Ligand competition assays indicate allosterism and insufficiency of the ternary complex model

Eyad Qunaibi\textsuperscript{1}
Roger Barber\textsuperscript{2}

\textsuperscript{1}Formerly (during the time of the study): School of Pharmacy, University of Houston, Houston, TX. At present: School of Pharmacy, Applied Sciences University, Amman, Jordan; \textsuperscript{2}Formerly (during the time of the study): Department of Integrative Biology and Pharmacology, University of Texas/Houston, Houston, TX, USA

\textbf{Background:} Many researchers have tried to correlate characteristics of ligand binding at G-protein–coupled receptor (GPCR) with ligand efficacy. The ternary complex model (TCM) is the traditional model for explaining the equilibrium of agonist-GPCR-G-protein interaction, and the effect of this interaction on agonist efficacy. However, no consistent correlation has been proven for various binding-efficacy data, so several extensions of the model have been proposed. These extensions are of descriptive value but their validity cannot be verified by binding-efficacy correlations. Therefore, we developed a novel approach to validate the TCM and its extensions.

\textbf{Methods:} We simulated the predictions of the TCM for relationships within binding parameters. According to the TCM, an increase in the difference between high and low agonist affinities for a receptor (ie, greater $K_L/K_H$) should be accompanied by stability or an increase in the fraction of receptors bound to the agonist with high affinity ($R_H$). To validate these predictions we performed ligand competition experiments for a set of $\beta_2$-adrenergic receptor (AR) agonists and analyzed the resulting binding data as well as data taken from relevant literature.

\textbf{Results:} No smooth relationship exists between $R_H$ and $K_L/K_H$ in our or others' data, indicating the insufficiency of the TCM and its extensions. We introduce the allosteric modulators model as an alternative.

\textbf{Conclusions:} To our knowledge, this is the first paper in which insufficiency of the TCM and its extensions based on binding data are shown, and the first in which the presence of allosteric modulators of ligand affinity is proven to be a necessity for explaining binding data at GPCRs.

\textbf{Keywords:} G-protein-coupled receptor, ternary complex model, allosteric modulators model, fraction of high affinity receptors, ratio of high and low receptor affinities for agonist, binding-functional correlations

Traditionally, ligand-binding assays have been used as a first line filter for the process of selecting new chemical entities (NCEs) that have high affinity for a receptor of interest, and for predicting their efficacy at that receptor. A wide variety of responses beyond the agonist-receptor level have been used to express agonist efficacy at guanyl nucleotide-binding protein (G-protein) coupled receptors. This involves, for example, agonist-induced binding of GTP to G-protein, adenylate cyclase activation, and inositol phosphate production.

Introduction of the ternary complex model (TCM) gave the theoretical basis for trying to correlate ligand efficacy with relative affinities of the ligand for receptors uncoupled versus coupled to G-protein ($K_L/K_H$) (where $K_L$ is the dissociation constant for binding of agonist to low affinity receptor sites and $K_H$ is the dissociation constant...
for binding of agonist to high affinity receptor sites) or, less commonly, the fraction of receptors with high affinity for the ligand \( R_{H} \) or the fraction of receptors binding the agonist with high affinity at saturating agonist concentrations) in numerous studies. However, these correlations have varied from highly significant to completely absent. Several extensions and assumptions have been proposed that accommodate to some extent, this variability in correlation.

One has to bear in mind, however, that the very core concept in the TCM of a ligand-receptor-G protein hierarchy does not put limits on the binding-efficacy correlation; ie, it does not predict a sole or even a restricted range of correlations, disproving that which invalidates the model itself. This precludes using binding-functional correlations to validate the TCM. For example, one can hypothesize that the receptor conformation induced by an agonist to couple to G-protein (the active conformation) is the same for all agonists. By this hypothesis, agonists differ in the fraction of receptors which they put in the active conformation. One could also hypothesize that higher stability of the ternary complex is equal to forming more of the active conformation which, therefore, causes more activation of G-protein and of the downstream effector system. It follows that the agonist which has a higher log \( K_{A} / K_{H} \) should have a higher efficacy in activating an effector system. Notice that these assumptions are not consequences of the TCM but limitations put on the model to enable deriving relationships between binding parameters and efficacy.

If, however, an agonist with a higher log \( K_{A} / K_{H} \) is found experimentally to be less efficacious, then explanations can be made that challenge the assumptions added to the TCM but not the TCM per se. For example, it can be said that different conformations are induced by the different agonists. In this context, an agonist with a higher log \( K_{A} / K_{H} \) can induce a conformation that couples highly to G-protein but activates it less efficiently than the conformation induced by an agonist with a lower log \( K_{A} / K_{H} \). Alternatively, it can be said that all agonists induce the same type of conformation that couples to G-protein, but that the receptor then needs to switch to another conformation that activates G-protein. In this context, it can be postulated that an agonist with a higher log \( K_{A} / K_{H} \) will be less efficacious in activating adenylate cyclase (A/C), not because it cannot induce coupling of receptor to G-protein, but because the coupling it induces is so tight that the receptor cannot switch to the form which activates G-protein.

The above-clarified fluidity of the binding-functional correlations precludes using them to validate the sufficiency of the TCM and its extensions and modifications. The TCM extensions are valuable in incorporating inevitable observations (like constitutive activity) and accommodating broadly variable data. To validate a model, however, it is not enough to show that it ‘accommodates’ data. Rather, its ‘predictions’ need to be proven. The interplay of the many equilibrium constants in the TCM extensions combined with the modifications (like different conformations and promiscuity) gives countless possibilities of efficacy outcomes rather than a single testable prediction.

In this paper, we introduce a novel approach to test the sufficiency of the TCM and its extensions. We show that, unlike with binding-functional correlations, the TCM predicts definite relationships within the binding parameters. We simulated these relationships and ran accurate binding experiments for a series of \( \beta_{2} \)-adrenergic receptor (\( \beta_{2} \)-AR) agonists, analyzing binding data for various GPCRs in the literature. We then compared our and others’ data with the simulations and formed conclusions on the sufficiency of the TCM.

**Materials and methods**

**Simulation of the relationship within binding parameters**

We here simulate the relationship between \( R_{H} \) and \( K_{A} / K_{H} \) according to the TCM. Following are the equilibrium and equations that describe the ternary complex model:

\[
\begin{align*}
R & \quad \text{K}_1 \quad \text{AR} \\
\text{RG} & \quad \text{K}_2 \quad \text{ARG} \\
\text{RG A} & \quad \text{K}_3 \quad \text{RG A} \\
\text{RG A} & \quad \text{K}_4 \quad \text{RG A}
\end{align*}
\]

\[
K_1 = \frac{[A][R]}{[AR]}, \quad K_2 = \frac{[R][G]}{[RG]}, \quad K_3 = \frac{[RG][A]}{[ARG]}, \quad K_4 = \frac{[AR][G]}{[ARG]}
\]

Where \( R \) is the receptor, \( A \) is the agonist, and \( G \) is the G-protein heterotrimer. We will refer to the association of the receptor with the agonist as binding and the association of the receptor with G-protein as coupling in the present study.

According to the TCM, the receptors that are coupled to G-protein have a high affinity for agonist \( K_{A} \) while those that are not coupled have a low affinity \( K_{C} \). Experimentally, incremental concentrations of this agonist can be incubated with a receptor system that is prebound to an antagonist and the curve of antagonist displacement by the agonist analyzed.
From this analysis we can determine $K_L$, $K_H$, and $R_H$, the apparent fraction of receptors that should bind the agonist with high affinity at saturating agonist concentrations.

To define the predictions of the TCM for the relationship between $K_L/K_H$ and $R_H$, we elaborate first on the affinity constants in the equilibrium above ($K_L$-$K_H$) and explain how they relate to the affinity constants ($K_L$ and $K_H$) obtained from a 2-site analysis of ligand competition curves. In the TCM equilibrium, a low $K_L$ value indicates that coupling of receptors to G-protein in the absence of agonist is highly likely, and is therefore agonist-independent (constitutive). A high $K_L$ value, in contrast, indicates that coupling of receptors to G-protein in the absence of agonist is highly unlikely, and is therefore agonist-dependent. $K_L$ of 2-site analysis is equal to $K_L$ according to TCM. On the other hand, correlating $K_H$ of 2-site analysis with the equilibrium above is more complex and depends on whether coupling of receptors to G-protein is agonist-dependent or agonist-independent. When coupling is completely agonist-independent, $K_H = K_L$. When coupling is agonist-dependent, $K_H$ is approximated by $K_L$ because formation of the ternary complex in this case depends on the energetically unfavorable coupling of receptor to G-protein (represented by $K_L$) and the energetically favorable binding of agonist to the coupled receptor (represented by $K_H$). For a system with a given $K_H$, a greater $K_L/K_H$ indicates that the preference of binding to coupled receptors is higher than when $K_L/K_H$ is smaller.

For any given membrane preparation, the relationship between $K_L/K_H$ and $R_H$ depends on whether the coupling of receptor to G-protein is agonist-dependent or agonist-independent. We present both extremes here to define the predictions of the TCM for the relationship between $K_L/K_H$ and $R_H$. For any given membrane preparation, the relationship between $K_L/K_H$ and $R_H$ depends on whether the coupling of receptor to G-protein is agonist-dependent or agonist-independent. We present both extremes here to define the predictions of the TCM for the relationship between $K_L/K_H$ and $R_H$.

In the Results section, we show experimental $R_H$ – log $K_L/K_H$ relationships along with an upper line and a lower curve representing, respectively, the extremes of agonist-dependent and agonist-independent coupling. For the TCM to be valid, experimental $R_H$s should form a smooth curve between these two extremes at a position that depends on the level of agonist-independent precoupling (the value of $K_L$).

To draw the upper and lower limits of $R_H$ throughout this project, we followed several steps. First, we assumed a 100% and −0% precoupling for upper and lower limits of $R_H$, respectively. Drawing the lower limit is laborious; −0% precoupling was simulated by first assuming a very large value for the equilibrium constant of precoupling (ie, $K_L = 1000$).

We assumed that the ratio of G-protein to receptor is equal to 110% of the $R_H$ of the experimental agonist with the highest $R_H$ value. We also assumed an equilibrium constant for binding of agonist to uncoupled receptor ($K_L$ in the equilibrium above) of $1 \times 10^{-6}$ M. This value is arbitrary, but selected to be at a fairly typical value for low affinity binding of an agonist. We then constructed a spreadsheet in which we put equations to solve for $[ARG]$ and $[AR]$ based on $K_L$, $K_H$, and $K_H$ values, theoretical agonist concentrations, and the assumed concentration of G-protein (derivations of equations are presented in Supplement 1). $K_L$ was varied to obtain a range of log $K_L/K_H$ values. From $[ARG]$ and $[AR]$, the spreadsheet was used to calculate fractions of sites available for antagonist at different agonist concentrations. When these fractions were plotted against the logarithm of agonist concentration, a 2-site curve was obtained. From the analysis of this curve (by GraphPad software), $R_H$ was obtained for each log $K_L/K_H$. $R_H$ was then plotted against log $K_L/K_H$ and the relationship was taken as the theoretical lower limit of $R_H$.

Drawing the upper limit of $R_H$ is straightforward. It is approximated by the plateau, with incremental log $K_L/K_H$ values, of $R_H$ values simulated for the extreme of no precoupling.

In Figure 1 we simulate the impact the degree of precoupling has, in the context of the TCM, on $R_H$ values for theoretical agonists with different log $K_L/K_H$ values. $R_H$ in this figure is obtained from quantitative derivations based on the TCM (Supplement 1) combined with 2-site fit. Assuming that we know the $R_H$ value (say 0.65) for an agonist (A) with a defined log $K_L/K_H$ (say 3.2) in certain experimental conditions, and want to know what the TCM predicts $R_H$ to be for an agonist (B) that has a lower log $K_L/K_H$ (say 0.7). As can be seen in Figure 1, the TCM does not predict a certain exact value, but a range of values for $R_H$ (in this case ranging from 0.4 to 0.65), depending on the extent of precoupling of the
receptors. This argument can be extended to any number of agonists, keeping in mind that the degree of receptor precoupling should have the same impact on all agonists regardless of its magnitude. Therefore, \( R_h \) versus log \( K_L/K_H \) relationship should form a smooth curve which falls between the two limits of 0% and 100% precoupling.

From this discussion, we can see that the TCM predicts definite relationships between the binding parameters of an agonist (\( R_h \) and \( K_L/K_H \)). If these relationships are shown not to be valid, the TCM is then insufficient.

Here we have two important notes. First, it may be argued that obtaining data inconsistent with our simulations invalidates a ‘restricted version’ of the TCM which included the arbitrary values denoted for G/R ratio, \( K_f \), and \( K_g \) in our simulations, so choosing a different set of equilibrium values would modify the lower limit curve and accommodate the data. In response, no matter how these values are manipulated, upper and lower limits will be obtained within which the \( R_h \) versus log \( K_L/K_H \) relationship should form a curve if the TCM is sufficient. Second, upper and lower relationship limits are also imposed by all TCM extensions and modifications which limit the interaction to a ‘ternary’ complex; ie, do not incorporate the concept of other players that modify receptor affinity for ligand. For example, in the modification that assumes ligand-specific conformations, the term for \( K_f \) is:

\[
K_f = K_a \times f_{RaA} + K_b \times f_{RhA} \ldots
\]

where \( K_a \) is the affinity constant for conformation \( a \), and \( f_{RaA} \) is the fraction of this conformation of all low-affinity conformations at saturating agonist concentrations. It follows that affinity and fraction terms are still related and the microscopic \( K_a' \)'s, \( K_b' \)'s, and \( R_h' \)'s for individual conformations are all reflected in the macroscopic \( K_L' \)'s, \( K_H' \)'s, and \( R_h' \)'s obtained from 2-site analysis.

In our simulations, we assume that \( R_h \) is equal to \( fRGA \) (fraction of RGA at saturation agonist concentrations). However, we should mention here that the extent of identity between \( R_h \) and \( fRGA \) depends on whether coupling of receptor to G-protein is agonist-dependent or agonist-independent. In brief, the divergence between \( R_h \) and \( fRGA \) increases with increased agonist dependence of receptor coupling to G-protein. This is due to the divergence in these conditions between equation 18 and the equation built in the Graph Pad software to obtain \( R_h' \):

\[
\left( \frac{Max_{high}[A]}{K_H + [A]} \right) + \frac{Max_{low}[A]}{K_L + [A]}
\]

where \( Max_{high} \) and \( Max_{low} \) are, respectively, the concentrations of receptors bound to the agonist with high and low affinities at saturating agonist concentrations.

Figure 2 is a simulation for the divergence between \( R_h \) and \( fRGA \) in the extreme of agonist-dependent coupling (a very large \( K_f \) value of 1000). The G-protein/receptor ratio had to be <1.0 to conform to the assumption of the TCM of limited G-protein. We assumed a fixed \( K_f \) value and then varied the value of \( K_g \). At each \( K_g \), we calculated the amount of agonist that should bind to the receptor (to form RA and RGA species) at incremental agonist concentrations and followed the same steps to obtain the fraction of high affinity receptors calculated from equations describing the TCM and that obtained from two-site fit in the extreme of agonist-dependent coupling. The values of \( K_f, K_g, r, \) and \( g \) were assumed at 10\(^{-6}\), 1000, 1, and 0.6, respectively.
steps as above to get \( K_r^H/K_r^H \) and \( R_n^H \) values at that given \( K_r \). 
\( f_{RGA} \) was simply taken to be the calculated fraction of RGA species (from the sum of RA and RGA) at saturating agonist concentrations and is given by the equation:

\[
f_{RGA} = \frac{r + g + K_4 - \sqrt{(r + g + K_4)^2 - 4rg}}{2}
\]

The same process was repeated for different \( K_4 \) values. The fraction of receptors with high affinity (calculated \( f_{RGA} \) and \( R_n^H \) obtained from Graph Pad analysis) was then plotted against log \( K_r^H/K_r^H \).

An important note needs to be made here. Although \( f_{RGA} \) and \( R_n^H \) in the simulation above are not identical, they are still proportional. Also, the magnitude of divergence shown in the simulation is at maximum because the extreme of no precoupling is assumed. Therefore, \( R_n^H \) should be considered a useful approximation of \( f_{RGA} \).

Analysis of binding data in the literature

To evaluate whether the relationships between \( R_n^H \) and log \( K_r^H/K_r^H \) in the literature are consistent with the predictions of the TCM, we analyzed data from studies on a variety of GPCRs including \( \alpha \)-adrenergic, \( \beta \)-adrenergic, muscarinic, \( \mathrm{D}_2 \)-dopamine, \( \mathrm{A}_1 \)-adenosine, and \( \mathrm{H}_1 \)-serotonergic receptors. We should mention that in none of these studies was the fact that the TCM imposes certain limits for the relationship between \( R_n^H \) and log \( K_r^H/K_r^H \) discussed, nor was such a relationship suggested for establishment. In only one instance, a note was made that the \( \beta \)-AR agonists with higher log \( K_r^H/K_r^H \) ratios had higher \( R_n^H \) values at that given \( K_r \). The authors considered this proportionality to signal the validity of the TCM.

Binding experiments

We performed our own binding experiments because we went one step further, involving introducing a binding parameter that correlates with agonist efficacy (manuscript in preparation). This step needed reliably accurate binding data, as well as choosing the suitable expression of efficacy. In that work, we explain what reservations we have on some efficacy expressions in the literature.

The \( \beta \)-AR agonists tested were: epinephrine, isoproterenol, fenoterol, procatetol, albuterol, terbutaline, zinterol, dobutamine, tulobuterol, and ephedrine. The \( \beta \)-AR-containing membranes were from S49 mouse lymphoma cells, BEAS.2B human bronchial epithelial cells, or human embryonic kidney cells transfected with hemagglutinin-tagged \( \beta \)-ARs (H\( \beta \)ARH cells). H\( \beta \)ARH membranes were either reconstituted with \( \alpha \)-stimulatory and \( \beta \gamma \)-subunits of G-protein (\( G_{\alpha} \) and \( G_{\gamma} \)) or not reconstituted.

The reason why we needed to reconstitute H\( \beta \)ARH membranes with \( H_b G_{\alpha} \) and \( G\beta\gamma \) in a set of experiments was the low \( R_n^H \) values obtained with the naïve membranes. As expected, reconstitution did increase \( R_n^H \) (from 28.08% to 58.25%) for epinephrine, thus increasing the sensitivity of these membranes for comparison of different agonists. However, we then harvested another H\( \beta \)ARH membrane batch in which epinephrine had an \( R_n^H \) of \(-50\%\), high enough to resolve differences, if any, between \( R_n^H \)s for different \( \beta \)-AR agonists without need for reconstitution. We call this batch of membranes ‘naïve’ hereafter in the study. The enhanced \( R_n^H \) values we observed with the second batch could be due to better preparation techniques that preserved coupling of receptors to endogenous G-protein.

The low \( \beta \)-AR densities in S49 and BEAS.2B membranes put a limit on the number of agonists that could be tested in these membranes.

Materials

S49 cells were obtained from Dr Henrey Bourne (University of California, San Francisco, CA). BEAS.2B cells, HEK cells transfected with hemagglutinin-tagged \( \beta \)-AR, hereafter referred to as H\( \beta \)ARH cells, and 125I-radioactive iodinated cyanopindolol, hereafter referred to as [125I]CYP, were kindly provided by Dr Richard Clarke (University of Texas at Houston, Health Science Center, Houston). Ham’s F-12 medium, aprotinin, and beta subtype 2 adrenergic receptors, hereafter referred to as \( \beta \)-AR agonists, were obtained from Sigma. Fetal bovine and donor horse sera were from Atlanta Biologicals (Norcross, GA). Penicillin and streptomycin were from Mediatech. Tris Base, GTP, and guanosine-51-O-(3-thio)triphasphate (GTP\( \gamma S \)) were from Boehringer-Mannheim Biochemicals. Tritiated dihydroalprenolol, hereafter referred to as [3H]DHA, and [32P]ATP were from DuPont NEN. Multiscreen 96-well plates were from Millipore. [3H]cAMP was from Moravek Biochemicals. The plasmid H6-Gst\( \varphi \)PQE60 and the bacteria E. coli B212-DE3/pREP4 were kindly given to the authors by Dr Carmen Dessauer (University of Texas at Houston, Health Science Center, Houston, TX). Ni-NTA agarose resin was purchased from QIAGEN.

Cell culture and membrane preparation

S49 cells were grown and membranes harvested as described by Krumins et al except that buffer B did not contain trypsin inhibitor or leupeptin.
BEAS.2B cells were grown to confluence in T150 flasks at 37°C in sodium bicarbonate-buffered Ham’s F-12 medium supplemented with penicillin, streptomycin, and 10% fetal bovine serum. To split the cells, the medium was removed and the cell monolayer washed with 10 mL phosphate buffer solution, then 2 mL of trypsin solution (trypsin 0.25% and EDTA 0.02%) was added to the cell monolayer for 3–5 minutes. Then 10 mL of fresh medium was added and cells were suspended into the medium. For membrane preparation, the cells were passed into cell culture dishes and grown for at least 48 hours. Then the medium was removed by aspiration and the cell monolayer washed twice with 10 mL cold HE solution (20 mM Hepes, pH 8 and 1mM EDTA, pH 7). The cells were then scraped into 6 mL HE containing the protease inhibitor leupeptin (10 µg/mL). The cells were then homogenized in a type B Dounce homogenizer. Membranes were obtained from the lysate and stored as with S49 lysate with the exception that centrifugation was for 20 minutes.

HβARH cells were grown and membranes prepared using the exact same procedures for BEAS.2B cells with two modifications; Hepes-buffered DMEM was used instead of Ham’s F-12 medium, and G418 sulfate was included in the growth medium to select for the cells that were stably transformed with hemagglutinin-tagged β2-ARs.

Preparation of H6-Gs and H6-Gβγ
Gs tagged with 6 residues of histidine (H6-Gs) was prepared as described by Lee et al.36 H6-Gβγ was prepared as described by Iniguez-Lluhi et al.37 Protein concentration was determined using the Bradford method.38

Reconstitution of HβARH membranes with H6-Gs and Gβγ
To reconstitute HβARH membranes with H6-Gs and Gβγ, a membrane quantity including ~ 0.66 pmole β2-AR, 1 nmole of each of H6-Gs and Gβγ and 10 µl 0.01 M MgCl₂ were vortexed in a vial for 3 minutes. The vial was then put in ice for 15 minutes to be used for one binding experiment.

Ligand competition
Binding analyses were carried out in 305 µl reactions with a fixed concentration of [125I]CYP or [3H]DHA (75.0 pM and 1.0 nM, respectively), increasing β2-AR agonist concentrations and an amount of membrane protein containing 8.76 fM of β2-AR (for S49 and HβARH membranes). The reaction mixture contained the following final concentrations of reagents: 18.0 mM Hepes pH 8.0, 2.2 mM MgCl₂, 143.0 µM 1-methyl-3-isobutylxanthine (MIX), 29.0 µM phentolamine, 2.9 µM ascorbate, 29.0 µM thiourea, and 1.2 mM EDTA pH 7.0. The reaction mixture was incubated for 40 minutes at 30°C. Nonspecific [125I]CYP binding was determined in the presence of 20 µM alprenolol. Not more than 10% of the amount added of [125I]CYP was bound to filter papers, except in case of BEAS.2B membranes where nonspecific binding was up to 35%. Reactions were terminated by vacuum filtration through GF/C filters in 96-well filter plates using Millipore vacuum filtration apparatus and the filters were washed three times with a solution of 10 mM Tris-Cl, pH 7.4 and 5mM MgCl₂. The filters were dried and radioactivity counted using a Beckman Gamma counter for 1 minute. For accuracy enhancement, 13–14 agonist concentrations in quintuplets were used. Specifically bound [125I]CYP was plotted against log [agonist] and two-site competition analysis using Graph Pad software version 3.02; Graph Pad, San Diego, CA, yielded values of Kᵣ, Kᵢᵣ, and Rᵣᵢᵣ.

Determination of dissociation constants for radioactive antagonists at β2-AR and β2-AR density
Similar reaction buffers and conditions were used as in ligand competition assays. Instead of running an agonist-antagonist competition, various concentrations of the radioactive antagonist (25–2700pM for [125I]CYP and [3H]DHA, respectively) were incubated with membranes in the presence or absence of 20 µM alprenolol. Specifically-bound radioligand concentration was plotted against the logarithm of the free radioligand concentration and a sigmoidal dose-response analysis using Graph Pad software yielded IC₅₀ values for the radioligands. Cheng-Prussof correction was used to obtain the overall dissociation constant for binding of ligand to receptor (Kᵣ) values.

To solve for receptor density we first calculated the concentration of radioactive antagonist bound to receptor at saturation. The receptor density was obtained by dividing the moles of receptor by the concentration of membrane protein.

Analysis of data: statistical significance
Relationships were considered significant at P < 0.05.

Results
Analysis of binding data in the literature
Our analysis of Rᵣ versus log Kᵣ/Kᵢᵣ relationships is represented in Figure 3 and we obtained the following main results. Only in one study11 was a relationship within the limits of the TCM obtained. In two other studies3,4 significant relationships of higher Rᵣᵢᵣ for agonists with higher log Kᵣ/Kᵢᵣ were obtained, but they fell out of the limits of the TCM. In
two other studies\textsuperscript{10,12} significant relationships of lower $R_H$ for agonists with higher log $K_L/K_H$ were obtained. In the other seven studies\textsuperscript{2a,2b,5,16,20,28,34} no significant relationship between $R_H$ and log $K_L/K_H$ was obtained.

**Binding experiments**

The relationship between the fraction of $\beta_2$-ARs with high affinity for an agonist ($R_H$) and the ratio between high and low affinities of $\beta_2$-ARs for the agonist (log $K_L/K_H$)

Figure 4 shows typical ligand competition curves obtained for the agonists tested in H$\beta$ARH membranes against $[^{125}\text{I}]$CYP to determine values of $R_H$ and log $K_L/K_H$ for these agonists.

Figure 5 shows that the experimental $R_H$s did not fall within the range predicted by the TCM for a series of $\beta_2$-AR agonists that vary in log $K_L/K_H$ in all tested membrane types (S49, BEAS.2B, naïve H$\beta$ARH, and reconstituted H$\beta$ARH membranes). Notice, however, that a subset of these agonists (epinephrine, fenoterol, albuterol, terbutaline, and dobutamine) consistently follows a trend of higher $R_H$ for agonists with higher log $K_L/K_H$.

Using $[^{3}\text{H}]$DHA as an antagonist, a significant relationship was obtained (Figure 6). However, it is most probable that had the out-players (zinterol, procaterol, and ephedrine) been tested, a result of no significant relationship would have been obtained as with $[^{125}\text{I}]$CYP.

**Determination of dissociation constants**

for radioactive antagonists at $\beta_2$-AR and $\beta_2$-AR density

Table 1 shows the dissociation constants ($K_d$) we obtained for $[^{125}\text{I}]$CYP at $\beta_2$-AR in different membrane types. $K_d$ For $[^{3}\text{H}]$DHA in naïve H$\beta$ARH membranes was 55.7 ± 7.1 pM. Also shown in Table 1 are the $\beta_2$-AR densities ($B_{max}$) in all four membrane types.

**Discussion**

Using a unique approach, in the present study we show the insufficiency of the traditionally-accepted TCM,
thus revealing the possible reasons behind inconsistent correlations in the literature between in vitro functional efficacy of GPCR agonists and binding parameters derived from the TCM. By careful analysis of binding data in the literature for various GPCRs, we have shown that the experimental relationships between binding parameters [log \( K_{i}/K_{H} \) and \( R_H \)] deviate from the simulations of the relationships that the TCM necessitates (Figure 3). Our own work obtained the same result for \( \beta_2 \)-AR agonists in a variety of membrane types and using two different radioactive antagonists (Figures 5 and 6). It is worth mentioning that having some experimental data that follow the predictions of the TCM does not validate the model in this case, since obtaining data inconsistent with an equilibrium model even once indicates its insufficiency.

The novelty of our approach lies in testing relationships between binding parameters (log \( K_{i}/K_{H} \) and \( R_H \)). The stringency imposed by the TCM of these relationships allowed us to reveal discrepancies that could not be revealed by the much less stringent binding-functional correlations. In other words, even the datasets in the literature that were thought to be consistent with the TCM (based on binding-functional correlations) are generally not so (based on binding-binding relationships).

Thermodynamically, the only way to explain the complex log \( K_{i}/K_{H} \) versus \( R_H \) relationships shown in this study is to recognize that the ternary complex is not simply ‘ternary’; ie, other players are included that allosterically modulate receptor affinity. A considerable amount of evidence is cumulating for allosteric modulation of affinity in GPCRs.28,39–46 In a review article different models that incorporated allosterism into the ternary complex model were discussed and its impact on ligand affinity was described. However, the authors finally pointed implicitly to a conclusion similar ours of discrediting the TCM after presenting experimental observations where ‘accessory molecules’ or ‘coupling partners’ modulated the affinities of receptors for agonists.41 The authors concluded: “Some other additions to the list of GPCR coupling partners.
Allosterism replacing the ternary complex model promise to quash the concept of the receptor-G protein signaling hierarchy altogether”.

So, our study is not the first to bring to focus the effect of allosterism on ligand affinity in GPCRs. However, we have two very significant additions to what have been discovered so far about allosteric modulators. First, we show here that allosteric modulation is concluded from analysis of simple binding experiments. This is in contrast with the above-mentioned citations which involved evaluations of the effect of ‘adding’ an allosteric modulator on receptor affinity for an agonist. Second, our analysis here shows that allosteric modulators exist naturally or in experimental environments for most GPCRs in most systems because, to our knowledge, their presence is the only way to explain complex log $K_L/K_R$ versus $R_H$ relationships (see below). This is in contrast with the citations above which show that a given molecule or ion in a given concentration ‘can’ modulate binding properties, but whether this modulation does exist naturally remains to be proven.

Now, to appreciate the importance of incorporating allosteric modulation in explaining binding properties, we have to show how it accommodates binding data not accommodated by the TCM and its extensions. As we can see from Figures 3, 5 and 6, the inconsistency of experimental data with the TCM can be summarized in that log $K_L/K_R$ does not predict $R_H$. This inconsistency is stylized in the simplest form in Figure 7, in which two agonists with the same log $K_L/K_R$ can have different $R_H$ values, inconsistently with the TCM, which necessitates that such agonists should have the same $R_H$.

Several assumptions have to be made to enable a model of allosteric modulation explaining Figure 7. These assumptions are substantiated by many observations as detailed below. First, there should be several allosteric modulators that associate
with a given receptor and modify its affinity for different agonists. Second, different allosteric modulators induce different receptor conformations. Third, the induction of a given conformation changes the difference between the affinities of two different agonists for the receptor as compared with before the association of the allosteric modulator. In other words, a receptor with an affinity for agonist A that is 10-fold higher than for agonist B before association with the allosteric modulator may have an affinity for A that is, say, 100-fold higher than for B after association with the modulator. Fourth, at least some allosteric modulators are limited (lower in concentration than the receptor). Fifth, an allosteric modulator can bind to coupled and/or uncoupled receptors (different observations require different assumptions regarding the receptor species to which the allosteric modulator binds). The ‘allosteric modulators model’ is the name we give for our model that includes the aforementioned assumptions.

Figure 7 can be explained by the allosteric modulators model as follows. An allosteric modulator (a) associates with the receptor (both coupled and uncoupled forms), increasing its affinity for agonist A more than for agonist B. The affinity of receptor species for A is as follows: R(a)G > R(a) > R. Similarly, an allosteric modulator (b) associates with the receptor (both coupled and uncoupled forms), increasing its affinity for B more than for A. The affinity for B is R(b)G > R(b) > R. For both agonists, the receptors associated with a modulator are recognized in 2-site analysis as high-affinity sites, whether or not they are coupled to G-protein. Also, (b) is less available than (a), and both are lower in concentration than the receptor. Moreover, we have to assume that the log KL/KH intrinsic to B (ie, in absence of (a) and (b)) is higher than the log KL/KH intrinsic to A. However, when the two agonists are compared at a receptor system including both (a) and (b), the following happens. The abundance of (a) compensates for the low intrinsic log KL/KH of A, thus bringing the log KL/KH for A measured in this system to the level of the measured log KL/KH for B, which is compromised by the shortage of (b). Also, the abundance of (a) causes the formation of a higher fraction of R(a)G and R(a), as compared with the fraction of R(b)G and R(b) and, therefore, the RH for A would be higher than the RH for B.

This type of explanation is the only way by which we have been able so far to account for the complex log KL/KH versus RH relationships obtained in our and others’ studies.

The several assumptions made in our model are substantiated by many observations in the literature. For example, agonist-specific conformations have been proposed in several studies.2,29,30,33

### Table 1 Dissociation constants (Kd) for [125i]CYP at β2-AR and densities (Bmax's) of β2-AR

<table>
<thead>
<tr>
<th>Membrane type</th>
<th>Naïve HβARH</th>
<th>Reconstituted HβARH</th>
<th>S49</th>
<th>BEAS.2B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kd for [125i]CYP (pM)</td>
<td>26.8 ± 2.0</td>
<td>11.3 ± 0.6</td>
<td>24.8 ± 1.7</td>
<td>15.8 ± 0.6</td>
</tr>
<tr>
<td>Bmax (pmole/mg protein)</td>
<td>4.76</td>
<td>4.40</td>
<td>0.45</td>
<td>0.24</td>
</tr>
</tbody>
</table>

**Notes:** Data are represented as means ± SEM of two experiments.
As for allosteric modulators that modulate $K_a/K_l$ and/or $R_H$, differently for different agonist, calcyon, a receptor cross-talk protein, reduced $R_H$ for dopamine and SKF82958 at D$_1$-dopamine receptor without affecting their $K_a$ or $K_l$ values. Importantly, calcyon decreased the difference between $R_H$ values of the two D$_1$-agonists from 22% to 2%.

In fact, the allosteric modulators do not need to be only newly-recognized entities, but a thermodynamic understanding of molecules already known to interact functionally with GPCR brings to conclusion that they are, in a sense, allosteric modulators. For example, it is well-established that GPCR agonists increase the affinity of GPCR for many molecules, such as PKA and βARK. Thermodynamics requires that any of these molecules should then similarly increase the affinity of the receptor for the agonist. This understanding has been made note of in a recent review of allosteric modulation by mentioning that the expanding list of GPCR-interacting molecules but can also be ions, or lipids. For example, absence of Ca$^{2+}$ decreased the affinity of GABA for GABAB receptor 25.2-fold while it had no effect on affinity of baclofen. With dopamine D$_4$ receptors, replacing Na$^+$ in the reaction mixture with N-methyl D-glucamine increased log $K_a/K_l$ by 0.21 for the partial agonist aplatidore and by 0.35 for dopamine. Yet this replacement increased $R_H$ disproportionately by 37.38% and 7.10% for aplatidore and dopamine, respectively. In a third example, a single transmembrane domain protein called RAMP3 (receptor-activity-modifying protein 3) increased the affinity of human calcitonin receptor for rat amylin but not for calcitonin. It can be appreciated now that the recognition of human calcitonin receptor for rat amylin but not for (receptor-activity-modifying protein 3) increased the affinity of human calcitonin receptor for rat amylin but not for calcitonin.

Allosteric modulators need not be only intracellular molecules but can also be ions, membrane proteins, or lipids. For example, absence of Ca$^{2+}$ decreased the affinity of GABA for GABAB receptor 25.2-fold while it had no effect on affinity of baclofen. With dopamine D$_4$ receptors, replacing Na$^+$ in the reaction mixture with N-methyl D-glucamine increased log $K_a/K_l$ by 0.21 for the partial agonist aplatidore and by 0.35 for dopamine. Yet this replacement increased $R_H$ disproportionately by 37.38% and 7.10% for aplatidore and dopamine, respectively. In a third example, a single transmembrane domain protein called RAMP3 (receptor-activity-modifying protein 3) increased the affinity of human calcitonin receptor for rat amylin but not for calcitonin. It can be appreciated now that the recognition of allosteric modulators allows much more flexibility in $R_H$ versus log $K_a/K_l$ relationship than allowed by the TCM and its extensions.

In our experimental settings, the concentration of ions and pH of buffers we used should have influenced the relationship between $R_H$ and log $K_a/K_l$. Had other concentrations and pH values been used we should have observed different relationships. However, we postulate that an observation will prove consistent no matter what conditions are used; ie, relationships that cannot be explained by the TCM or its extensions.

Our work draws attention to binding-binding relationships as very useful tools for understanding receptor theory and shows that they can be simpler and more definite than the traditionally-applied binding-functional correlations. We did not aim to construct a mass-action scheme for our model since incorporating allosterism in a model is associated with extreme complexity and is unlikely to have significant practical predictive applicability. On the other hand, the restricted simple forms, such as the allosteric 2-state model, will inevitably fail to explain some allosteric behaviors, as pointed out in a recent review.

Finally, the importance of our work lies in four achievements. First, we invented a novel approach that proved the insufficiency of the ternary complex model and its extensions. Second, this insufficiency of the TCM may account for inconsistency of efficacy-affinity correlations. Third, we provided a model that accounts for binding data inconsistent with the TCM and, at the same time, reveals allosterism intrinsic to various receptor systems. Fourth, our model provides the theoretical basis for deriving a novel binding parameter that correlates with agonist efficacy in our and others’ work more significantly and consistently than the parameters used so far (manuscript in preparation).

### Acknowledgments

The authors thank the Department of Integrative Biology and Pharmacology, University of Texas/Houston, Houston, TX, for financial support. The authors also thank Dr Richard Clark and Ms Jacky Friedman (University of Texas at Houston, Health Science Center, Houston) for providing binding and functional protocols as well as $^{[25]}$IICYP.

### Disclosure

The authors report no conflicts of interest in this work.

### References

Supplement 1

Here we present our derivation of equations that we used in our spreadsheets to relate the quantities of different receptor species in the context of the TCM:

To calculate $R_H$ predicted by the TCM for an agonist with a given log $K_L/K_H$, we need to calculate the fraction of receptors that is bound to the agonist ($[RA] + [RGA]$) at different agonist concentrations. The fraction left for binding to radioactive antagonist is then calculated (using a spreadsheet) by subtraction from unity. Then this fraction is plotted against agonist concentration, and $R_H$ as well as log $K_L/K_H$ are obtained using Graph Pad software. So all we need to do mathematically is to solve the equations, based on equilibrium equations and the rule of mass conservation of the TCM, for $[RH]$ and $[RGH]$.

The ternary complex model is described diagrammatically as:

$$
\begin{align*}
K_1 & \quad R \leftrightarrow AR \\
K_2 & \quad \uparrow K_4 \\
RG & \leftrightarrow ARG \\
K_3 & 
\end{align*}
$$

So the equilibrium conditions are:

$$
\begin{align*}
K_1 &= \frac{[R][A]}{[RA]} \quad (1) \\
K_2 &= \frac{[R][G]}{[RG]} \quad (2) \\
K_3 &= \frac{[RG][A]}{[RGA]} \quad (3) \\
K_4 &= \frac{[RA][G]}{[RGA]} \quad (4)
\end{align*}
$$

and the mass conservation conditions are:

$$
\begin{align*}
r &= [R] + [RA] + [RG] + [RGA] \quad (5)
\end{align*}
$$

where $r$ is the total receptor amount

$$
\begin{align*}
g &= [G] + [RG] + [RGA] \quad (6)
\end{align*}
$$

where $g$ is the total G-protein amount

In order to solve for $[RGA]$, we use the equilibrium equations to get expressions for $[RA]$, $[RG]$, and $[R]$ in terms of $[RGA]$ as follows:

From 4, $[RA] = \frac{K_1[RGA]}{[G]}$.

From 1 and 4, $[R] = \frac{K_1[R]}{[A]} = \frac{K_1K_4}{[A][G][RGA]}$.

Insertion of these relationships into equation 5 gives:

$$
r = [RGA]\left(\frac{K_4}{[G]}\left(1 + \frac{K_1}{[A]}\right) + \frac{K_3}{[A]}\right)
$$

which may be rewritten as:

$$
r = [RGA]\left(\frac{K_4}{[G]}\left(1 + \frac{K_1}{[A]}\right) + 1 + \frac{K_3}{[A]}\right)
$$

Now only the elimination of $[G]$ remains. From 6 and 3 we can determine that:

$$
[G] = g - [RG] - [RGA] = g - \left(1 + \frac{K_3}{[A]}\right)[RGA]
$$

Substituting 9 into 8 gives:

$$
r = [RGA]\left(\frac{K_4}{[G]}\left(1 + \frac{K_1}{[A]}\right) + 1 + \frac{K_3}{[A]}\right)
$$

Writing $(1+(K_1/[A]))$ as $B_1$ and $(1+(K_3/[A]))$ as $B_3$ gives:

$$
r = [RGA]\left(\frac{K_4B_1}{g - [RGA]B_3} + B_3\right)
$$

Multiplying through by $g-[RGA]B_3$ gives:

$$
rg - rB_3[RGA] = K_4B_1[RGA] + gB_3[RGA] - B_3^2[RGA]^2
$$

Then, rearranging these figure:

$$
B_3^2[RGA]^2 - (rB_3 + gB_3 + K_4B_1)[RGA] + rg = 0
$$

Solving using the standard solution to a quadratic gives:

$$
\frac{rB_3 + gB_3 + K_4B_1 - \sqrt{(rB_3 + gB_3 + K_4B_1)^2 - 4rgB_3^2}}{2B_3^2} = \frac{[RGA]}{B_3}
$$

This rearranges to:

$$
[RGA] = \frac{1}{B_3} \left(\frac{r + g + K_4B_1}{B_3} \sqrt{\frac{(r + g + K_4B_1)^2}{4} - 4rg} - \frac{4rg}{2}\right)
$$
In order to calculate the total binding of agonist we also need to know \([RA]\). We calculate it as follows:

The quantity of receptors not coupled to G-protein (here called \(x\)) is equal to \([R] + [RA]\).

From the equilibrium condition (1), \([R]\) is equal to \([RA]/K_1/\text{[A]}\). Therefore:
\[
x = \frac{[RA]K_1}{[A]} + [RA] = [RA] \left( \frac{K_1 + [A]}{[A]} \right)
\]

It follows that \([R] + [RA] = [RA] \left( \frac{K_1 + [A]}{[A]} \right)\).

Therefore: \([RA] = \frac{([R] + [RA])A}{K_1 + [A]}\)

The quantity of receptors not coupled to G-protein ([R] + [RA]) is also equal to \(r - [RG] - [RGA]\).

Therefore:
\[
[R] = [RGA] - [RG] = \frac{[A]}{K_1 + [A]}
\]

But \(1 + (K_1/[A])\) is \(B_3\) and \([A]/(K_1 + [A])\) is \(1/B_1\). Therefore equation 15 becomes:
\[
[R] = \frac{r - B_3[RGA]}{B_1}
\]

By inserting the known solution for \([RGA]\) (equation 14) and rearranging we get:
\[
[R] = \frac{r - B_3[RGA]}{B_1} + \frac{1}{B_1} \left( \frac{1}{B_1} - \frac{1}{B_1} \right)
\]

Finally, the total amount of receptor bound by agonist at a given agonist concentration is given by the sum of 14 and 17:
\[
[RGA] + [R] = \frac{r + g + K_4B_3}{B_3} - \frac{\left( r + g + K_4B_3 \right)^2 - 4rg}{2}
\]