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Quantitative Resolution of Beta-Adrenergic Receptor Subtypes by Selective Ligand Binding: Application of a Computerized Model Fitting Technique

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SUMMARY


Frog myocardium appears to possess both $\beta_1$ and $\beta_2$ receptors, based on the potency order of several adrenergic agonists to compete for [$\text{H}]$dihydroalprenolol binding. Selective beta-blocking agents are able to distinguish two receptor subtypes in frog myocardium, but only one site in rat ventricle. Computer modeling using a PDP 11/45 indicates that all rat $\beta$ receptors are $\beta_1$, whereas only 15%-25% of frog ventricular $\beta$ receptors are of the $\beta_1$ subtype. Computerized curve fitting can provide a more accurate estimate of receptor parameters than currently available graphical methods of analysis.

INTRODUCTION

The use of radiolabeled ligands has facilitated the study of various properties of the beta-adrenergic receptors in many tissues (1). One of the characteristics of beta receptors investigated by this method has been the distinction between $\beta_1$ and $\beta_2$ receptors originally proposed from physiological observations by Lands et al. (2). For example, the adenylate cyclase-coupled beta-adrenergic receptor of the frog erythrocyte appears to possess binding properties of the $\beta_2$ type (3), whereas the rat heart demonstrates binding affinities for ligands predicted for $\beta_1$ receptors (4).

Until recently, it has been believed that individual tissues contain only one of the $\beta$ receptor subtypes. However, pharmacological studies by Caisson et al. (5) demonstrated a mixture of $\beta_1$ and $\beta_2$ receptors in kitten, but not rat heart. Similar physiological techniques have indicated that frog myocardium might contain a small $\beta_1$ component in addition to a predominant population of $\beta_2$ receptors (6).

Using radiolabeled ligand techniques, Barnett et al. (7) recently demonstrated a mixture of 25% $\beta_1$ and 75% $\beta_2$ receptors in rat lung, but rat heart studies demonstrated only one class of sites. A graphical method derived from the classical Scatchard data analysis ("pseudo-Scatchard") was used to estimate the relative proportions of receptor subtypes in these ligand binding experiments.

In the present study, we have applied a computerized model fitting technique to estimate receptor parameters more accurately than currently available graphical methods.
In the present application, for each curve the number "m" of ligands is two, ligand 1 being the labeled ligand (DHA) and ligand 2 being the competitor. The number "n" of classes of binding sites is set to either 1 or 2, but could be larger. A Scatchard transformation of data (not shown) from saturation studies resulted in a straight line, indicative of high affinity binding of DHA with equal affinity for all receptors. Secondly, in the presence of a competitive ligand (e.g., propranolol) there was an apparent decrease in the affinity of DHA for the receptors without any change in the maximum amount of DHA bound, as predicted for true competitive binding. DHA appears to be non-selective for either beta1 or beta2 receptor subtypes and the same value was assigned to its two affinity constants, $K_{11}$ and $K_{12}$, for sites 1 and 2, respectively. The deviations of the observed points from the predicted values were weighted according to the reciprocal of the predicted variance (13). The data were repeatedly fit using the model for one, two, or more classes of binding sites. The model providing the best fit was chosen on the basis of the lowest value of mean squares of residuals. The computer programs provided the best estimates (with their standard error) for the affinity constants of each ligand and the concentration of receptors in each subtype. All computations were performed using an interactive program in PL/1 using a PDP 11/45.

RESULTS

Binding of DHA to membrane vesicles from both frog and rat ventricle demonstrated appropriate stereoselectivity and a high affinity for DHA. The $K_D$'s obtained from Scatchard analysis (data not shown) were $3.6 \text{ nM}$ and $2.6 \text{ nM}$ in the frog and rat, respectively. The reciprocal of the $K_D$'s were utilized as the affinity constants of DHA in subsequent computer analyses. The maximum number of binding sites for DHA was approximately $100 \text{ fmole/mg protein}$ in frog ventricle and $35 \text{ fmole/mg protein}$ in the rat.

Displacement curves of agonist competition against approximately $3 \text{ nM}$ DHA revealed a different pattern for the two species. Figure 1 illustrates the ability of four adrenergic agonists to compete for DHA binding in the frog ventricle. The pattern observed is similar to that found with beta2 systems such as the frog erythrocyte (3). Estimates of the EC50's from dose response curves indicated a potency ratio for hydroxybenzylisoproterenol:isoproterenol:epinephrine:norepinephrine of $1200:70:7.7:1$. By contrast the pattern observed in the rat ventricle was as expected for beta1 receptor binding (Fig. 2), i.e., the relative agonist potencies of hydroxybenzylisoproterenol:isoproterenol:epinephrine:norepinephrine were $30:25:1.7:1$.

The ability of three beta-blocking agents to compete for DHA binding to membrane vesicles was also different in the two species. Figure 3 illustrates dose-response competition curves for approximately $3 \text{ nM}$ DHA binding in frog ventricle. The potency order of propranolol:butoxamine:practolol was $2000:6.7:1$. In the rat myocardium, butoxamine and practolol were approximately equipotent, and approximately 1000 fold weaker than propranolol (Fig. 4). In the experiments using rat heart the three antagonist dose-response curves appeared to differ only in the potency of the competitors, i.e., all three curves were parallel (Fig. 4). In the frog heart, however, the displacement of DHA by butoxamine and practolol is more complex than that obtained with propranolol. Dose response curves (Fig. 3) indicate a second component with butoxamine and practolol. In order to analyze the interaction of beta-receptor agents with DHA binding sites a computer modeling system was developed. Figures 1 through 4 illustrate the ability of the model to fit the experimental observations. The lines indicate the best fit from the computer model, whereas the symbols represent the actual data points. Predicted values for ligand affinities and proportions of beta1 and beta2 receptors obtained from agonist and antagonist competition curves are...
FIG. 1. Competition curves for specific DHA binding to frog ventricular membranes by beta-adrenergic agonists. The ordinate indicates the percent of maximal specific DHA binding, 0.0221 nM. (Specific binding is defined as the difference between binding in the absence of any competing ligand and binding in the presence of 10 M propranolol.) The abscissa is the molar concentration of various agonists. The lines are computer modeled best fits. The symbols indicate the means of actual data points for 2 (hydroxybenzylisoproterenol), 11 (isoproterenol, U), 9 (epinephrine, A), and 10 (norepinephrine, [ ]). Separate experiments with each agonist.

FIG. 2. Competition curves for specific DHA binding to rat ventricular membranes by beta-adrenergic agonists. The ordinate indicates the percent of maximal specific DHA binding, 0.0083 nM. The abscissa is the molar concentration of various agonists. The symbols indicate the means of actual data points derived from two separate experiments with each agonist (hydroxybenzylisoproterenol, [ ], isoproterenol, U, epinephrine, A, norepinephrine, [ ]) are given in Tables 1 and 2.
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