Ligand Binding to Cytochrome P450 3A4 in Phospholipid Bilayer Nanodiscs

THE EFFECT OF MODEL MEMBRANES

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The membrane-bound protein cytochrome P450 3A4 (CYP3A4) is a major drug-metabolizing enzyme. Most studies of ligand binding by CYP3A4 are currently carried out in solution, in the absence of a model membrane. Therefore, there is little information concerning the membrane effects on CYP3A4 ligand binding behavior. Phospholipid bilayer Nanodiscs are a novel model membrane system derived from high density lipoprotein particles, whose stability, monodispersity, and consistency are ensured by their self-assembly. We explore the energetics of four ligands (6-([3-cholamidopropyl]-dimethylammonio)-1-propanesulfonate; ANF, miconazole, and bromocriptine) binding to CYP3A4 incorporated into Nanodiscs. Ligand binding to Nanodiscs was monitored by a combination of environment-sensitive ligand fluorescence and ligand-in-membrane effects on ligand binding and turnover by cytochrome P450s have generally involved measuring binding $K_D$ values and turnover $K_m$ values for protein incorporated into liposomes, over a
range of lipid concentrations. Extrapolation to a lipid-free system provides qualitative information as to how the membrane affects the apparent affinity of a membrane protein for a substrate. Of particular interest is the analysis by Kühn-Velten (5) on progesterone binding to CYP17 in liposomes using a combination of absorbance spectroscopy, ultracentrifugation, and equilibrium dialysis to measure the concentration of ligand bound to protein, bound to the membrane, and free in solution. The apparent $K_D$ value was some 3 orders of magnitude lower than the true $K_D$ value corrected for the free progesterone concentration.

It should be noted that the lipid mixtures widely used in CYP3A4 turnover studies (7–9) are useful empirical functional tools in terms of solubilizing CYP3A4 and enhancing activity of recombinant CYP3A4 in vitro, but they are not suitable model membranes for investigations of ligand binding. They contain detergents such as cholic acid or CHAPS well below their critical micellar concentrations (10, 11), along with smaller amounts of phospholipids. These mixtures cannot form canonical mixed micelles with the phospholipids (12, 13), but they are unlikely to exist as liposomes because the detergent concentrations are much higher than the phospholipid concentrations (14). The consequent uncertainty about the structure and composition of the lipid phase in reconstituted systems greatly complicates attempts to describe small molecule binding to these systems, making a rigorous analysis of their effect on ligand binding to CYP3A4 intractably complex.

Phospholipid bilayer Nanodiscs (15–26), promising new model membranes, may clarify our understanding of ligand binding to CYP3A4. Nanodiscs resemble nascent discoidal high density lipoprotein particles (see Fig. 1a) and consist of a POPC bilayer about 10 nm in diameter surrounded by two monomers of a 23-kDa membrane scaffold protein (MSP). The protein coat ensures that Nanodiscs are monodisperse, relatively stable, and consistent between preparations; it also allows the determination of the affinity and stoichiometry with which small molecules bind to the Nanodisc membrane. As an additional benefit, incorporation of CYP3A4 into Nanodiscs prevents its oligomerization, which can affect its reduction kinetics (21) and substrate turnover (27).

Here we study the binding of four small molecule ligands (TNS, ANF, miconazole, and bromocriptine; structures in Fig. 1b) to CYP3A4-Nanodiscs, to determine the true affinity of these compounds to CYP3A4 incorporated into a membrane, and to determine how bound ligand partitions between the CYP3A4 active site and a lipid bilayer. TNS is a well characterized fluorescent probe of protein structure that fluoresces in nonpolar environments but is quenched and red-shifted in solution. ANF is a CYP3A4 substrate and effector of testosterone metabolism, which fluoresces in solution and is quenched and blue-shifted in nonpolar environments. Miconazole is an azole drug that is a known inhibitor of CYP3A4. Bromocriptine, an ergot alkaloid used as a dopamine receptor agonist, is also a substrate (28) and potent inhibitor of CYP3A4 (29).

FIGURE 1. a, model of Nanodisc structure, based on a model of discoidal high density lipoprotein particles (52). Two MSP monomers (gray helices) form an amphipathic helical ring around a DPPC bilayer (white surface). Nanodiscs are about 10 nm in diameter and 4 nm thick. b, structures of TNS, ANF, miconazole, and bromocriptine.
MSP and POPC were mixed in a 1:65 molar ratio with 50 mM cholate and incubated on a shaker for 1 h at 4 °C. After incubation with 0.8 g/ml Amberlite XAD-2 for 4 h on ice, nickel column chromatography was used to separate CYP3A4-Nanodiscs (which possess a His tag at the CYP3A4 C terminus) from excess Nanodiscs. The 5-fold excess of Nanodiscs to CYP3A4 ensures that only one monomer of CYP3A4 is incorporated into a given Nanodisc. Size exclusion was used to purify the CYP3A4-Nanodiscs and verify stable and monomeric incorporation. The absolute absorbance spectrum of CYP3A4 did not change significantly upon incorporation into Nanodiscs (data not shown). Unless otherwise stated, the concentration of CYP3A4-Nanodiscs in experiments was 1.4 μM.

**Ligand Binding to Nanodiscs**

**Ligand Binding to Nanodiscs Monitored by Fluorescence Spectroscopy**—An SLM-Aminco AB/2 fluorimeter (SLM-Aminco, Urbana, IL) was used for all experiments, and the concentration of Nanodiscs used for titrations was 1.0 μM unless otherwise stated. Data were corrected for the primary and secondary inner-filter effects by the method of Lakowicz (32) and normalized for the change in volume over the course of a titration.

TNS fluorescence (λ_ex = 320 nm, λ_em = 440 nm) increases upon binding to Nanodiscs. To determine the affinity of the first mode of TNS binding to Nanodiscs, TNS fluorescence was monitored, whereas Nanodiscs were titrated into 0.5 μM TNS (Fig. 3a). Data were fit to the hyperbolic binding equation. The fluorescence of tryptophan residues (λ_ex = 295 nm) in MSP is quenched upon TNS binding, via a Forster resonance energy transfer to TNS. Relative quenching of the MSP Trp fluorescence at 340 nm upon addition of TNS to Nanodiscs was used to monitor binding (Fig. 3b). (There are two Trp residues in each MSP monomer, and we assume that they are quenched equally upon ligand binding.) Data were fit to kinetic simulations (see below) of a three-site sequential binding model.

ANF fluorescence is quenched upon binding to Nanodiscs. 0.5 μM ANF was mixed with varying concentrations of Nanodiscs between 0 and 12.5 μM and excited at 320 nm. The relative quenching of ANF emission between 400 and 500 nm (Fig. 4a) was fit to the quadratic binding equation, because the apparent KD value was close to the concentration of ANF. ANF binding also quenches MSP Trp fluorescence; ANF was titrated into 0.5 μM Nanodiscs, and the resulting quenching of Trp fluorescence at 340 nm (Fig. 4b) was fit to the multisite quadratic binding to determine the stoichiometry of ANF binding to Nanodiscs.

The affinity of miconazole for Nanodiscs was measured using a competitive binding assay with ANF. 1.0 μM Nanodiscs were mixed with 20 μM ANF and excited at 320 nm. The recovery of ANF fluorescence at 440 nm was monitored as aliquots of miconazole were added (Fig. 5a). Data were fit to the hyperbolic binding equation.

Bromocriptine also quenches MSP Trp fluorescence upon binding to Nanodiscs. Bromocriptine was separately titrated into 0.83, 1.7, and 3.3 μM Nanodiscs, and the three binding curves (Fig. 6a) were globally fit to kinetic simulations of a five-site sequential binding model.

**Ligand Binding to CYP3A4**—Ligand binding was monitored by absolute absorbance spectroscopy of the heme Soret band.
Data were collected on a Cary 3E spectrophotometer (Varian, Cary, NC). Unless otherwise stated, the sample cuvette contained 1.4 μM total CYP3A4-Nanodiscs, whereas the reference cuvette contained an equal concentration of Nanodiscs. Equal aliquots of ligand were added to both cuvettes, and absorbance was recorded from 350 to 600 nm. Absolute absorbance spectroscopy minimizes interference from any ligand absorbance that overlaps with the heme. This is especially useful for ligands that display environment-sensitive absorbance, such as ANF and TNS.

All of the absorbance scans from a titration were smoothed over a 4 nm window, baseline-corrected, corrected for the effect of solvent, and normalized for the change in volume. Difference spectra were calculated by subtracting the absorbance signal for CYP3A4 alone from each scan in the titration, and the peak-to-trough ΔA was plotted against ligand concentration.

Data analysis was performed using scripts written in the Python programming language, and curve fitting was performed using Gepasi (33) for kinetic simulations and gnuplot for analytical equations. When fitting to kinetic simulations, Gepasi was used to model the relevant binding scheme. All bimolecular on-rates were set to 1 μM⁻¹ s⁻¹, and suitable selected off-rates and scaling factors were varied so as to minimize the χ² between steady-state metabolite concentrations and experimental data, using Levenberg-Marquadt, evolutionary programming, and Nelder and Mead fitting algorithms. Because the data are from equilibrium binding experiments, the time scales and the absolute values of rate constants in these simulations are arbitrary. Equilibrium binding constants for any given step are given by the ratios of relevant rate constants. This procedure obviates the need to derive analytical binding equations for complex binding schemes, making it especially useful when the free ligand approximation is inapplicable because of high affinity binding to CYP3A4 or to Nanodiscs.

RESULTS

The affinity of an amphiphile binding to a lipid bilayer is traditionally described by a membrane/solvent partition coefficient $K_p$, but equilibrium association ($K_A$) or dissociation constants ($K_D$) can be used instead when the molar volume ($V_{memb}$, with units of concentration⁻¹) of the model membrane can be estimated using the equations $K_p = K_A / V_{memb} = 1 / (V_{memb} K_D)$ (34–38). We describe multiple small molecules binding to the Nanodisc membrane as a series of sequential binding modes, each with an associated $K_D$ value. Scheme 1 presents the framework we use to describe ligand binding to CYP3A4 in Nanodiscs and the competition between binding to the membrane and to CYP3A4. $K_1$ is the dissociation constant of ligand binding to the membrane. $K_1$ is the dissociation constant of ligand binding to CYP3A4 in Nanodiscs. Inset, TNS fluorescence as a function of Nanodisc concentration. $b$, relative quenching of MSP tryptophan fluorescence ($λ_{ex} = 295$ nm, $λ_{em} = 340$ nm) was monitored as a function of TNS concentration. Data were fit to a three-site sequential binding model, with $K_i$ values of 6.1 μM for the second and third binding events. Inset, MSP Trp fluorescence is quenched in response to TNS addition (indicated by arrow). $c$, TNS binding to 1.4 μM CYP3A4-Nanodiscs. The difference between $ΔA$ at 440 nm and 414 nm was plotted against TNS concentration. Data were fit to kinetic simulations of the binding model in Scheme 2, with $K_1$ of 4.0 μM. Inset, the type II calculated difference spectra induced by TNS binding to CYP3A4 in Nanodiscs. A.U., arbitrary units.
Ligand Binding to CYP3A4 in Nanodiscs

The overall membrane partition coefficient $K_P$ can be calculated from these $K_i$ values by using the equation $K_P = 1/(V_{\text{memb}}K_i)$ for each of the three binding modes and summing the resultant individual partition coefficients. Assuming a molar volume for POPC of 1263 Å$^3$ (39) and 130 POPC molecules per Nanodisc, the volume of a Nanodisc is $1.64 \times 10^{-22}$ liters, and therefore the molar volume $V_{\text{memb}}$ is 98.9 liters/mol. Consequently, the overall $K_P$ for TNS is $6.8 \times 10^3$. This closely matches the $K_P$ values for TNS-binding phospholipid vesicles ($\approx 6.5 \times 10^3$) (37, 40, 41), implying that Nanodiscs are suitable model membranes for the study of small molecule binding to lipid bilayers.

binding to the protein, and can be directly compared with $K_D$ measurements made using other model membranes, or in the absence of model membranes, inasmuch as all represent the affinity of drug for the active site under those specific conditions. $K_1 = K_i^*/K_i$ is a unitless equilibrium constant describing the ratio of ligand bound to the membrane and to the protein. In cases where multiple ligands can bind the Nanodisc membrane, a different $K_2$ is defined for each occupancy state of the CYP3A4-Nanodisc complex.

Steady-state fluorescence spectroscopy could not adequately distinguish ligand bound to the Nanodisc bilayer from ligand bound to CYP3A4 for any of the small molecules under consideration. Therefore, the same general strategy was used to obtain models for each of the various ligands binding to CYP3A4 in Nanodiscs. Ligand binding to free Nanodiscs (Fig. 3, a and b, Fig. 4, a and b, Fig. 5a, and Fig. 6a) was used to determine $K_i$. Binding to CYP3A4 in Nanodiscs (Figs. 3c, 4c, 5b, and 6b) was monitored via ligand-induced changes in the absorbance of the heme Soret band. These data were fit to kinetic simulations of suitable binding models, to recover $K_i'$, $K_i^*$, and $K_2$.

**FIGURE 4.** a, ANF binding to Nanodiscs. The integrated fluorescence of 0.5 μM ANF ($\lambda_{ex} = 320$ nm) from 400 to 500 nm was monitored, and relative quenching was plotted against Nanodisc concentration. Data were fit to the quadratic binding equation, with a $K_i$ of 0.81 μM. Inset, ANF fluorescence is quenched as a function of Nanodisc concentration. b, Trp fluorescence quenching ($\lambda_{ex} = 295$ nm, $\lambda_{em} = 340$ nm) of 0.5 μM Nanodiscs was monitored as a function of ANF concentration. Data were fit to the multisite quadratic binding equation to determine that about 14 ANF molecules bind to each Nanodisc. Inset, MSP Trp fluorescence is quenched in response to ANF addition (indicated by arrow). c, ANF binding to 1 μM CYP3A4-Nanodiscs. The difference between $\Delta A$ at 388 and 417 nm was plotted against ANF concentration. Data were fit to kinetic simulations of the binding model in Scheme 3, with $K_i^*$ of 5.8 μM. Inset, type I calculated difference spectra induced by ANF binding to CYP3A4 in Nanodiscs. A.U., arbitrary units.
TNS binding to CYP3A4 in Nanodiscs caused a type II spectral change, with an increase in absorbance at 440 nm and a decrease at 414 nm (Fig. 3c). Data from the optical titration were fit to the model in Scheme 2, incorporating the $K_1$ values obtained from the experiments with Nanodiscs alone. The fit yielded a $K_1'$ value of $4.0 \pm 0.4$ $\mu$M; this is the dissociation constant of TNS binding to the active site of CYP3A4 in Nanodiscs. The equivalent value measured for CYP3A4 in solution is 25.4 $\mu$M (42). This apparent difference in affinity may be due to structural changes in CYP3A4 caused by incorporation into a lipid bilayer. The $K_2$ values calculated from these $K_1$ and $K_1'$ values vary between 1.4 $\pm$ 0.1 (for the singly occupied CYP3A4-Nanodisc complex) and 0.66 $\pm$ 0.07 (for doubly and triply occupied complexes). Values of $K_2$ close to 1 indicate that TNS does not have a strong thermodynamic preference for either the Nanodisc bilayer or the CYP3A4 active site.

ANF—As for TNS, the affinity with which a single molecule of ANF bound to Nanodiscs was determined by titrating Nanodiscs into a fixed concentration of ANF and monitoring the decrease in integrated ANF fluorescence between 400 and 500 nm (Fig. 4a). Fitting the resulting curve to the quadratic binding equation yielded a $K_1$ of 0.81 $\pm$ 0.20 $\mu$M. In the converse titration, ANF binding to Nanodiscs was monitored by Trp fluorescence quenching at 340 nm (Fig. 4b) and fit to the multsite quadratic binding Equation 1,

$$Q = \frac{Q_{max}}{2 + [M]} \times \left( K_1 + n + [M] + [ANF] \right) - \sqrt{(K_1 + n + [M] + [ANF])^2 - 4 \times n + [M] \times [ANF]} \quad (Eq. 1)$$

Here [M] is the Nanodisc concentration, and $n$ is the stoichiometry of ANF binding to Nanodiscs. The recovered value of $n$ was 14.3 $\pm$ 0.6, indicating that about 14 molecules of ANF bind to each Nanodisc. This value was confirmed by kinetic simulations. Assuming 14 molecules of ANF bind to a Nanodisc, each with a $K_1$ of 0.81 $\mu$M, the overall membrane partition coefficient is $1.7 \times 10^5$.

ANF binding to CYP3A4 in Nanodiscs caused a high spin (type I) spectral change, with an increase in absorbance at 388 nm and a decrease at 417 nm (Fig. 4c). Data from this titration were fit to the model in Scheme 3, and the recovered $K_1'$ value was 5.8 $\pm$ 0.4 $\mu$M. ANF binding to CYP3A4 in solution has been studied extensively (43–48) and is thought to be cooperative in nature with at least two distinct ANF-binding sites in each CYP3A4 monomer. This interaction has been described frequently (43, 46, 48) in terms of the Hill equation, with $n$ values around 1.8 and $S_{50}$ values around 5 $\mu$M, but the latter are not $K_D$.

**FIGURE 5.** a, miconazole binding to Nanodiscs. Miconazole was titrated into a mixture of 1 $\mu$M Nanodiscs and 20 $\mu$M ANF, and a recovery of ANF fluorescence ($\lambda_{ex} = 320$ nm, $\lambda_{em} = 440$ nm) was monitored as a function of miconazole concentration. b, miconazole binding to 1.4 $\mu$M CYP3A4-Nanodiscs. The difference between miconazole-induced heme absorbance changes at 438 and 408 nm was plotted against miconazole concentration. c, miconazole binding to 1.4 $\mu$M CYP3A4 in solution. The difference between $\Delta A$ at 430 and 408 nm was plotted against miconazole concentration. Data were fit to the hyperbolic binding equation, with a $K_1$ of 9.0 $\mu$M. Inset, ANF fluorescence increases in response to increased miconazole concentration (indicated by arrow).
values and cannot be directly compared with $K_1$ values. More recently, Roberts and Atkins (47) proposed a two-site model for ANF binding to CYP3A4 as follows: a high affinity (1 M) peripheral site that weakly perturbs the heme, and a lower affinity site close to the heme with a $K_D$ of 55 M. This study cannot prove or disprove the existence or effect of the high affinity peripheral site when CYP3A4 is incorporated into a bilayer, because it has not been possible to resolve ANF bound in the putative peripheral site from ANF bound to the bilayer. Importantly, the results in the nanodiscs should not be taken as evidence against multiple binding of ANF. Rather, the multiple binding observed in other experimental models is likely to be masked by the membrane binding here. As with TNS, the difference between a $K_1$ of 5.8 M and a $K_D$ of 55 M for the active site may reflect differences between CYP3A4 structure or active-site environment in solution and in Nanodiscs. The calculated $K_2$ value was 7.2, indicating that ANF preferentially binds to the Nanodisc bilayer. The free energy difference between binding to the membrane and to the CYP3A4 active site is $RT \ln(K_2)$, 1.2 kcal/mol. Note that the free energy values reported in this study refer specifically to the CYP3A4-Nanodisc system described here, and because they are ultimately calculated using $K_1$ values, they depend on the dimensions of the Nanodiscs used. Therefore, they are not strictly equivalent to free energy values for an idealized “infinite” lipid bilayer.

Miconazole—Miconazole displaces ANF from the Nanodisc bilayer, resulting in an increase in ANF fluorescence (Fig. 5a).

Fitting the resulting curve to the hyperbolic binding equation yielded a $K_1$ value of 9.0 ± 0.4 M (and hence a membrane partition coefficient of 1.1 × 10³). Miconazole binding to CYP3A4 in Nanodiscs causes a type II spectral change, with an increase in absorbance at 430 nm and a decrease at 408 nm (Fig. 5b). These data were fit to the model in Scheme 5 and resulted in a $K_1$ value of 0.45 M. (For CYP3A4 in solution, the equivalent $K_D$ is about 0.04 M (Fig. 5c).) The calculated $K_2$ value was...
Ligand Binding to CYP3A4 in Nanodiscs

SCHEME 2. Model of TNS binding to CYP3A4 in Nanodiscs. L (hexagon) represents TNS, ME (prism on white disk) represents the CYP3A4-Nanodisc complex; L·ME represents a single TNS molecule bound to the Nanodisc bilayer; ME·L represents TNS bound in the CYP3A4 active site; Ln·ME represents n TNS molecules bound to the Nanodisc bilayer, and Ln·ME·L represents one TNS bound in the CYP3A4 active site and n bound to the bilayer. Three TNS molecules bind sequentially to the Nanodisc bilayer, with K

0.05 ± 0.003, indicating that miconazole prefers binding to CYP3A4 active site by a ΔG of −1.8 kcal/mol.

Bromocriptine—Like ANF and TNS, bromocriptine quenches Trp fluorescence upon binding to Nanodiscs. However, bromocriptine’s fluorescence itself is not sufficiently altered upon binding to allow for an accurate observation of the first binding mode, as was performed for ANF and TNS. Therefore, to arrive at a complete picture of bromocriptine binding, the ligand was titrated into three different concentrations of Nanodiscs, and the resulting quenching data (Fig. 6a) were globally fit to a variety of binding models. The best fit was obtained using a model where five molecules of bromocriptine bound to each Nanodisc, each accounting for one-fifth of the total quenching, with two initial high affinity binding modes (each with a K

DISCUSSION

Qualitatively, our results agree well with previous experimental studies of the membrane effect on CYP ligand binding (4–6). The presence of model membranes can significantly alter the apparent affinity with which a ligand binds; the extent of this effect varies depending on the ligand. Kominami et al. (4) reported that whereas the apparent KD values for progesterone and 17α-hydroxyprogesterone binding to CYPs from bovine adrenocortical microsomes vary between about 25 nM and 0.4 µM as the membrane content of the system is increased, the corrected KD values were in the 30-90 µM range (assuming these substrates access CYP active sites via the membrane). The extensive analysis by Kuhn-Velten (5) showing a similar effect on progesterone binding to CYP17 in liposomes has already been mentioned. Margolis and Obach (6) studied membrane effects on the inhibition of bufuralol 1′-hydroxylation by CYP2D6 by four drugs: the more lipophilic the drug, the more the apparent K

of 2.9 µM for the first binding event and 6.1 µM for the second and third binding modes (indicating apparent negative cooperativity). K

values between 0.09 ± 0.009 (for singly and doubly occupied CYP3A4-Nanodisc complexes) and 0.03 ± 0.003 (for higher occupancy states). Thermodynamically, bromocriptine prefers binding to the CYP3A4 active site by a ΔG between −1.4 kcal/mol and −2.1 kcal/mol.
The equilibrium constant $K_2$ is a useful and concise descriptor of this competition for ligand binding between the protein and the membrane; if $K_2 > 1$, the ligand will preferentially bind to the membrane, whereas if $K_2 < 1$, binding to the protein is more favorable. For example, consider Scheme 2, our proposed model for TNS binding to the CYP3A4-Nanodisc complex. The various $K_2$ values describe the equilibrium between TNS bound at the CYP3A4 active site and in the Nanodisc bilayer at different occupancies of the complex as a whole. For the singly occupied complex, a $K_2$ of 1.4, being greater than 1, indicates that TNS slightly favors binding to the bilayer. For the doubly and triply occupied complexes, $K_2$ values indicate that ANF preferentially binds the CYP3A4 active site, with a $\Delta G$ of $-1.8 \text{ kcal/mol}$.

The affinities with which some ligands bind to CYP3A4 in solution differ considerably from the values of $K_1'$, the dissociation constant for binding to the CYP3A4 active site, obtained in this study. For TNS, $K_D$ in solution is 25 $\mu$M, whereas $K_1'$ is 4.0 $\mu$M; for ANF, $K_D$ in solution is 55 $\mu$M, whereas $K_1'$ is 5.8 $\mu$M; for miconazole, $K_D$ is 0.04 $\mu$M, whereas $K_1'$ is 0.45 $\mu$M. These altered affinities may be caused by changes in CYP3A4 structure and/or dynamics or the environment of the active site upon incorporation into the Nanodisc bilayer, and presumably...
better reflect the true in vivo affinities than data from experiments with CYP3A4 in solution. Therefore, extrapolation of in vitro data to predictions of in vivo pharmacokinetics would be better served by using $K_1$ values than by solution $K_D$ values. Ideally, any turnover $K_m$ values for the membrane proteins involved in the metabolism of a drug would also be measured for proteins incorporated into lipid bilayers, while taking drug partitioning into the membrane into account. If experimental considerations make this difficult, prediction accuracy may be improved by scaling $K_m$ by $K_1/K_D$ to reflect how CYP structure and dynamics are affected by incorporation into a membrane.

This work also illustrates the importance of characterizing ligand binding to the model membrane. A titration with protein incorporated into a model membrane does not provide enough information by itself to arrive at an accurate binding model. For example, a simple fit of the sigmoidal binding curve in Fig. 4c to the Hill binding equation results in an $S_{50}$ of 19 μM and an $n$ of 3.3, implying a much more cooperative and lower affinity interaction than we propose. These artificial conclusions would result from a failure to properly analyze the effect of the membrane phase. Understanding ligand binding to the membrane is a necessary prerequisite to obtaining accurate models of binding to a membrane protein. An attempt to fit a more complex binding model (such as one that accounted for ligand binding to the membrane) to the same single binding curve would be grossly overparametrized, and recovered values would not be meaningful. Combining data from Nanodiscs alone with data

**Scheme 5. Model of bromocriptine binding to CYP3A4 in Nanodiscs.** L (hexagon) represents bromocriptine; ME (prism on white disk) represents the CYP3A4-Nanodisc complex; $L_n\cdot ME$ represents n bromocriptine molecules bound to the Nanodisc bilayer, and $L_n\cdot ME\cdot L$ represents one bromocriptine bound in the CYP3A4 active site and n bound to the bilayer. Five bromocriptine molecules bind to the Nanodisc bilayer, with $K_1$ values of 5.2 μM for the first two binding events and 15 μM for the last three events. $K_1$ is 0.45 μM, compared with a solution $K_D$ of 0.18 μM. $K_2$ varies between 0.09 (for singly and doubly occupied complexes) and 0.03 (for higher occupancies), indicating a $\Delta G$ for the CYP3A4 active site between $-1.4$ kcal/mol and $-2.1$ kcal/mol.

**Figure 7. Summary of membrane/CYP3A4 equilibria.** The Gibbs free energy difference between one ligand molecule bound to the Nanodisc membrane and to the CYP3A4 active site is plotted on the ordinate for all four ligands used in this study. The prism represents CYP3A4; the disk represents the Nanodisc, and hexagons represent molecules of ligand. ANF preferentially binds to the membrane, and its $K_2$ is therefore greater than 1. TNS binds with almost equal affinity to either site, and so its $K_2$ is about 1. Miconazole and bromocriptine preferentially bind to CYP3A4, giving them $K_2$ values less than 1.
from CYP3A4-Nanodiscs ensures that none of the fits to data were overparametrized, and in fact no more than two fitting parameters were obtained from any given binding curve.

We recognize that this approach relies on the assumption that the presence of the membrane protein does not significantly alter the thermodynamics of ligand binding to the model membrane. Ideally, $K_2$ would be measured by simultaneously measuring occupancy of the active site and membrane phase of the CYP3A4-Nanodisc complex. Unfortunately, with steady-state fluorescence spectroscopy we have not been able to resolve CYP3A4-bound ligand from membrane-bound ligand for the small molecules in this study. CYP3A4 adds three additional Trp residues to the complex, each of which may respond differently to ligand (TNS, ANF, or bromocriptine) binding: TNS and ANF fluoresce with differing intensities in the membrane and in the CYP active site. These additional variables mean that although steady-state fluorescence titrations with CYP3A4-Nanodiscs are consistent with the models presented here, some uncertainty may be introduced because of CYP-dependent effects on ligand-Nanodisc interactions.

More advanced techniques, such as time-resolved fluorescence, fluorescence anisotropy, or NMR $T_1$ relaxation experiments may allow us to simultaneously measure occupancy of the protein-binding site and the membrane for these or other CYP3A4 ligands. This would provide a more rigorous measurement of model parameters, as well as insight into how incorporated proteins affect amphiphile binding to lipid bilayers. It is difficult to predict what this effect would be a priori, although the presence of an incorporated protein might be expected to decrease the membrane area available for ligand binding (and thereby decrease a ligand’s affinity), the ordering effect (49–51) of a membrane protein on nearby lipids could either promote or hinder ligand binding. Taking these factors into account, the presented strategy is a reasonable compromise that is convenient to apply to a broad range of ligands and provides valuable insight into membrane effects on ligand binding.

The approach presented here improves upon earlier attempts (2, 3) to theoretically describe ligand binding to cytochrome P450s for two reasons. The first is that the monodisperse and consistent size of the lipid phase in Nanodiscs leads to a well-defined lipid volume competing with the CYP3A4 active site for ligand binding, allowing for the determination of specific equilibrium constants ($K_2$) for ligand partitioning between the active site and the membrane. The second is that fitting experimental data to kinetic simulations of binding models (33) removes the need to derive analytical binding equations for each of the various binding models considered. These analytical equations can become intractably complex when the free ligand approximation is not applicable (as when lipid is not present in great excess relative to the protein or when a ligand binds with high affinity to either protein or membrane). Independence from the free ligand approximation means that the binding models presented here do not depend on the route of substrate entry into the CYP3A4 active site, and so are true equilibrium binding models.

This work demonstrates how a well-defined, consistent model membrane such as phospholipid bilayer Nanodiscs can be used to understand the details of ligand binding to a membrane protein. It also illustrates how the presence of a model membrane can alter the apparent ligand binding behavior of incorporated proteins, by competing with them for ligand binding.

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