THE ^{99m}Tc-DTPA DYNAMIC RENAL SCAN WITH DECONVOLUTION ANALYSIS

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Dynamic renal studies were performed with ^{99m}Tc-diethylenetriaminepentaacetic acid (^{99m}Tc-DTPA). The results were analyzed by the method of mathematical deconvolution in order to obtain the impulse response function of the kidney. Regional analysis of the kidney was attempted by evaluating the independent responses of the renal parenchyma and renal pelvis to a bolus injection of ^{99m}Tc-DTPA.

The technetium chelate, ^{99m}Tc-diethylenetriaminepentaacetic acid (^{99m}Tc-DTPA), has been used to study renal function. The biologic behavior of DTPA, together with the physical characteristics of ^{99m}Tc, make this compound a useful agent for renal studies (*1*). The DTPA is cleared in a truly glomerular manner by the kidneys (*2*), in contrast to Hippuran, most molecules of which pass through the tubular cells into the urine (*3*).

Dynamic renal studies with ^{99m}Tc-DTPA yield results that readily lend themselves to analysis by the method of mathematical deconvolution. This technique allows one to derive the response of a kidney to a bolus injection of DTPA into the renal artery from the renogram which results from the time-varying input of DTPA from the blood into the kidneys.

Deconvolution analysis has been previously applied to bloodflow measurements (*4*) and to tracer-kinetics studies in gastroenterology (*5*). In particular, deconvolution analysis has recently been used to study renal function by Fleming and Goddard (*6*) and Kenny et al (*7*). These workers used ^{123}I-Hippuran as the tracer and employed Laplace transforms to derive the retention function. In contrast, the present communication describes the renal handling of ^{99m}Tc-DTPA and uses the matrix algorithm of deconvolution.

MATERIALS AND METHODS

The renal scan. The patient, who is hydrated before the study, is positioned with his back to the scintillation camera so that both kidneys and the abdominal aorta are in the field of view. The camera used in this investigation is a Selektronik Radicamera (Denmark) having a 13-in.-diam NaI(Tl) crystal; it was used in conjunction with a high-sensitivity parallel-hole collimator specifically designed for dynamic studies. Approximately 2 mCi of ^{99m}Tc-DTPA in about 0.5 ml of saline is injected into an antecubital vein and sequential 20-sec frames are stored in the computer (a PDP/E computer used with the Nukab-2530 data-analysis software). The study proceeds for approximately 20 min, and at the end of the study, time–activity curves of each kidney and the aorta are obtained for analysis. Following a program written in FORTRAN for the mathematical analysis, the computer program takes 2 min to calculate and display the relevant information on renal function.

Derivation of the retention function. The deconvolution of the renal scan requires that the kidney be regarded as a linear system, i.e., the amplitude of the renogram is assumed to be directly proportional to the administered dose. This linearity is implicitly assumed in practice since the amount of tracer normally injected is very much less than the volume of distribution. If the foregoing is true, it follows that the observed renogram will be a convolution of the input function from the blood to the kidney with the impulse response function (or retention function) of the kidney. Thus, the renal activity R(t) at time t is given by

$$R(t) = \int_0^t B(t - T)H(T)dT, \qquad (1)$$

where B is the activity in the blood and H is the kidney retention function. The retention function H is the form of the renogram that would be obtained if a bolus of DTPA could be injected directly into the renal artery: it represents renal function in its simplest form. Equation 1 may be solved for H in a number of ways, and two of these have been investigated in this department.

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The first method for obtaining H is by means of Laplace transforms (*6,7*). Since the expression is a standard convolution integral, the retention function is the inverse Laplace transform of the ratio of the Laplace transforms of R and B. This method requires that the blood activity B to be represented by some reasonably simple function of time. However, no simple function directly applicable in all cases has been found. In view of this, the matrix algorithm of deconvolution (*8*) is preferred for the solution of H.

In this second method, the linear matrix H is evaluated in a successive manner, starting with H(0) and working through to the final element H(N). Thus, H(t) is given by

$$H(t) = [R(t) - \sum_{T=0}^{t-1} B(t - T)H(T)]/B(0). \quad (2)$$

This method does not assume previous knowledge of the form of the data, and perturbations occurring in both the blood curve and renogram (due to patient movement, for example) will not be reflected in the retention function. On one occasion, for example, a patient was given a subcutaneous injection of DTPA due to a clinical error. The activity in the blood, monitored over the aorta, continued to rise during the 20-min study, resulting in a renogram indicative of an obstructed kidney. Using the matrix algorithm of deconvolution, however, the retention function indicated a normally functioning kidney, confirmed a few days later by repeating the examination with an intravenous injection.

Filtering of the data. A common problem in the analysis of experimental results is the presence of unwanted frequencies or noise in the data. We found data-bounding to be of use in overcoming this problem (*9*). Data-bounding is a process whereby noise components exceeding a certain bound are eliminated from the data; it is an iterative process in which the bound for rejecting noise is decreased on successive passes through the data. The effect of data-bounding is illustrated in Fig. 1. The upper half of this figure gives the result of deconvoluting the raw data, where it may be seen that the retention function provides very little information. The lower half presents the retention function calculated after the renal and blood curves have been data-bounded. The retention function now clearly indicates a normally functioning kidney with a mean transit time of 3 min. Moreover, there is no significant loss of structure in either the renal curve or blood curve. The amplitudes of all curves presented here were plotted on an arbitrary scale for the purposes of clear illustration.

Blood-background subtraction. It is customary in conventional renography to subtract the contribution

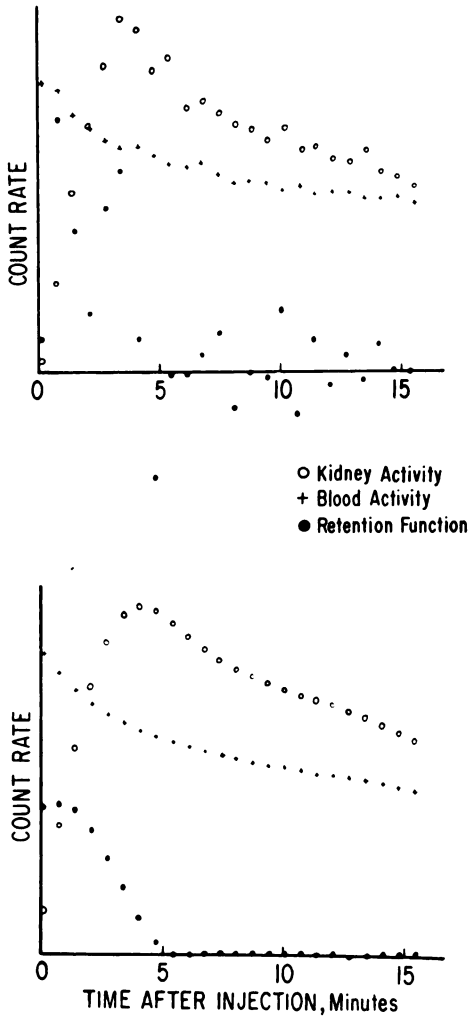

FIG. 1. Effect of data-bounding on deconvoluted retention function. (Top) Deconvolution of raw data; (bottom) deconvolution after kidney and blood activity curves have been data-bounded.

of the included extrarenal tissues in order to obtain the net renogram (*10*). However, if it is assumed that the variation of blood background with time is qualitatively the same as the arterial blood activity, then the blood activity overlying the kidney represents a constant offset at all frequencies, which appears only in the first element of the deconvoluted retention function. In order to eliminate the blood-background contribution, the first element of the retention function is set equal to the second element. Thus, it is not necessary to delineate the kidney exactly as a region of interest. In fact, a very large area may be deconvoluted, provided only one kidney is contained within the region. Of course, the subtracted renogram can be derived by convoluting the calculated retention function with the blood activity curve, as indicated by Equation 1.

Absolute renal function. If the arterial blood activity curve is computed by flagging an equal area

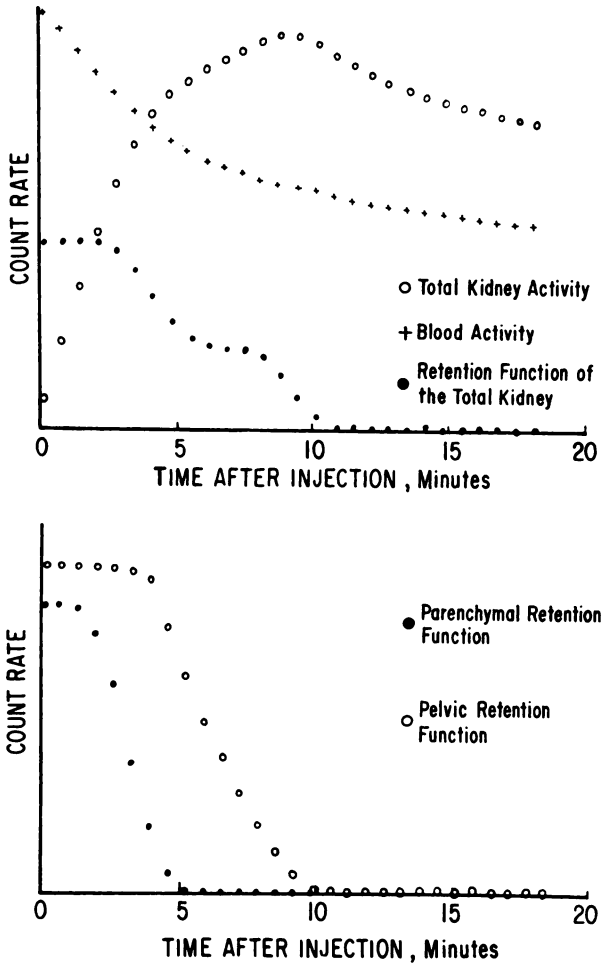

FIG. 2. Deconvolution of kidney with dilated renal pelvis. (Top) Whole kidney; (bottom) retention functions of renal parenchyma and renal pelvis.

on every scan, the amplitude of the retention function at the time of injection will be related to the number of functioning nephrons present in the kidney. In a study of 34 patients with normal renal function, these initial amplitudes exhibited a standard deviation of 20% of the mean. If the mean of these amplitudes is taken to represent "normal" renal function, it then becomes possible to specify the function of any other kidney.

In a normally functioning kidney the retention function should have a zero amplitude after about 5 min (Fig. 1, bottom). In some cases, however, there may be uptake and retention of DTPA with a very poor clearance. In this case the amplitude of the retention function may be well above zero at the end of the study. The ratio of the amplitude of the retention function at the end of the study to that at the beginning is related to the fraction of renal function that is compromised by obstruction.

Regional analysis of the kidney. With the scintillation camera, the kidney can be delineated in its coronal plane, where regional separation of the kidney may be attempted. However, since the resolution of the scintillation camera is of the order of 1 cm at best, the cortical and medullary functions cannot be separated. Analysis of the regional physiology of the kidney has been attempted from time–activity curves of the renal parenchyma and renal pelvis. Satisfactory separation of these areas is sometimes questionable, but in certain cases regional deconvolution can aid diagnosis. In particular, comparison between the DTPA clearances of the parenchyma and pelvis may help distinguish parenchymal DTPA retention from pelvic obstruction.

In common with other workers, we have observed that in a few cases the retention function of the total kidney has a negative excursion of about 20% of the amplitude of the retention function at the time of injection. That is, the rate of removal of DTPA from the kidney exceeds the rate of input from the blood. This phenomenon may be caused by such factors as increased urine flow rate due to transient fluctuations in the salt and water reabsorption in the nephrons, changes in renal blood flow as the psychologic state of the patient alters during the study, or peristalsis of the renal pelvis producing nonlinear passage of urine. When this happens, the simple linear model of the kidney no longer holds.

CLINICAL EXAMPLES

Figure 2 (top) shows the renogram, blood curve, and retention function of the right kidney of a patient with carcinoma of the cervix. The intravenous pyelogram showed a normal left kidney, but the right kidney apparently had an enlarged pelvis. The problem was to determine the presence or absence of obstruction on the right side.

The deconvolution of the whole kidney shows a prolonged retention function with two clear populations of transit times, these being more clearly resolved by regional analysis of the kidney. Figure 2 (bottom) shows the retention functions of the renal parenchyma and renal pelvis of this right kidney. The retention function of the pelvis is obtained by deconvoluting the renogram of the pelvis with the renogram of the parenchyma, thus deriving the response of the pelvis to a bolus injection of DTPA directly into the pelvis. The retention function of the parenchyma indicates normal function, whereas the pelvic response function shows that the mean lifetime of a DTPA molecule in the dilated pelvis is about 5 min, considerably longer than that observed in a normal pelvis (about 1.5 min).

Since the parenchymal function is entirely normal, there is no delay for the DTPA molecule in reaching the pelvis. This would not have been the case had

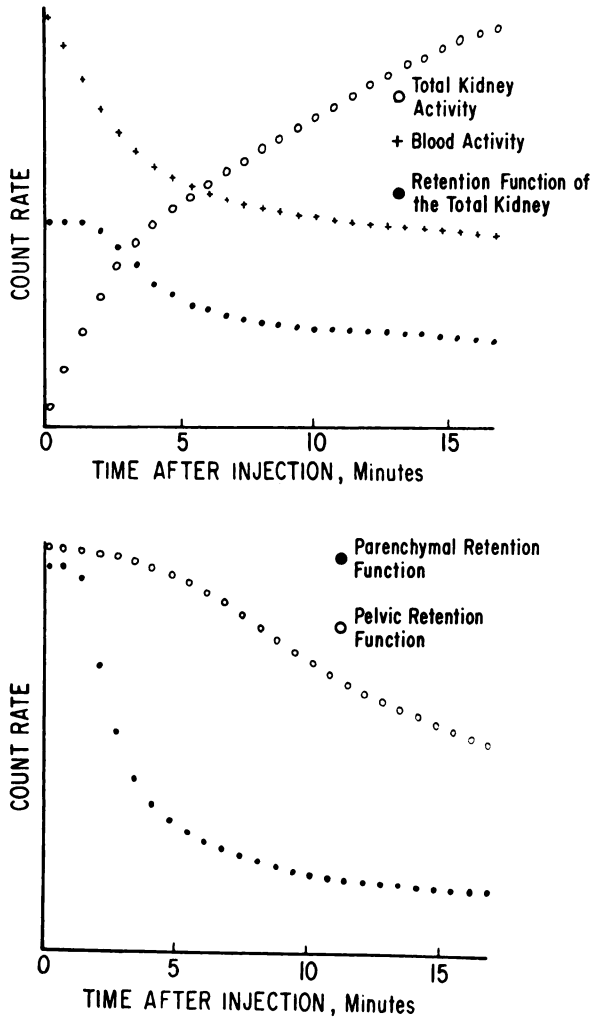

FIG. 3. Deconvolution of kidney with hydronephrosis. (Top) Whole kidney; (bottom) retention functions of renal parenchyma and renal pelvis.

the function of the parenchyma been reduced due to the inability of the pelvis to discharge its contents down the ureter. Thus, this case shows a pelvis larger on one side than the other but without obstruction.

The use of regional analysis in a case of proven hydronephrosis is illustrated in Fig. 3. The first half shows the renogram, blood curve, and retention function of the hydronephrotic left kidney. However, the retention function of the parenchyma, shown in the second half, indicates an element of functional impairment resulting from the back-pressure of urine in the renal pelvis. The retention function of the pelvis shows very slow clearance of urine.

CONCLUSIONS

The introduction of DTPA as a dynamic renal-scanning agent permits the whole nephron to be studied, in contrast to Hippuran, only a small fraction of which is filtered through the glomerulus. The different mechanisms of handling DTPA and Hippuran by the kidney lead to shorter renal transit times for Hippuran. Kenny et al (*7*) have shown that the mean renal transit time in 19 normal patients injected with ^{123}I-Hippuran is 2.23 ± 0.27 min, whereas we observed that the mean renal transit time of DTPA in 14 normal patients is 3.0 ± 0.5 min.

Interpreting renograms depends largely on experience and pattern recognition, since the shape of the renal curve is related to tracer clearance from the blood. Deconvolution reduces the renogram to a curve that is more easily interpreted. Small changes in renal function (particularly nephron transit times) are more clearly seen in the retention function than in the integral renogram. The method of deconvolution is a further step forward in the understanding of the renogram, following the introduction of blood-background subtraction a few years ago.

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