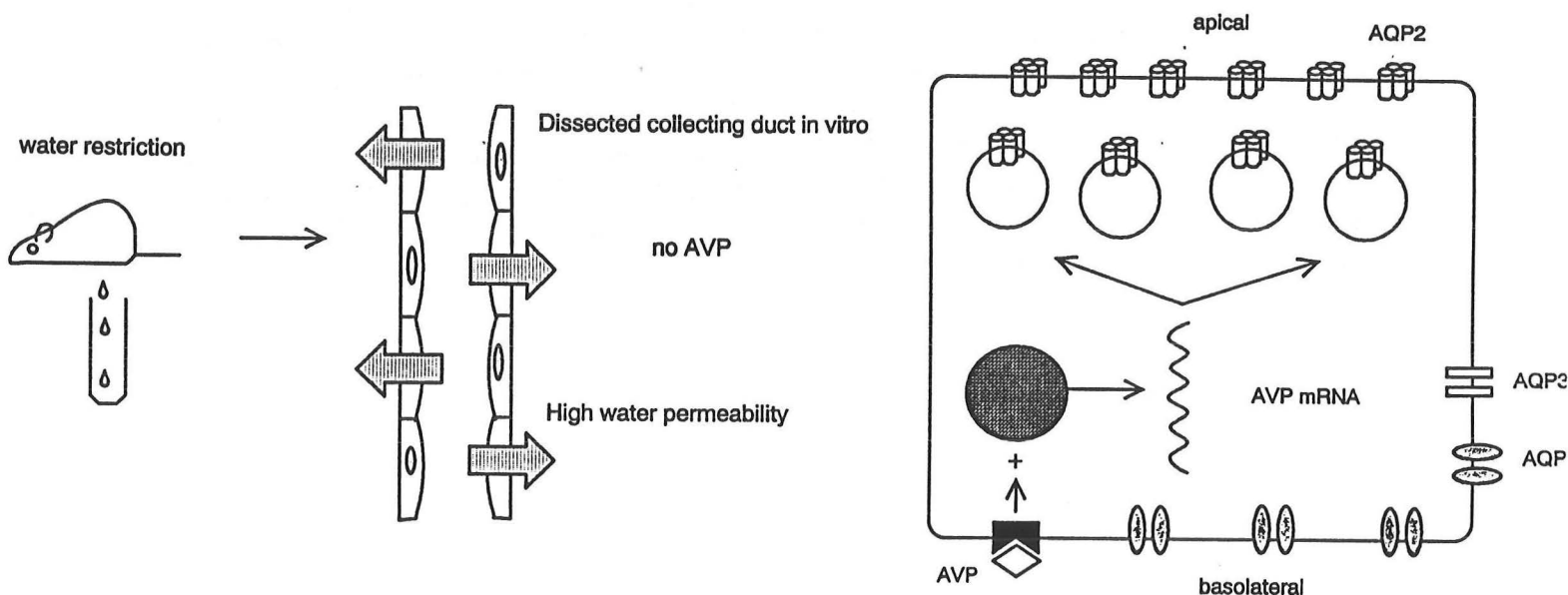
## Acute regulation of AQP2 by AVP

Acute regulation refers changes that occurs in a few minutes. Water permeability of the collecting duct increases within 40 seconds, with a maximal response of an 8-fold increase in about 40 mins (Flamion 1990, Wall 1992). Upon removal of AVP, the response is fully reversible in about the same time frame. These transepithelial permeability changes are due almost entirely to changes in apical membrane and not the basolateral membrane (Flamion 1990). The shuttle hypothesis that were proposed in the early 80's (Wade 1981, Brown 1983) are now confirmed by specific reagents. Subapical vesicle containing AQP-2 are rapidly fused to the surface increasing the number of water channel in the apical membrane (Nielsen 1993, Sabolic 1995, Nielsen 1995). The mechanism responsible for the insertion is currently unknown. Acute phosphorylation by protein kinase A appears to be necessary for increasing AQP2-mediated water permeability (Kuwahara 1995). It is presently not known whether phosphorylation by protein kinase A induces insertion, modulates gating of existing channels, or both. Vesicle-associated membrane protein (VAMP's) or synaptobrevins are believed to determine the specificity of vesicular traffick, docking, and fusion to membrane (Nielsen 1995, Jo 1995).



## Chronic regulation of AQP2

Another mode of regulation takes place over days or at least 24 hrs. It is well known that renal collecting ducts taken from thirsted animals persist to have high water permeability *in vitro* long after the removal of AQP2 (Langford 1991, Knepper 1993, Han 1994). This is due an adaptation in vivo in response to sustained high levels of AVP leading to increase abundance of intramembrane cluster (Wade 1994), increased AQP2 mRNA and protein abundance on the apical membrane and the whole cell (Nielsen 1993, Hayashi 1994, Terris 1996).

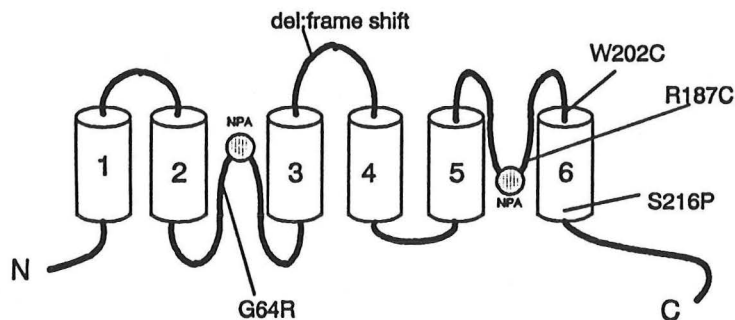


In central diabetes insipidus, the absence of AVP is not the only reason why the kidney cannot concentrate urine. When AVP levels are chronically low such as in the Brattle boro rat with congenital diabetes insipidus, AQP2 virtually disappears from the kidney (Digiovani 1994). When the animal is then repleted with exogenous AVP, it takes about one to two days before adequate AQP2 levels are established. The clinical observation is that in patients with established central diabetes frequently do not respond to DDAVP immediately or only have partial responses. Reasons such as medullary "wash-out" have frequently been proposed due to the loss of solutes in the renal medulla after prolonged water diuresis (Valtin 1966, Fanton 1987) and prolonged treatment with vasopressin re-establishes medullary tonicity and antidiuresis (Harrington 1965, Harrington 1968). Suppressed AVP also prevents interstitial urea accumulation in the inner medulla via AVP-sensitive urea transport at the terminal medullary collecting duct (Morgan 1968, Knepper 1987, Knepper 1990). A more attractive or at least a supplementary explanation for the apparently lack of response to AVP after chronically low AVP from either central diabetes insipidus or water loading is a normal physiologic delay in AVP-induced AQP2 expression.

## Autosomal recessive nephrogenic diabetes insipidus from mutations in AQP-2

A number of inactivating mutations have been identified in patients who are either homozygous or compound heterozygotes.

Nephrogenic diabetes insipidus: Mutations in AQP2



With the exception of the frameshift deletion, all these mutations are situated around or at the region. All these mutant proteins are predicted to be either improperly processed, non-functional, or both. The mechanistic details are just being uncovered. Bichet et al have identified defective trafficking as one mechanism (Bichet, personal communication).

### Urinary AQP-2 levels

Since apical membrane proteins from renal epithelial cells are detectable in normal urine, a sensitive radioimmunoassay can actually measure AQP2 levels in human urine. Kanno and coworkers studied urinary AQP2 in normals, subjects with central and nephrogenic diabetes insipidus (Kanno 1995). All were given a single dose of DDAVP. Urinary AQP2 levels rose in the first two groups but the profile was completely flat in the patients with nephrogenic diabetes insipidus. This clinical test is currently not widely available it is highly promising as an investigative tool for further human studies of water metabolism.

## **ACQUIRED NEPHROGENIC DIABETES INSIPIDUS**

Much more common than congenital diabetes insipidus is the acquired form. That applies to both central and nephrogenic. Acquired diabetes insipidus with a hypotonic urine (polyuria with paucity of solutes in the urine) can be broadly classified into two pathophysiologic categories:

1. Loss of medullary hypertonicity
2. Lack of permeability of the collecting duct (central vs. nephrogenic)

Since the discovery of aquaporins has enhanced our knowledge of the pathophysiology of nephrogenic diabetes insipidus, the role of AQP2 in three common clinical forms of nephrogenic diabetes insipidus will be described.

### **Lithium-induced nephrogenic diabetes insipidus**

One common acquired form of nephrogenic diabetes insipidus is the Li-induced type which has been described up to 50% of patients on lithium although not all of them have overt clinical presentations (Boton 1987, Walker 1993). The urinary concentration defect is resistant to AVP and likely multifactorial in nature including impairment of cAMP generation (Christensen 1985, Christensen 1988, Sugawara 1988, Goldberg 1988) and enhanced prostaglandin E2 effects (Sugawara 1988, Yamaki 1991). Recently, AQP2 has been shown in an animal model to be an effector in this disorder (Marples 1995). Chronic Li therapy led to a urinary concentration defect, polyuria and polydipsia that was paralleled by a dramatic reduction of collecting duct AQP2 levels. The recovery of AQP2 is slow and incomplete within after one week of cessation of Li therapy. During chronic Li therapy, a 7 days sustained pharmacologic infusion of AVP which normally induces AQP2 protein to supraphysiologic levels only partially restored the AQP2 levels and partially reversed the concentration defect while the animals were on Li. This study suggests that Li has a dramatic effect on AQP2 expression that is more than pure antagonism of tonic levels of AVP.

### **Nephrogenic diabetes insipidus from K depletion**

K depletion has long been known to induce a urinary concentration defect. Like lithium, the urinary concentration defect is multifactorial including loss of medullary solutes (Mannitus 1960), deranged papillary blood flow (Whinery 1979), and stimulation of prostaglandin synthesis (Ferris 1978) although species variations do exist (Berl 1980). In a rat model of K deficiency (Marples 1996), AQP2 levels were significantly suppressed after 2 weeks of a low K diet. In the presence of chronically suppressed AQP2 levels, the kidney failed to mount a urinary concentrating response respond to acute water restriction. Only upon K repletion and restoration of AQP2 levels could normal urinary concentration be operative.

## **Post-obstructive nephrogenic diabetes insipidus**

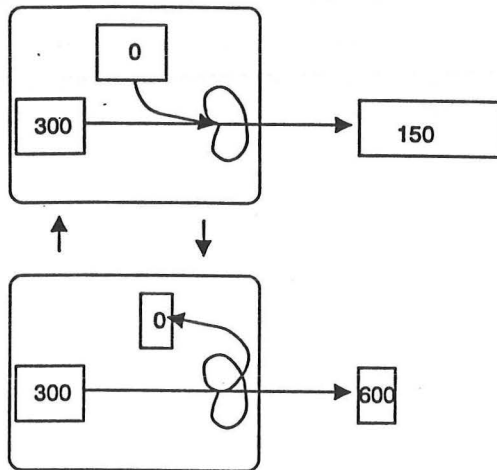
A diuretic phase after relief of urinary obstruction is a common clinical problem characterized by inability to concentrate urine (Wilson 1951, Wilson 1975). All segments of the nephron appear to be involved in the diuretic phase; proximal tubule, loop of Henle, and the collecting duct (Jaenike 1972, Yarger 1972, McDougal 1972, Wilson 1975, Sonnenberg 1976, Buerkert 1977, Buerkert 1978, Hanley 1982). The role of AQP2 in this disorder was recently shown in a rat model of transient bilateral ureteral ligation (Frøkiær 1996 ). One day after obstruction was induced, AQP2 levels fell to <30% of control. Upon relief of this obstruction, AQP2 levels remained extremely low for 48 hours. The diuresis in the first 24 hrs was due to solute diuresis with a significantly elevated *Cosm*. However, 48 hours post obstruction, the diuresis is predominantly a water diuresis; most likely attributable to the low AQP2 levels. Even after 7 days of relief of the obstruction, AQP2 levels still have not returned to baseline. Although there is no significant diuresis at this point, rats with a history of obstruction 7 days ago still cannot respond to an 18 hour water deprivation with antidiuresis likely due to the low AQP2 levels.

## SUMMARY

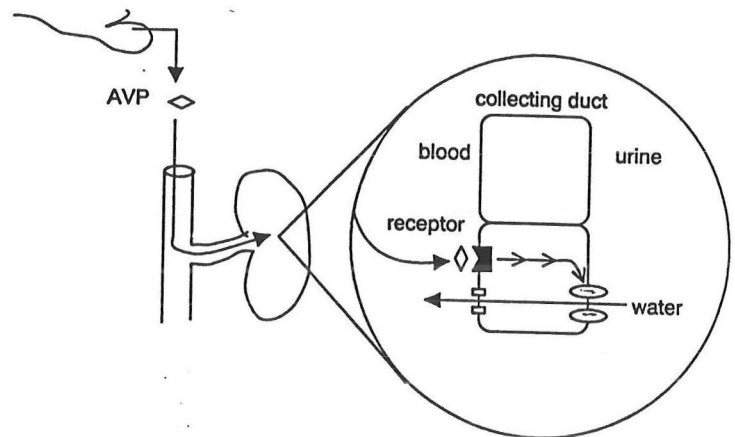
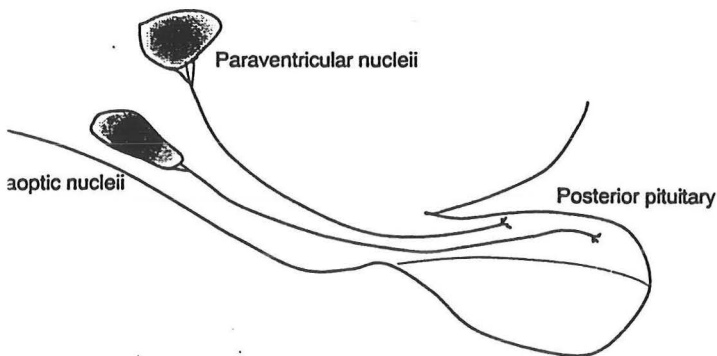
1. Plasma  $[Na]$  is a clinical marker for total body water.
2. Regulation of total body water is achieved by a dual system of thirst and renal water excretion or generation.

	Major defense
Water excess	Kidney
Water deficit	Thirst

3. Kidney can add or remove water from plasma.



4. Posterior pituitary-collecting duct axis: Determinant of the fate of water in the kidney.



Congenital diabetes insipidus

Mutations in the carrier protein of AVP:

Mutations in the V2 receptor:

Mutations in the AQP2 water channel:

autosomal dominant central

X-linked nephrogenic

autosomal recessive

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