

[Fig. 1] (Fig. 1A). We hypothesized that a tracer with these properties could have its myocardial kinetics analyzed with a simple compartmental model in which the neurons act kinetically as a single irreversible compartment (Fig. 1B). In addition, these properties would allow the application of the Patlak graphical method for estimating the tracer's net neuronal uptake rate (7).

To this end, our studies of a series of ^{11}C -labeled phenethyl-guanidines identified N - ^{11}C -guanyl(-)-*meta*-octopamine (^{11}C -GMO, Fig. 2) as a promising tracer exhibiting the 2 targeted properties (8). The goal of the current study was to test our hypothesis that ^{11}C -GMO would exhibit myocardial kinetics that could be successfully analyzed with tracer kinetic techniques. We also evaluated the ability of quantitative measures from analyses of ^{11}C -GMO kinetics to track declines in available NET densities, induced pharmacologically with the potent NET inhibitor desipramine.

MATERIALS AND METHODS

Radiochemistry

^{11}C -GMO and ^{11}C -MIBG were synthesized as previously described (8). ^{11}C -HED was prepared using previously published methods (9). Specific activities for these compounds were 18.5–55.0 TBq/mmol. ^{18}F -FDG was prepared as previously described (10).

Animal Care. The care of all animals used in this study was done in accordance with the Animal Welfare Act and the National Institutes of Health's *Guide for the Care and Use of Laboratory Animals* (11). Animal protocols were approved by the University Committee on Use and Care of Animals at the University of Michigan.

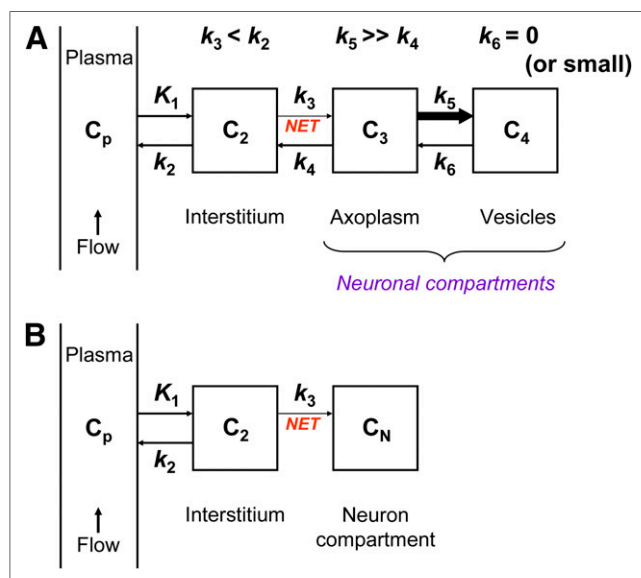


FIGURE 1. (A) Comprehensive compartmental model of sympathetic nerve radiotracer with optimal kinetic properties. Arrow thicknesses are drawn in approximate proportion to magnitude of rate constants. If NET transport rate of tracer (k_3) is less than efflux rate from interstitium back into plasma (k_2), this prevents tissue uptake of tracer from being flow-limited. Furthermore, if vesicular storage rate (k_5) is rapid relative to efflux from neuronal axoplasm (k_4), and tracer is effectively trapped in vesicles ($k_6 = 0$ or small), 2 neuronal compartments kinetically behave as single trapping compartment. This allows use of simplified compartmental model (B) for quantitative analysis of kinetic data from PET studies.

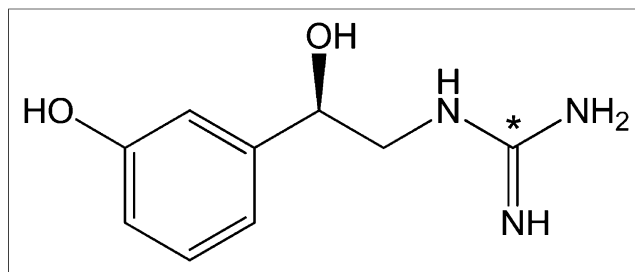


FIGURE 2. Structure of ^{11}C -GMO. ^{11}C label is incorporated into guanidine group (*).

Isolated Rat Heart Studies

Kinetic studies of the neuronal uptake and retention of ^{11}C -GMO, ^{11}C -HED, and ^{11}C -MIBG were performed with an isolated working rat heart system (8,12) under moderate workload conditions (10 cm H_2O preload, 100 cm H_2O afterload). For comparison, a study with ^{18}F -FDG was performed under identical conditions except that the perfusate glucose concentration was changed from 5 to 10 mM. A 10-min constant infusion of tracer at low concentrations was performed to measure neuronal uptake rates. The heart was then switched to a second perfusion circuit with normal perfusate for 120 min to study tracer clearance from sympathetic nerve terminals. Coincidence counting rate data (cps/heart) from 2 opposing 5.1 \times 5.1 cm cesium fluoride detectors were corrected for random coincidences and normalized to the activity concentration in perfusate (cps/mL perfusate) and the heart's wet mass (g wet/heart) to express heart uptake of tracer as an apparent distribution volume (mL perfusate/g wet). Neuronal uptake rates K_{up} (mL perfusate/min/g wet) were determined as the linear slope of the apparent distribution volume data between 1 and 4 min of the constant infusion study. Clearance kinetics were fit to multiple exponential decay processes to characterize clearance rates. For the nerve tracers, 54 μM corticosterone was added to perfusate to block extraneuronal uptake (uptake-2) into myocytes (13), which competes with neuronal uptake (uptake-1) in rat hearts but is absent in nonhuman primate and human hearts (6).

PET Imaging

PET imaging was performed using a Concorde Microsystems microPET P4 primate scanner (19-cm field of view, 7.8-cm axial extent, 1.75-mm intrinsic spatial resolution, and 2.25% peak system sensitivity) (14). After the monkey was anesthetized, a percutaneous angiocatheter was placed in the saphenous vein of each leg (1 for tracer injection, 1 for blood sampling). Heart rate (bpm), blood oxygen saturation levels (SpO_2), and body temperature were monitored continuously (V3404P; SurgiVet). A transmission scan was acquired using a rotating $^{68}\text{Ge}/^{68}\text{Ga}$ rod source for attenuation corrections. Dynamic PET data were acquired in list-mode for 60 min after ^{11}C -GMO injection (24–44 MBq/kg). List-mode emission data were rebinned into a 24-frame dynamic sequence (12 \times 10, 2 \times 30, 2 \times 60, 2 \times 150, 2 \times 300, and 4 \times 600 s). Rebinning emission data were corrected for attenuation and scatter, and transaxial images were reconstructed using maximum a posteriori reconstruction (15), an iterative method that accounts for the detector point spread function in the model of the system.

Radiometabolite Analyses

Before imaging, a blood sample (1.5–2.0 mL) was drawn, and 3.7 MBq of ^{11}C -GMO were added. This was incubated at 37°C for 60–70 min to determine tracer stability in blood. During the PET scan, 4 venous blood samples (1.5–2.0 mL) were drawn at 5, 15, 30, and 55 min to assess radiometabolites in plasma and partitioning of

^{11}C -GMO between plasma and red blood cells (RBCs). Blood samples were centrifuged for 1 min at 12,000g to separate plasma and RBCs. Plasma was deproteinized by adding perchloric acid (HClO_4 ; final concentration, 0.4N) and centrifuging for 5 min at 12,000g. The supernatant was neutralized with KOH (pH 7.0–7.5), filtered twice (0.22- μm filters; Millipore Millex/GS), and analyzed by high-performance liquid chromatography (HPLC) (10 μ Hydro-RP column [Synergi]; 4.6 \times 250 mm, 60 mM sodium phosphate buffer, pH 5.4, with 3% ethanol; flow rate, 1.0 mL/min) and radiation detection (905-4 NaI (TI) detector; Ortec). The sample spiked with ^{11}C -GMO was processed in the same way. Aliquots (0.1 mL) of whole blood, plasma, final supernatant, and pellets were counted in a γ -counter. Count data (decay-corrected) were used to determine the relative concentrations of ^{11}C -GMO in plasma and whole blood (C_p/C_{wb}). HPLC and radiation detection data (decay-corrected) were processed for peak analysis (ACD/ChromProcessor, version 10; ACD Inc.) to determine the percentage of activity associated with intact ^{11}C -GMO (f_{intact}). A mathematic function describing the time course of the metabolic breakdown of ^{11}C -GMO in plasma, $f_{\text{intact}}(t)$, was obtained by nonlinear regression analysis (Prism 3.0; GraphPad Software).

Tracer Kinetic Analyses

Summed images of the final 4 PET frames were used to draw regions of interest on the myocardial wall and on the blood pool in the basal left ventricular chamber to extract time–activity curves for myocardial tissue $C_t(t)$ and whole blood $C_{wb}(t)$. The plasma concentration of intact ^{11}C -GMO versus time, $C_p(t)$, was estimated by multiplying $C_{wb}(t)$ by the metabolic breakdown function, $f_{\text{intact}}(t)$, and the mean ratio of activity concentrations in plasma and whole blood, C_p/C_{wb} . Thus, $C_p(t) = C_{wb}(t) \cdot f_{\text{intact}}(t) \cdot [C_p/C_{wb}]$. The plasma time–activity curve, $C_p(t)$, was used with the tissue time–activity curve, $C_t(t)$, for compartmental modeling. Nonlinear regression analysis with the simplified compartmental model (Fig. 1B) provided estimates of the rate constants K_1 (mL/min/g), k_2 (min^{-1}), k_3 (min^{-1}), and a blood volume fraction, BV (dimensionless), using in-house analysis software. Rate constant estimates were used to calculate a net uptake rate constant K_i (mL/min/g) = $(K_1 k_3)/(k_2 + k_3)$, which reflects the rate of ^{11}C -GMO accumulation into nerve terminals. Tissue and plasma kinetics of ^{11}C -GMO were also analyzed using Patlak graphical analysis (7). After construction of a Patlak plot, the last 9 points of the plot were analyzed with linear regression to determine the Patlak slope, K_p (mL/min/g). Under ideal conditions, the Patlak slope, K_p , is a direct measure of the net uptake rate constant, K_i , and thus for the model structure shown in Figure 1B is also equal to $(K_1 k_3)/(k_2 + k_3)$.

Control and Pharmacologic Blocking Studies

In addition to control conditions ($n = 4$), NET blocking studies were performed with the NET inhibitor desipramine. The goal of these studies was to assess the ability of the quantitative parameters from kinetic analyses to track progressively lower cardiac NET densities induced pharmacologically by increasing desipramine doses. All studies were performed in the same monkey to minimize biologic variation between studies and to make initial assessments of the reproducibility of quantitative measures of NET density. The desipramine dose (dissolved into 2.0 mL of sterile saline) was infused intravenously over 20 min using an infusion pump. ^{11}C -GMO was injected 10 min after the end of the desipramine infusion. Desipramine doses used were 0.010 mg/kg ($n = 2$), 0.0316 mg/kg ($n = 2$), 0.10 mg/kg ($n = 2$), 0.316 mg/kg ($n = 1$), and 1.0 mg/kg ($n = 1$). The measured kinetic parameters K_i from compartmental modeling and K_p values from Patlak analysis, as a function of desipramine dose, were fit to a sigmoidal dose–response model with variable slope using nonlinear regression (Prism 3.0; GraphPad Software).

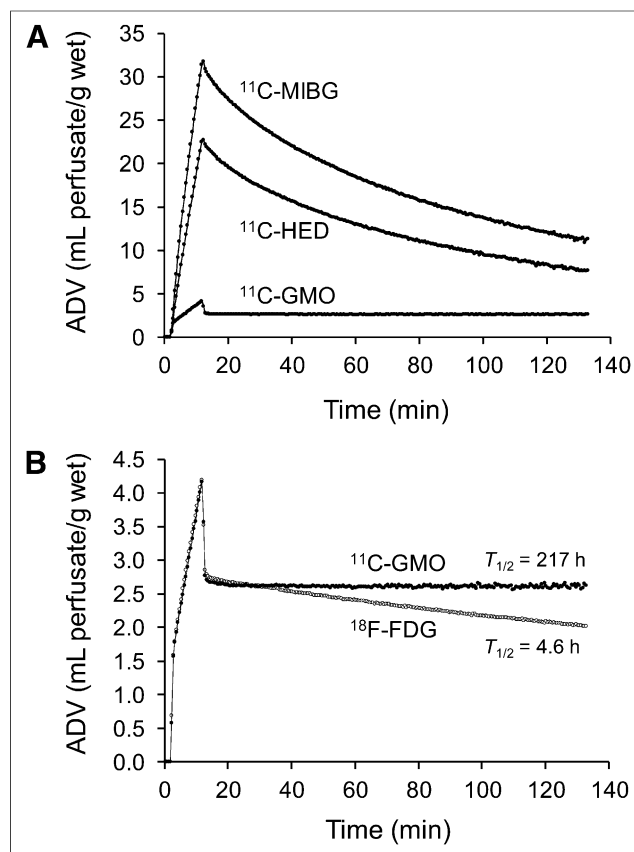


FIGURE 3. (A) Kinetics of ^{11}C -MIBG, ^{11}C -HED, and ^{11}C -GMO in isolated working rat hearts. In each case, 10-min constant infusion of tracer was performed to measure neuronal uptake rates (K_{up} ; mL/min/g wet), then heart switched to normal heart perfusate to study efflux rates from neuronal spaces. (B) For comparison, isolated rat heart kinetics of ^{11}C -GMO are shown along with those of ^{18}F -FDG. Note different y-axis scales used in A and B.

RESULTS

Isolated Rat Heart Studies

The neuronal uptake and retention kinetics of ^{11}C -GMO in the isolated rat heart are shown in Figure 3A, in comparison to those of ^{11}C -MIBG and ^{11}C -HED. ^{11}C -GMO possesses a much slower neuronal uptake rate (K_{up}) than the other 2 tracers (Table 1), about 8 times slower than ^{11}C -HED and 12 times slower than ^{11}C -MIBG. ^{11}C -GMO also has a much longer neuronal retention time than ^{11}C -MIBG and ^{11}C -HED (Table 1). A slower neuronal uptake rate and a long retention time are the 2 kinetic properties we hypothesized a nerve tracer would require for its kinetics to be analyzed successfully with tracer kinetic techniques. It is also in-

TABLE 1
Uptake Rates and Major Clearance Half-Times in Isolated Rat Hearts, as Shown in Figure 3

Tracer	K_{up} (mL/min/g)	Major clearance half-time (h)
^{11}C -MIBG	3.65	2.1
^{11}C -HED	2.35	1.1
^{11}C -GMO	0.30	217
^{18}F -FDG	0.31	4.6

interesting to compare the kinetics of ^{11}C -GMO with those of the well-established cardiac tracer ^{18}F -FDG (10 mM glucose, no insulin) in this model (Fig. 3B). The uptake kinetics of the 2 tracers are almost identical, whereas ^{18}F -FDG clears from the myocardium with a major half-time of 4.6 h, compared with a neuronal clearance half-time of more than 200 h for ^{11}C -GMO (Table 1). Because coronary flow rates are more than 10 times physiologic levels in this system, tracers diffusing from tissue spaces tend to be cleared from the isolated heart at faster rates than would be seen in vivo. Thus, storage of ^{11}C -GMO inside vesicles is an effective trapping mechanism leading to extremely long neuronal retention times.

^{11}C -GMO Metabolism

[Fig. 4] In monkey studies, ^{11}C -GMO was metabolized into 1 major and 2 minor metabolites, all of which were more polar than the parent compound (Fig. 4A). The half-time for the metabolic breakdown of ^{11}C -GMO averaged 16.0 ± 3.0 min (range, 11.0–22.5 min). In most cases, the fraction of plasma activity associated with intact ^{11}C -GMO versus time was fit to the following function (Fig. 4B):

$$f_{\text{intact}}(t) = \text{span} \times \left(\frac{B^n}{t^n + B^n} \right) + \text{plateau}. \quad \text{Eq. 1}$$

For the study using a desipramine dose of 1.0 mg/kg, it was necessary to use an alternative function:

$$f_{\text{intact}}(t) = \text{span} \times \left(\frac{Ue^{-At} - Ae^{-Ut}}{U - A} \right) + \text{plateau}. \quad \text{Eq. 2}$$

The fitted curve for $f_{\text{intact}}(t)$ was used in preparing the input function, $C_p(t)$, for kinetic analyses. HPLC analyses of blood samples spiked with ^{11}C -GMO showed only the parent compound, indicating that it is stable in blood and plasma. Similar to ^{123}I -MIBG and ^{11}C -HED, ^{11}C -GMO is metabolically stable inside neurons. The guanidine group in the side chain of ^{11}C -GMO prevents metabolism by neuronal enzymes such as monoamine oxidase, although some phenethylguanidines are reversible monoamine oxidase inhibitors (16). ^{11}C -GMO lacks the catechol structure of catecholamines such as norepinephrine, so it is not metabolized by catechol-*O*-methyl-transferase.

^{11}C -GMO Partitioning in Blood

Analysis of ^{11}C -GMO concentrations in whole blood, plasma, and RBCs demonstrated that ^{11}C -GMO stays primarily in plasma, with little uptake into RBCs. The ratio of plasma and whole-blood activity concentrations, $C_p(t)/C_{\text{wb}}(t)$, tended to be constant throughout the PET study. For all of the blood samples drawn during PET scanning, the average ratio was 1.47 ± 0.08 . Similarly, for all spiked blood samples, the mean ratio was 1.41 ± 0.07 . Desipramine block of cardiac NET had no effect on the blood partitioning of ^{11}C -GMO. Blood partitioning data for each study was used in the preparation of input functions for kinetic analyses.

Effects of Desipramine Infusion and ^{11}C -GMO Injection

Body temperature and SpO_2 levels were stable during all studies. For desipramine levels at 0.10 mg/kg and below, desipramine infusion caused no change in heart rate. However, for desipramine doses of 0.316 and 1.0 mg/kg, starting 3 min into the de-

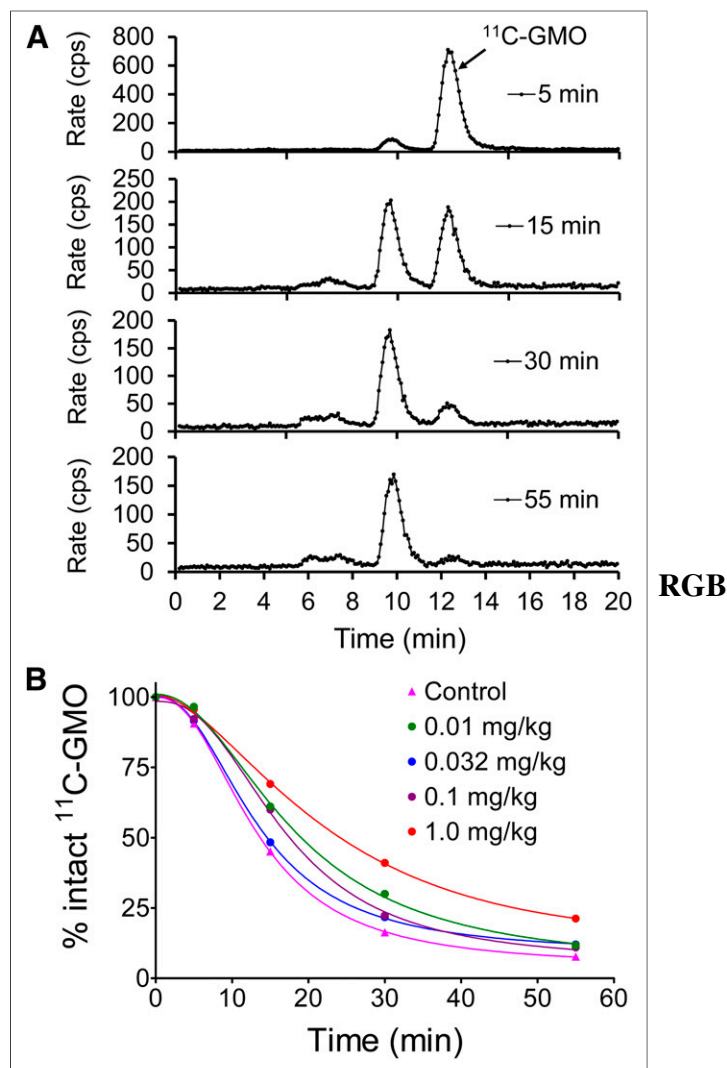


FIGURE 4. (A) Reversed-phase HPLC and radiodetection analysis of radiometabolite formation in plasma. (B) Fraction of activity associated with intact ^{11}C -GMO was determined for each sample, and percentage intact vs. time data fit to mathematic function to characterize metabolic breakdown of ^{11}C -GMO.

desipramine infusion, heart rate steadily rose from a baseline of around 100 bpm up to 122–125 bpm at 1 min after desipramine infusion. Heart rate then slowly declined 4–8 bpm over the next 60 min. Intravenous injection of ^{11}C -GMO had no effect on heart rate, with only a transient increase of 1–2 bpm for 1 min observed during the desipramine study using a dose of 0.316 mg/kg.

Imaging Properties

Representative transaxial PET images from a control study and progressively higher desipramine block studies are shown in Figure 5. The images clearly show a desipramine dose-dependent decline in the cardiac retention of ^{11}C -GMO. In controls, heart-to-blood ratios of 3.01 ± 0.18 and heart-to-liver ratios of 0.89 ± 0.24 were seen in the final image ($n = 4$). If the relatively high liver uptake of ^{11}C -GMO also occurs in human subjects, this could be a minor drawback because the liver is often close to inferior or inferoseptal segments of the left ventricle, leading to some spillover of counts from liver into these segments.

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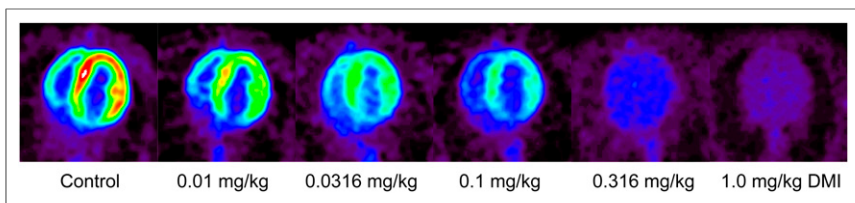


FIGURE 5. Representative transaxial small-animal PET images of cardiac ^{11}C -GMO retention. Shown are summed images (final 4 dynamic frames) for control study (far left) and for blocking studies with progressively higher doses of NET inhibitor desipramine.

Kinetic Analysis: Compartmental Modeling

Compartmental modeling of ^{11}C -GMO kinetics proved to be robust in the sense that the nonlinear regression algorithm converged in a few iterations to a single global minimum. Myocardial time–activity curves and corresponding compartmental model fits for a control study and 3 of the desipramine blocking doses are presented in Figures 6A–6D. Model parameter estimates for all studies are given in Table 2. Parameter estimates were fairly consistent within groups, but values of k_3 , which ideally should reflect cardiac NET density, did not decrease with increasing desipramine doses. However, the net uptake rate constant K_i calculated from the combination of estimated rate constants ($K_1 k_3$)/($k_2 + k_3$) did provide a quantitative measure that sensitively tracked reductions in available cardiac NET in a desipramine dose–dependent manner (Table 2; Fig. 6E). Declines in K_i values (Y) versus increasing desipramine doses were well described by a sigmoidal dose–response model with variable Hill slope (n_H), where $X = \log$ [desipramine dose]:

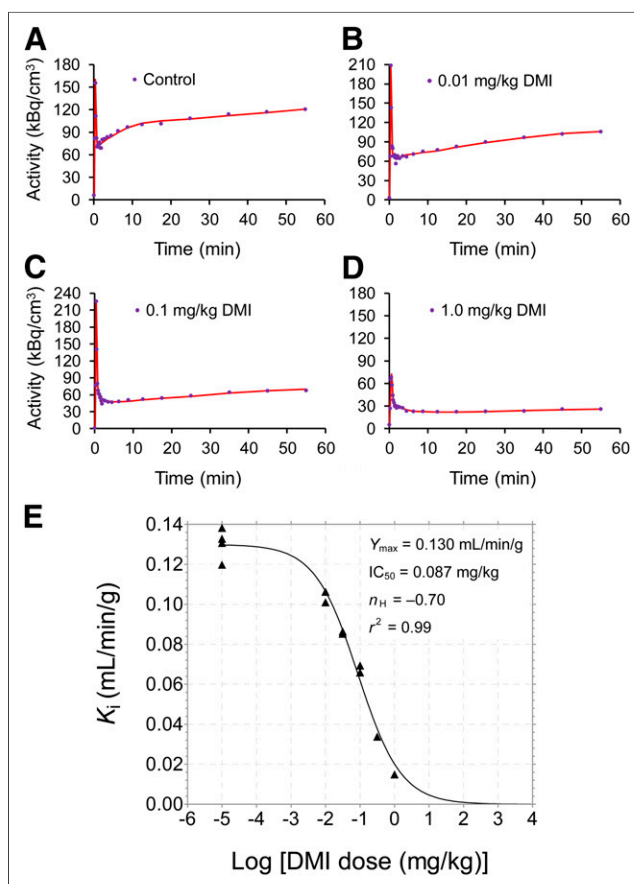
$$Y = \frac{Y_{\max}}{1 + 10^{|\log(\text{IC}_{50}) - X| \times n_H}} \quad \text{Eq. 3}$$

For the K_i data, nonlinear regression analysis yielded parameter estimates of $\text{IC}_{50} = 0.087 \pm 0.012$ mg/kg desipramine, Hill slope $n_H = -0.70 \pm 0.07$, and a maximum net uptake rate constant $Y_{\max} = 0.130 \pm 0.003$ mL/min/g ($r^2 = 0.99$). Because the Hill slope is less than -1.0 , this indicates that the dose–response curve is more shallow than the standard 1-site competition dose–response curve used frequently for in vitro competitive displacement assays. The observation that estimates of the individual model parameters K_1 , k_2 , k_3 , and BV were variable and that k_3 estimates alone did not serve as the index of NET density was not unexpected, because a similar situation exists for analyses of ^{18}F -FDG kinetics in assessments of cardiac glucose utilization (17).

Kinetic Analysis: Patlak Graphical Analysis

Patlak analysis of ^{11}C -GMO kinetics provided highly linear Patlak plots under all experimental conditions, with linear correlation coefficients $r > 0.99$ in all cases (Fig. 7A). Measured Patlak slopes K_p (mL/min/g) are shown in Table 2. Similar to the K_i values from compartmental modeling, the measured Patlak slopes K_p declined along a sigmoidal dose–response curve (Fig. 7B) with increasing doses of desipramine: $\text{IC}_{50} = 0.068 \pm 0.010$ mg/kg desipramine, Hill slope $n_H = -0.54 \pm 0.05$, and a maximum Patlak slope $Y_{\max} = 0.104 \pm 0.002$ mL/min/g ($r^2 = 0.99$). There was a strong linear correlation between the measured Patlak slopes and the calculated K_i values from compartmental modeling: $K_p = (0.757)K_i + 0.001$, with linear correlation coefficient $r = 0.99$ (data not shown).

[Fig. 6]
[Table 2]



RGB

FIGURE 6. Compartmental modeling of ^{11}C -GMO kinetics using simplified model shown in Figure 1B. Myocardial ^{11}C -GMO kinetics (blue dots) and corresponding compartmental model fits (red lines) are shown for control study (A) and 3 different desipramine blocking doses (B–D). (E) Relationship between net uptake rate constants K_i (mL/min/g) calculated from compartmental model parameter estimates and \log [desipramine dose (mg/kg)]. Decline in K_i values was well described by sigmoidal dose–response curve with variable Hill slope (n_H). Estimated parameter values for dose–response curve fit are shown.

DISCUSSION

This study was designed to test whether quantitative measurements derived from analyses of myocardial ^{11}C -GMO kinetics are capable of sensitively tracking cardiac sympathetic nerve densities over the full dynamic range seen in normal subjects and in patients with heart disease. The experimental approach used was to pharmacologically induce varying degrees of cardiac NET inhibition using the NET inhibitor desipramine. Our findings demonstrated that 2 measures of the net uptake rate constant K_i —obtained either by calculation from compartmental modeling results or as the Patlak slope K_p from Patlak graphical analysis—each appear to serve as robust and reproducible measures of regional cardiac sympathetic nerve density. To the best of our knowledge, ^{11}C -GMO is the first sympathetic nerve radiotracer to possess myocardial kinetics that can

track reductions in available cardiac NET in a desipramine dose–dependent manner (Table 2; Fig. 6E). Declines in K_i values (Y) versus increasing desipramine doses were well described by a sigmoidal dose–response model with variable Hill slope (n_H), where $X = \log$ [desipramine dose]:

TABLE 2
Results from Compartmental Modeling and Patlak Analysis of ¹¹C-GMO Kinetics

Study	Compartmental modeling				Patlak analysis, K_p (mL/min/g)	
	K_1 (mL/min/g)	k_2 (min ⁻¹)	k_3 (min ⁻¹)	BV		
Control						
A	0.392	0.145	0.074	0.322	0.133	0.104
B	0.345	0.123	0.082	0.283	0.138	0.111
C	0.306	0.082	0.061	0.278	0.131	0.102
D	0.282	0.117	0.087	0.252	0.120	0.099
Desipramine dose						
0.01 mg/kg						
A	0.245	0.129	0.099	0.343	0.106	0.077
B	0.259	0.138	0.089	0.356	0.101	0.073
0.0316 mg/kg						
A	0.271	0.255	0.114	0.361	0.084	0.062
B	0.256	0.188	0.094	0.326	0.085	0.064
0.1 mg/kg						
A	0.417	0.794	0.149	0.411	0.066	0.047
B	0.217	0.240	0.113	0.370	0.069	0.051
0.316 mg/kg						
A	0.662	2.228	0.120	0.215	0.034	0.030
1.0 mg/kg						
A	0.102	0.435	0.074	0.592	0.015	0.017

Net uptake rate constants K_i were calculated from estimated parameter values as $(K_1 k_3)/(k_2 + k_3)$.

be analyzed in a straightforward and robust manner using conventional kinetic analysis methods.

Isolated rat heart studies demonstrated that NET transports ¹¹C-GMO at a rate about 8 times slower than ¹¹C-HED (Fig. 3A). Similarly, NET transport assays using a rat C6 glioma cell line stably transfected with the cloned human NET (C6-hNET cells) showed that ¹¹C-GMO was transported at a rate about 9 times slower than ¹¹C-HED (18). We believe that this large reduction in the NET transport rate reduces the rate constant k_3 in the compartmental model to a magnitude that is less than k_2 (Fig. 1B). When $k_3 < k_2$, the tracer's net tissue uptake is not confounded by flow-limitation effects. As shown in Table 2, for all studies performed, k_3 was estimated to be less than k_2 , which is consistent with the hypothesis that the net neuronal uptake of ¹¹C-GMO is not flow-limited. Thus we believe that the quantitative parameters K_i and K_p are likely to be sensitive measures of regional cardiac nerve density, capable of detecting mild-to-moderate nerve losses earlier in the progression of denervation than is currently possible with flow-limited tracers such as ¹¹C-HED or ¹²³I-MIBG. The dose-response curves shown in Figures 6E and 7B support this contention. Desipramine-induced declines in both K_i and K_p were well described by a sigmoidal dose-response model, with $r^2 > 0.99$ in each case. This means that more than 99% of the total variance in the net influx constants (K_i , K_p) is explained by variation in the desipramine dose (as modeled by the dose-response function), demonstrating the high sensitivity of these measures.

Not surprisingly, there was a high correlation between K_i and K_p , which are essentially 2 measures of the same aggregate combination of the model rate constants, $(K_1 k_3)/(k_2 + k_3)$. In most cases, Patlak slopes K_p were a little lower than their corresponding K_i values. For Patlak analysis, we did not make any corrections to the tissue kinetics for the presence of radioactivity in blood vessels or for spillover effects between blood pool and myocardium. This resulted in a modest downward bias in the

Patlak slopes. The compartmental model's BV parameter corrects for blood-borne radioactivity in tissue and for spillover effects (19). Although K_p was lower than K_i for most studies, for the highest desipramine concentration (1.0 mg/kg), K_p was higher than K_i (0.17 mL/min/g vs. 0.15 mL/min/g, respectively; Table 2). In this study, tissue activity levels were actually lower than blood activity levels late in the study, leading to a higher than average BV estimate, reflecting net spillover from blood into tissue. It appears that the compartmental modeling approach appropriately accounts for blood volume and spillover effects, and thus the calculated K_i constant should be more accurate than the Patlak slopes. That said, both measures are seen to provide an excellent index of NET transport rate.

We postulated that the main factor causing quantitative analyses of a tracer such as ¹¹C-HED to fail was its rapid NET transport rate, resulting in flow-limited uptake. The present results demonstrate that the slower NET transport rate of ¹¹C-GMO, combined with its efficient trapping in storage vesicles, leads to myocardial kinetics that can be analyzed successfully. However, it is possible that another factor may contribute to successful analysis of ¹¹C-GMO kinetics—the tendency of the tracer to stay in plasma throughout the study, with little trapping in RBCs, allowing intact ¹¹C-GMO molecules in plasma to accumulate slowly into nerve terminals during the entire PET study. ¹¹C-HED on the other hand tends to equilibrate with RBCs, reaching a C_p/C_{wb} ratio of 1.0 several minutes after tracer injection (20). If ¹¹C-HED molecules associated with RBCs are unavailable for extraction into tissue, preventing further accumulation into neurons, this may explain in part why cardiac ¹¹C-HED levels do not climb significantly after the rapid cardiac uptake seen early in a PET study (21). The uptake of ¹¹C-HED into RBCs may simply be due to passive diffusion, because it is more lipophilic than ¹¹C-GMO. However, the biogenic amines dopamine, norepinephrine, and epinephrine are all actively transported into RBCs (22), so it is possible that this mechanism is also involved.

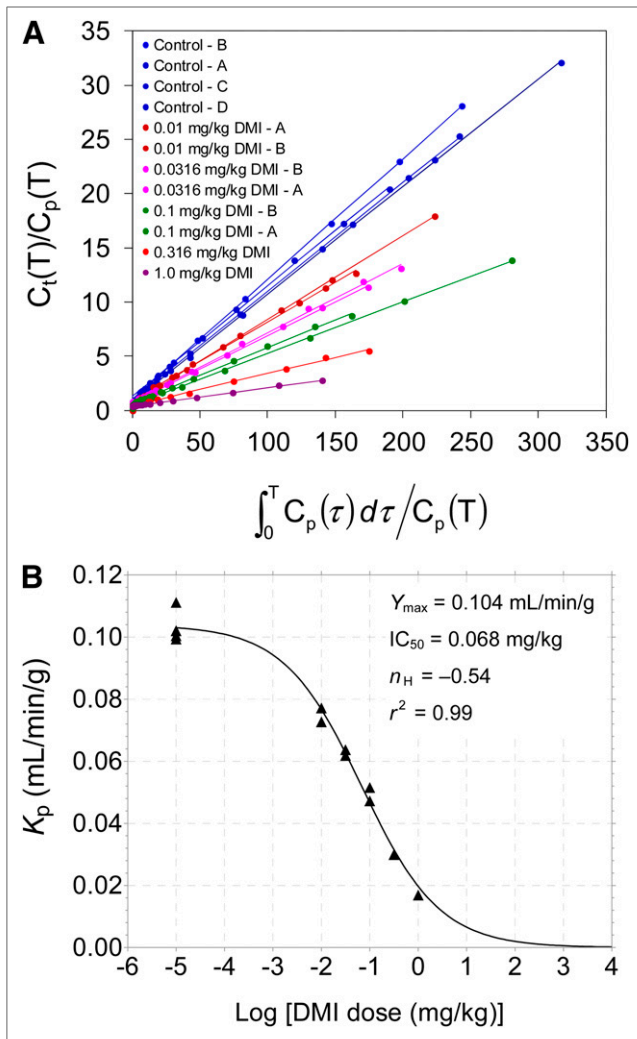


FIGURE 7. (A) Patlak plots of ^{11}C -GMO kinetics for all studies. Legend values are listed in order of highest Patlak slope to lowest, corresponding to values given in Table 2. (B) Relationship between Patlak slopes K_p (mL/min/g) and \log [desipramine dose (mg/kg)]. Reductions in measured K_p values vs. desipramine dose were again well described by sigmoidal dose-response curve with variable Hill slope (n_H). Estimated parameter values for dose-response curve are shown.

Measurement of Regional Norepinephrine Uptake Rates

In cardiac PET studies of glucose metabolism with ^{18}F -FDG, it has been shown that regional metabolic rates of glucose utilization $r\text{MR}_{\text{glu}}$ ($\mu\text{mol}/\text{min}/\text{g}$) can be calculated from net uptake rate constants K_i (or measured Patlak slopes K_p) (23). For such calculations, it is necessary to know the value of the lumped constant (LC) in the heart (the correction factor that relates the observed ^{18}F -FDG kinetics to those of glucose) and the subject's plasma glucose concentration C_{glu} ($\mu\text{mol}/\text{mL}$). Then $r\text{MR}_{\text{glu}}$ can be calculated as:

$$r\text{MR}_{\text{glu}} (\mu\text{mol}/\text{min}/\text{g}) = K_i (\text{mL}/\text{min}/\text{g}) \times \frac{C_{\text{glu}} (\mu\text{mol}/\text{mL})}{\text{LC}} \quad \text{Eq. 4}$$

In a similar fashion, it may be possible to use regional K_i values from compartmental modeling of ^{11}C -GMO kinetics (or Patlak

slopes K_p) to noninvasively estimate regional norepinephrine (NE) uptake rates ($r\text{UR}_{\text{NE}}$) in the heart, in units of pmol NE/min/g. This would require knowledge of the relative NET transport rates of norepinephrine and ^{11}C -GMO, here termed a relative transport constant $\text{TC} = \text{UR}_{\text{GMO}}/\text{UR}_{\text{NE}}$. In addition, the plasma concentration of norepinephrine C_{NE} (pmol NE/mL) would need to be measured for the subject. Then $r\text{UR}_{\text{NE}}$ could be calculated as:

$$r\text{UR}_{\text{NE}} (\text{pmol NE}/\text{min}/\text{g}) = K_i (\text{mL}/\text{min}/\text{g}) \times \frac{C_{\text{NE}} (\text{pmol NE}/\text{mL})}{\text{TC}} \quad \text{Eq. 5}$$

As a starting point, TC can be approximated from isolated rat heart kinetics. In this system, ^{11}C -GMO has a NET-mediated uptake rate constant K_{up} equal to 0.30 mL/min/g (8), whereas the value for ^3H -norepinephrine is 4.44 mL/min/g (24), so that $\text{TC} = 0.30/4.44 = 0.068$. Plasma norepinephrine levels C_{NE} for female rhesus macaques held in captivity have been reported to be approximately 1.2 pmol/mL (25). Using $K_i = 0.130$ mL/min/g for ^{11}C -GMO, we can estimate $r\text{UR}_{\text{NE}}$ in the rhesus macaque heart as:

$$r\text{UR}_{\text{NE}} (\text{pmol NE}/\text{min}/\text{g}) = (0.130 \text{ mL}/\text{min}/\text{g}) \times \frac{(1.2 \text{ pmol}/\text{mL})}{0.068} = 2.3 \text{ pmol}/\text{min}/\text{g}$$

Values for comparison are difficult to find, but Eisenhofer et al. estimated a whole-heart $\text{UR}_{\text{NE}} = 819$ pmol/min in the human heart using ^3H -norepinephrine spillover techniques (26). Taking a nominal mass of 300 g for a normal adult human heart, an estimated regional $r\text{UR}_{\text{NE}}$ value would be $(819 \text{ pmol}/\text{min})/(300 \text{ g}) = 2.7 \text{ pmol}/\text{min}/\text{g}$. These 2 estimates of $r\text{UR}_{\text{NE}}$ agree well enough to suggest that this approach may provide a noninvasive method of measuring regional norepinephrine uptake rates in human subjects. Further work is needed to validate this approach. Although such measurements might not find routine clinical use, they may find application in clinical studies of the effects of diseases on regional norepinephrine reuptake rates or on the efficacies of drug therapies designed to improve or otherwise modulate norepinephrine reuptake rates.

CONCLUSION

^{11}C -GMO appears to be the first cardiac sympathetic nerve tracer possessing kinetics that can be analyzed in a straightforward manner to provide robust and sensitive quantitative measures of regional cardiac sympathetic nerve density. These quantitative measures will likely be able to detect mild-to-moderate sympathetic nerve losses that occur early in the course of cardiac denervation, which is not possible with existing tracers such as ^{11}C -HED and ^{123}I -MIBG. In addition, ^{11}C -GMO may find application in monitoring the efficacy of novel drug therapies designed to halt or reverse cardiac denervation in diseases associated with enhanced risk of sudden cardiac death, such as diabetic autonomic neuropathy and heart failure. Finally, it may be possible to non-invasively quantify regional norepinephrine reuptake rates through extension of the methodology currently used for measuring glucose metabolic rates from parameters measured from ^{18}F -FDG kinetics.

DISCLOSURE

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