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The Origins of Diversity and Specificity in G Protein-Coupled Receptor Signaling

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Abstract

The modulation of transmembrane signaling by G protein-coupled receptors (GPCRs) constitutes the single most important therapeutic target in medicine. Drugs acting on GPCRs have traditionally been classified as agonists, partial agonists, or antagonists based on a two-state model of receptor function embodied in the ternary complex model. Over the past decade, however, many lines of investigation have shown that GPCR signaling exhibits greater diversity and “texture” than previously appreciated. Signal diversity arises from numerous factors, among which are the ability of receptors to adopt multiple “active” states with different effector-coupling profiles; the formation of receptor dimers that exhibit unique pharmacology, signaling, and trafficking; the dissociation of receptor “activation” from desensitization and internalization; and the discovery that non-G protein effectors mediate some aspects of GPCR signaling. At the same time, clustering of GPCRs with their downstream effectors in membrane microdomains and interactions between receptors and a plethora of multidomain scaffolding proteins and accessory/chaperone molecules confer signal preorganization, efficiency, and specificity. In this context, the concept of agonist-selective trafficking of receptor signaling, which recognizes that a bound ligand may select between a menu of active receptor conformations and induce only a subset of the possible response profile, presents the opportunity to develop drugs that change the quality as well as the quantity of efficacy. As a more comprehensive understanding of the complexity of GPCR signaling is developed, the rational design of ligands possessing increased specific efficacy and attenuated side effects may become the standard mode of drug development.

The heptahelical G protein-coupled receptors (GPCRs) constitute the most diverse form of transmembrane signaling protein. An estimated 1% of the mammalian genome encodes GPCRs, and about 450 of the approximately 950 predicted human GPCRs are expected to be receptors for endogenous ligands (Takeda et al., 2002). GPCRs detect an extraordinarily diverse set of stimuli in the external environment, from photons of light and ions to small molecule neurotransmitters, peptides, glycoproteins, and phospholipids. In addition, nearly 40% of all current therapeutics target GPCRs (Brink et al., 2004).

The mechanism by which GPCRs transduce extracellular messages into intracellular cellular responses was initially envisioned as a simple linear model in which agonist binding promotes transition of the receptor from an “off” to an “on” state capable of engaging heterotrimeric

guanine nucleotide-binding (G) proteins, whose dissociated $G\alpha$ and $G\beta\gamma$ subunits in turn activate or inhibit various downstream effector molecules. Implicit in this model is the concept that a GPCR agonist will impact every consequence of receptor activation in the same fashion, whether G protein coupling, receptor desensitization, internalization, or trafficking. Recently, however, experimental evidence documenting the existence of multiple active receptor states, alternative mechanisms of signaling, and preorganization of GPCR signaling units has dramatically expanded our notions of the complexity and texture of GPCR signaling and forced a reexamination of even the fundamental concepts of agonism and antagonism. It is increasingly clear that for a given GPCR, the optimal receptor conformation for G protein activation differs between G protein pools and that synthetic and, in some cases, naturally occurring ligands can selectively promote different coupling conformations of the receptor (vide infra). Many examples now exist of “agonists” that activate only a subset of potential G protein partners or induce G protein coupling without triggering desensitization and endocytosis or of “antagonists” that cause receptor desensitization or initiate apparently G protein-independent signals without producing detectable activation of heterotrimeric G proteins. Herein, we examine current insights into the source of GPCR signaling diversity and specificity and discuss the impact of these factors on the classic concepts of agonism and the process of drug discovery.

The Evolution of Receptor Theory

The Ternary Complex Model of GPCR Function

GPCRs transmit signals intracellularly by functioning as ligand-activated guanine nucleotide exchange factors (GEFs) for heterotrimeric G proteins. G protein activation is initiated through hormone-driven changes in the tertiary structure of the transmembrane heptahelical receptor core that are transmitted to the intracellular transmembrane loops and carboxyl terminus. These conformational changes alter the ability of the receptor to interact with intracellular G proteins and catalyze the exchange of GDP for GTP on the heterotrimeric G protein α subunit. The GTP-bound α subunit stimulates its cognate downstream effectors, e.g., adenylate cyclase or phospholipase C, conveying information about the presence of an extracellular stimulus to the intracellular environment.

In the simplest conceptualization, a membrane receptor functions as a switch, existing in either an empty off state or an agonist-bound on state. Such early allosteric models of membrane receptor function were introduced in the late 1960s (Karlin, 1967). Evidence that GPCR behavior was more complex originated with the finding that β -adrenergic receptors exhibit two affinity states for agonists, the relative proportions of which are modulated by the presence of guanine nucleotides (DeLean et al., 1980). The model advanced to explain these phenomena predicted that in the presence of GDP, agonist binding promotes the formation of a long-lived ternary complex between agonist (H), GPCR (R), and heterotrimeric G protein (G) that exhibits high agonist binding affinity. In the absence of the G protein, or when the presence of GTP allows for receptor-catalyzed G protein activation, the H-R-G complex is dissociated, and the receptor resides in a low-affinity (H-R) state.

The Extended Ternary Complex Model

Efforts to employ receptor chimeras to explore the structural basis of specificity in receptor-G protein coupling led to the unexpected finding that α_{1b} -adrenergic receptors carrying relatively conservative substitutions of β_2 -adrenergic receptor-derived amino acid sequences in the C-terminal portion of the third intracellular loop activate Gq/11 proteins in the absence of agonist. Indeed, mutation of a single residue, Ala293, of the α_{1b} -adrenergic receptor to any other amino acid increased the agonist affinity of the receptor and produced constitutive stimulation of phosphatidylinositol hydrolysis (Kjelsberg et al., 1992). Using analogous

constitutively active mutants of the β_2 -adrenergic receptor, it was subsequently possible to demonstrate that some ligands that seem to be classic competitive antagonists on native receptors show selective high affinity for the inactive receptor and suppress basal receptor activity (Samama et al., 1994). Ligands possessing these properties have been termed “negative antagonists” or “inverse agonists”.

This and subsequent work involving a large number of GPCRs has affirmed the hypothesis that the receptor exists in spontaneous equilibrium between two conformations (active, R^* ; inactive, R) that differ in their ability to activate G proteins (Samama et al., 1993). In the native state, the receptor is maintained predominantly in the R conformation by intramolecular interactions within the transmembrane helical bundle; i.e., the spontaneous equilibrium heavily favors the inactive R state. Agonist binding, or selective mutagenesis, relieves these constraints, allowing the receptor to “relax” into the R^* conformation that enables G protein coupling. The extended ternary complex model developed to explain these phenomena proposes that the intrinsic efficacy of a ligand reflects its ability to alter the equilibrium between R and R^* (Lefkowitz et al., 1993). According to the model, *full agonists* stabilize the R^* conformation, pulling the equilibrium toward the active state to generate full receptor activation and a maximal response; *partial agonists* have lower intrinsic efficacy than full agonists, thus producing a submaximal system response and potential attenuation of full agonist activation; *antagonists* bind indiscriminately to both R and R^* , producing no physiological response but blocking the response to agonists; and *inverse agonists* act as antagonists in nonconstitutively active systems but have the added property of actively reducing receptor-mediated constitutive activity of GPCR systems by binding preferentially to R and pulling the equilibrium toward the inactive state. Even the behavior of “Protean agonists”, ligands that act as partial agonists in some systems and as inverse agonists in others can be accounted for within the extended ternary complex model if one assumes that the active receptor conformation produced by ligand binding ($H\text{-}R^*$) is of a lower efficacy than the spontaneously formed R^* state (Kenakin, 1995c). Under conditions of low basal activity, i.e., little or no spontaneously formed R^* , such a ligand would behave as a partial agonist, whereas under conditions of high basal activity, it would behave as an inverse agonist.

Three-State to Multistate Models

Although the ternary complex model can sufficiently explain the properties of agonism, antagonism, partial agonism, and inverse agonism, it is still limited in that it accommodates the existence of only two functional receptor states. However, several lines of experimental evidence suggest that multiple active states of GPCRs can exist.

Many GPCRs, either at physiologic levels or when overexpressed, are promiscuous; i.e., they stimulate different signaling pathways by activating more than one G protein pool. In a two-state model, where only a single R^* conformation exists, the agonist pharmacology of a receptor should be the same regardless of the response being measured. Yet a paradoxical reversal of relative efficacy of agonists has been described for several GPCRs that activate more than one stimulus-response element, including the 5-HT_{2C} receptor (Berg et al., 1998), pituitary adenylate cyclase-activating polypeptide receptor (Spengler et al., 1993), dopamine D2 receptor (Meller et al., 1992), and neurokinin (NK)-1 receptor (Sagan et al., 1999). Although differential stimulus pathway activation can occur through a strength-of-signal type of mechanism (i.e., a highly efficacious agonist might activate two pathways, whereas a weaker agonist may activate only the more sensitive one), the reversal of the relative efficacy of different agonists acting on the same receptor cannot be explained on the basis of a two-state model.

The demonstration that GPCRs exhibit ligand-specific activation states led to the proposal that three or even more active states of the same receptor may exist. In these three-state or multistate

models, certain agonists are predicted to induce distinct active conformations of the receptor by differentially exposing regions of the intracellular domains involved in coupling to different G protein pools. Indeed, multiple G protein-coupled states of the α_2 -adrenergic receptor can be distinguished using a variety of guanine nucleotide analogs (Seifert et al., 1999). Similarly, several receptor mutations have been described that produce constitutive activity that is restricted to a single signaling pathway among those ordinarily activated by the receptor (Perez et al., 1996). These mutations presumably restrict conformational isomerization of the receptor to a certain subset that promotes specific G protein-coupling conformations. Although the behavior of a mutated receptor cannot be extrapolated a priori to its wild-type counterpart, these data clearly demonstrate that subtle changes in receptor structure outside of the G protein-coupling domains, as might occur upon binding different agonist ligands, can alter G protein selectivity (Kenakin, 2002).

Biophysical evidence also supports the concept that different GPCR ligands induce distinct populations of receptor microconformation (Ghanouni et al., 2001). Fluorescence lifetime spectroscopy of β_2 -adrenergic receptors fluorescently labeled at Cys265 reveals a Gaussian distribution of environments for the probe, reflecting continuous fluctuations in receptor conformation. The addition of agonist or antagonist ligands changes the distribution of receptor conformations, reflecting the stabilization of a specific subset of conformations. Moreover, different agonists select different arrays of receptor conformation, consistent with the induction of ligand-selective active states.

The existence of multiple active receptor conformations makes it plausible that agonists can change not only the degree, but also the “quality”, of receptor activation. It is known that different areas of the cytosolic loops on receptors activate different G proteins (Wade et al., 1999). It is thus predictable that agonists producing distinct tertiary conformations of a receptor could expose these different G protein-activating sequences to produce differential activation of G proteins. This multistate model of GPCR activation provides the theoretical basis for the concept of signaling-selective agonism, also referred to as “agonist-specific trafficking of receptor signaling” (Kenakin, 1995a, b).

The Origins of GPCR Signaling Diversity

In contrast to the large number of GPCR sequences in the genome, there are comparatively few genes encoding heterotrimeric $G\alpha$ subunits. With input from a large number of receptors converging on a limited number of transducer elements, how do GPCRs generate diverse responses under different conditions and in different tissues?

Diversity in a Two-State Model

Numerous factors expand the signaling repertoire of heptahelical GPCRs. First is the sheer complexity of the receptors themselves. The majority of GPCR families consist of multiple receptor subtypes, often with different G protein-coupling specificities. For example, there are at least 12 different mammalian genes encoding serotonin receptors. Additional complexity derives from alternative splicing of receptor genes and RNA editing, generating multiple receptor isoforms with distinct biochemical properties from the same gene (Paasche et al., 2001).

Another layer of complexity arises from the ability of each G protein class to activate multiple downstream effectors. Both $G\alpha$ and $G\beta\gamma$ subunits contribute to the modulation, in a synergistic or antagonistic fashion, of either the same or unrelated effectors, resulting in dual intracellular signaling. An example is the simultaneous G_i/o -mediated inhibition of adenylate cyclase via the $G\alpha$ subunit and stimulation of phospholipase $C\beta$ via the $G\beta\gamma$ subunit (Exton, 1996). Further complexity arises from secondary modulation of intracellular effectors, for example, the

indirect activation of phospholipase A₂ following a rise in intracellular Ca²⁺ concentration (Clark et al., 1991).

Finally, there is the capacity for simultaneous activation of multiple G protein pools. Some Gi/o-coupled receptors, for example, mediate phosphoinositide hydrolysis through a pertussis toxin-insensitive pathway in addition to mediating pertussis toxin-sensitive inhibition of adenylate cyclase (Jones et al., 1991). Quantitative analysis of agonist-induced guanine nucleotide exchange on G α subunits has provided more definitive evidence. The dual coupling to Gs and Gq/11 family G proteins (Jin et al., 2001) or to Gi/o and Gq/11 family G proteins (Offermanns et al., 1994) has now been reported for many GPCRs. In some cases, a single receptor has been found to simultaneously activate members of three or even four unrelated classes of G protein (Gs, Gi/o, Gq/11, and G12) (Laugwitz et al., 1996).

A persistent question is whether such multiple G protein coupling represents pleiotropy (i.e., physiologic activation of different G protein species) or promiscuity (i.e., low-efficacy activation of nonpreferred G protein species as a result of receptor or G protein overexpression). In experimental systems, an agonist activating one GPCR that stimulates multiple G proteins frequently elicits signals downstream of each G protein with differing efficacy and/or potency (Offermanns et al., 1994). Unless there is reversal of agonist efficacy, such behavior is consistent with a two-state model in which the receptor can interact with both preferred and secondary transducers. Indeed, the emergence of a dual signaling commonly occurs as the level of receptor expression increases, suggesting that most GPCRs are promiscuous (Zhu et al., 1994; Cordeaux et al., 2000). Similar phenomena arise from changes in the expression levels of the participating G proteins (Nasman et al., 2001). On the other hand, many studies have demonstrated dual or multiple coupling in systems where the GPCR is constitutively expressed at low levels, consistent with physiologically relevant pleiotropic G protein coupling (Laugwitz et al., 1996; Jin et al., 2001).

Diversity Due to Multiple Receptor Conformations

Consistent with models of agonist-specific trafficking of receptor signaling, a number of structurally modified agonists for promiscuous peptide and nonpeptide GPCRs have been shown to promote selective G protein coupling (Spengler et al., 1993; Chakrabarti et al., 1995; MacKinnon et al., 2001). A similar phenomenon is signal-selective antagonism, in which an antagonist blocks only a subset of the signaling pathways elicited by an agonist. This has been clearly described for the cholecystokinin (CCK)-B (Pommier et al., 1999) and NK-1 receptors (Sagan et al., 1996).

Other examples of ligand-selective GPCR regulation include ligands that promote coupling to one G protein pool while antagonizing coupling to another. The gonadotropin-releasing hormone (GnRH) receptor “antagonist” Ant135-25 acts as an antagonist with respect to Gq coupling by the GnRH receptor but functions as an agonist in cellular contexts where the receptor is coupling to Gi (Maudsley et al., 2004). Similarly, the β_2 -adrenergic receptor antagonist ICI-118-551, which behaves as an inverse agonist for coupling to Gs, was recently found to act as an agonist for β_2 -adrenergic receptor coupling to Gi (Gong et al., 2002).

Studies of agonist-induced GPCR desensitization and endocytosis have likewise demonstrated the existence of ligand-specific receptor conformations. In a two-state model, it would be expected that the relative propensity of agonists to induce desensitization would parallel their relative efficacy for signaling. For μ -opioid receptor agonists, this is generally true, with the notable exceptions of methadone, ι - α -acetyl methadone, and buprenorphine, which induce disproportionate receptor phosphorylation and desensitization (Yu et al., 1997). Similarly, both enkephalins and morphine stimulate δ - and μ -opioid receptors, but only enkephalins induce rapid receptor internalization (Keith et al., 1996). Disparities between primary pathway

activation and desensitization have been also demonstrated for NK-1 (Maudsley et al., 1998) and serotonin 5-HT_{2C} receptors (Stout et al., 2002). Studies of the recovery from desensitization also suggest that agonists differentially affect receptor conformation. Whereas the resensitization of 5-HT₃ receptors after prolonged stimulation with partial agonists is monoexponential, desensitization induced by full agonists recovers with sigmoid kinetics, suggesting at least three transitional steps and up to four states (van Hooft and Vijverberg, 1996). Even more dramatic are GPCR antagonists that stimulate receptor internalization. The CCK receptor antagonist D-Tyr-Gly-[(Nle28,31,D-Trp30)cholecystokinin-26–32]-phenylester, which blocks CCK-mediated G protein activation, nonetheless causes profound receptor internalization (Roettger et al., 1997). Certain competitive antagonists of the angiotensin AT1a receptor, such as [sarcosine 1, Ile4, Ile8] Ang II, exhibit similar properties (Holloway et al., 2002).

The finding that synthetic ligands can induce two or more functionally distinct receptor conformations suggests the possibility that native hormones interacting with the same GPCR may exhibit agonist-specific trafficking. Does this phenomenon occur in nature? Some data suggest so. For example, fully processed follicle-stimulating hormone, a glycopeptide, has different effects on adenylate cyclase and phospholipase C activity than the less abundant circulating nonglycosylated form of follicle-stimulating hormone, which can even act as a receptor antagonist. These data suggest that post-translational processing in the gonadotrope modulates signaling by an endogenous peptide agonist (Arey et al., 1997). A more compelling case can be made for the chemokine type 7 (CCR7) receptor. CCL19 and CCL21, two endogenous CCR7 ligands that exhibit equivalent potency and efficacy with respect to calcium mobilization, differ dramatically in terms of their ability to cause receptor phosphorylation and desensitization. Moreover, only the “desensitizing” ligand CCL19 robustly activates the mitogen-activated protein (MAP) kinases extracellular signal-regulated kinases 1 and 2 (ERK1/2), hinting that desensitization itself may be a discretely regulating signaling event (Kohout et al., 2004).

Diversity Arising from Receptor Dimerization

Coprecipitation studies, complementation experiments using mutated or chimeric receptors, and fluorescence energy transfer measurements all support the hypothesis that many, if not most, GPCRs can form homodimers, heterodimers, or higher-order multimers (Angers et al., 2002). The assembly of receptor multimers establishes another level of conditioning that can affect GPCR ligand recognition, signaling, and intracellular trafficking. In the limit case, receptor dimerization is a prerequisite for the functionality of the receptor. The GABA_BR1 and GABA_BR2 receptors are nonfunctional as monomers. Only GABA_BR1-R2 heterodimers, which assemble in the endoplasmic reticulum-Golgi apparatus, are capable of membrane expression and signaling (Jones et al., 1998).

Numerous, less dramatic examples exist wherein dimerization alters receptor pharmacology and signaling. Dimerization of the μ - and δ -opioid receptors decreases the affinity for certain agonists, presumably by altering the conformation of extracellular receptor domains (George et al., 2000). The converse is true for heterodimers of the adenosine A_{2A} and dopamine D1 receptors, where selective agonist affinities are increased (Franco et al., 2000). Agonist efficacy can also be altered by GPCR dimerization. For example, heterodimerization between somatostatin SSTR5 and SSTR1 (Rocheville et al., 2000) and between μ - and δ -opioid receptors (George et al., 2000) increases both the intrinsic efficacy and apparent potency of some agonists.

Cross-talk between heterodimeric GPCR pairs can positively or negatively modulate the response to agonists binding to either member of the pair, resulting in either enhanced G protein activation or cross-inhibition (Ferre et al., 1998; Jordan and Devi, 1999). Even qualitative

changes in G protein-coupling specificity have been reported. Whereas μ - and δ -opioid receptors couple to pertussis toxin-sensitive G proteins when expressed individually, coexpression of these receptors results in opioid signaling in the presence of pertussis toxin, suggesting that μ - δ heterodimers can activate pertussis toxin-insensitive G proteins (George et al., 2000). Finally, heterodimerization can affect receptor desensitization and trafficking, thus modulating the duration of GPCR signaling. For example, the nonselective opioid agonist etorphine, which causes internalization of δ -, but not κ -opioid receptors, does not cause δ -opioid receptor internalization when it is coexpressed with the κ receptor (Jordan and Devi, 1999).

Nonreceptor Modifiers of GPCR Signaling

The pharmacology of at least two GPCRs is not determined exclusively by the intrinsic structure of receptor but by their interaction with the nonreceptor RAMP (receptor activity modifying protein) and RCP (receptor component protein) proteins (McLatchie et al., 1998; Evans et al., 2000). RAMPs form complexes with the calcitonin receptor-like receptor (CRLR) and calcitonin receptor and control receptor trafficking and function. RAMP binding to the CRLR is required for transport of nascent receptors to the plasma membrane. Furthermore, the specific CRLR-RAMP complex determines the ligand specificity of the receptor. The CRLR-RAMP1 complex acts as a receptor for the calcitonin gene-related peptides, a pleiotropic family of neuropeptides with homology to calcitonin, amylin, and adrenomedullin. When CRLR is coexpressed with RAMP2 and RCP, it functions as an adrenomedullin receptor. Similarly, complexes between a naturally occurring splice variant of the calcitonin receptor and RAMP1 or RAMP3 yield a functional amylin receptor. RAMP expression is modified under physiologic stress and in response to glucocorticoids, suggesting that cellular responsiveness to certain hormones can be regulated through the control of accessory protein expression.

Desensitization as a Modifier of Signal Quality

Mechanisms to dampen GPCR signals exist at every level, from receptor to G protein and effector. At the receptor level, two processes, termed heterologous and homologous desensitization, respectively, have been shown to play a role not only in limiting signal duration and intensity, but also in the determination of signal quality. Both processes are initiated by receptor phosphorylation. The activation of second messenger-dependent protein kinases, such as protein kinase A and protein kinase C, leads to phosphorylation of serine and/or threonine residues in the cytosolic loops and C-terminal tail of many GPCRs. Phosphorylation of these sites is sufficient to inhibit receptor-G protein coupling, and agonist occupancy is not required. Thus, unliganded receptors, even those for other ligands, can be desensitized in this manner. In contrast, homologous desensitization is specific for agonist-occupied GPCRs. It is a two-step process in which the receptor is first phosphorylated by one of a family of G protein-coupled receptor kinases (GRKs) and then binds to an arrestin protein that exhibits high affinity only for the agonist-occupied, GRK-phosphorylated form of the receptor (Stoffel et al., 1997). Arrestin binding serves both to sterically inhibit G protein coupling and to target the receptor to clathrin-coated pits for internalization (Ferguson, 2001).

The observation that protein kinase A phosphorylation of small peptides derived from the intracellular loops of the β_2 -adrenergic receptor converts them from *in vitro* activators of Gs to activators of Gi suggested the hypothesis that heterologous desensitization might cause a “switch” in β_2 -adrenergic receptor-G protein-coupling selectivity. Using both protein kinase A phosphorylation-site mutants expressed in cellular systems and purified recombinant receptors and G proteins *in vitro*, it has been possible to demonstrate that protein kinase A phosphorylation of the β_2 -adrenergic receptor both impairs Gs coupling and promotes receptor coupling to Gi (Daaka et al., 1997; Zamah et al., 2002). Not only does switching enhance desensitization by converting the receptor from an activator to an inhibitor of adenylyl cyclase,

it confers novel signaling properties on the receptor, such as the ability to stimulate Gi-dependent ERK1/2 activation. An analogous mechanism has been described for the Gs-coupled murine prostacyclin receptor. In this case, protein kinase A phosphorylation of Ser357 of the receptor is required for receptor coupling to Gi and Gq/11, but not to Gs (Lawler et al., 2001). Other GPCRs demonstrate type-selective desensitization of G protein coupling following protein kinase A or C activation. For example, Gq/11-mediated glutamate release by the subtype 1a metabotropic glutamate receptor (mGluR1a) is progressively desensitized by protein kinase C-mediated receptor phosphorylation, whereas a simultaneous inhibitory signal mediated through Gi/o coupling remains unaffected. The result is that in the presence of a persistent stimulus, the mGluR1a receptor switches from an activator to an inhibitor of glutamate release (Herrero et al., 1998). Collectively, these data suggest that regulation of the G protein-coupling specificity by receptor phosphorylation adds an additional level of control that permits the temporal resolution of cellular signaling elicited during the sustained stimulation of a receptor.

GPCR Coupling to Non-G Protein Effectors

A final source of GPCR signaling diversity arises from data suggesting that GPCRs transmit “G protein-independent” signals and that coupling to certain non-G protein effectors exhibits features consistent with agonist-specific trafficking. The intracellular domains of several GPCRs have been shown to bind to proteins that might function as alternative GPCR signal transducers, among which include GEFs for small G proteins, nonreceptor tyrosine kinases, and several proteins that function as adaptors or scaffolds. A specific peptide motif in the C terminus of the β_1 -adrenergic receptor binds directly to the postsynaptic density protein of 95 kDa/disc-large/zona occludens-1 (PDZ) domain of the cAMP-regulated Ras GEF (cyclic nucleotide-Ras GEF), allowing the receptor to stimulate guanine nucleotide exchange on the small G protein Ras (Pak et al., 2002). Another PDZ domain-containing protein, the Na⁺/H⁺ exchanger regulatory factor/ezrin binding protein 50, binds to the C terminus of β_2 -adrenergic and parathyroid hormone/parathyroid hormone-related protein receptors and confers the ability to regulate Na⁺/H⁺ exchanger 3 activity (Hall et al., 1998; Mahon et al., 2002). Stimulation of the Janus tyrosine kinase/signal transducer and activator of transcription pathway of transcriptional regulation by angiotensin AT1a receptors involves tyrosine phosphorylation of AT1a receptor tail by an Src family kinase, followed by association of Janus tyrosine kinase 2 with the receptor (Ali et al., 1997).

The most compelling evidence to date for G protein-independent signaling, however, involves the utilization of arrestins as alternative signal transducers. The two nonvisual arrestin isoforms (β -arrestin 1 and 2) can bind to several signaling proteins and recruit them to agonist-occupied GPCRs (Luttrell and Lefkowitz, 2002). Src family nonreceptor tyrosine kinases (Luttrell et al., 1999), components of the c-Jun N-terminal kinase 3 and ERK1/2 MAP kinase cascades (DeFea et al., 2000; McDonald et al., 2000), the E3 ubiquitin ligase mdm2 (Shenoy et al., 2001), and the phosphodiesterase 4D3 and 4D5 isoforms of cAMP phosphodiesterase (Perry et al., 2002) are recruited to GPCRs in this manner. In this distinctive model of GPCR signaling, β -arrestin binding is thought to confer enzymatic activity upon the receptor at the same time that it uncouples the receptor from its cognate G proteins. Indeed, the finding that arrestin-bound M₂ muscarinic acetylcholine receptors exhibit increased affinity for agonists, but not antagonists, has led to the speculation that the agonist-receptor-arrestin complex represents an “alterative ternary complex” (Gurevich et al., 1997).

Evidence that arrestin-bound GPCRs signal independently from G protein activation comes from several sources. Stimulation of a G protein-uncoupled Asp-Arg-Tyr/Ala-Ala-Tyr mutant of the AT_{1a} receptor with angiotensin II fails to induce detectable G protein loading but still promotes β -arrestin 2 recruitment, receptor internalization, and ERK1/2 activation that is

abolished when β -arrestin 2 is selectively depleted by RNA interference (Wei et al., 2003). In an analogous fashion, exposure of the wild-type AT1a receptor to the antagonist [sarcosine 1, Ile4, Ile8] Ang II induces β -arrestin 2 recruitment and ERK1/2 activation in the absence of detectable G protein activation. This signal too is abolished by the depletion of β -arrestin 2 by RNA interference. Analogous results have been reported for the β_2 -adrenergic receptor, where the inverse agonist, ICI-118-551, acts as a partial agonist for ERK1/2 activation (Azzi et al., 2003). The ERK1/2 response is absent in β -arrestin 1/2 null murine embryo fibroblasts but can be restored by expression of β -arrestin 2. This β -arrestin-dependent ERK1/2 activation has a slower onset and more sustained duration than G protein-mediated ERK1/2 activation (Ahn et al., 2004). For GPCRs, such as the NK-1, AT1a, and V2 vasopressin receptors, all of which form stable GPCR-arrestin complexes, the β -arrestin-dependent “signalsome” seems to remain intact as the receptor transits the endosomal compartment, resulting in activation of a spatially constrained, extranuclear pool of activated ERK1/2 (DeFea et al., 2000; Tohgo et al., 2002). In contrast, G protein-dependent ERK1/2 activation tends to promote nuclear translocation of the kinase and ERK1/2-dependent transcriptional responses. Thus, signal strength, duration, subcellular localization, and functional consequence are all dictated by the mechanism of signal propagation.

The Origins of Signaling Specificity

The converse of signaling diversity is signaling specificity, the constraint of responses to specific cells or tissues, even when the stimulus itself may be systemic, as in the case of a circulating hormone. In essence, there must be mechanisms to limit “signal spread” and work against promiscuity.

There are numerous factors, both intracellular and extracellular, within the classic conceptualization of GPCR signaling that promote specificity. For example, the highly localized release and rapid reuptake or extracellular degradation of neurotransmitters within the synaptic space provides a highly effective means of confining signals spatially. For systemic hormones, tissue-selective expression of receptor subtypes comes into play. A typical cell may express more than 10 different GPCR genes, different combinations of G protein subunits, and multiple isoforms of effector molecules. The differential expression of these various proteins imposes signal specificity at many levels, resulting in hormone responses that are customized for the specific cell type. Signal duration and intensity are selectively modulated through rapid receptor desensitization and internalization and more slowly by down-regulation of receptor expression (Ferguson, 2001). Nonetheless, GPCR signaling systems seem to exhibit higher levels of preorganization than can be accounted for by control of ligand availability and tissue-specific expression of transducer elements. Numerous studies have indicated that different GPCRs coupling to the same G protein in a single cell can elicit different biochemical or cellular responses (Harper et al., 1985; Steinberg and Brunton, 2001). A one-dimensional view of GPCR signal organization cannot readily account for such observations. At least two additional factors, compartmentalization of signaling proteins within membrane microdomains and preorganization of GPCR signaling units through interactions with anchoring and scaffolding proteins, seem to play important roles in GPCR signaling specificity.

Specificity Arising within Membrane Microdomains

For most of the early years, GPCR signal transduction was conceptualized along the lines of a “Brownian motion” model in which the random thermodynamic collision of signaling proteins within the plane of the plasma membrane was responsible for the flow of information from receptor to G protein to effector. Such a random process, however, would be energetically expensive for complex organisms that require rapidity and specificity of signaling function. Furthermore, mounting experimental evidence indicates that GPCRs, G proteins, and effectors are not randomly distributed in the plasma membrane. Indeed, it has been suggested that GPCR

signaling mainly occurs within specialized microdomains, implying that the efficiency and specificity of signal transduction are dictated by the stoichiometry of transducer elements within spatially discrete membrane regions (Neubig, 1994; Ostrom et al., 2000).

One of the most studied forms of membrane microdomain are regions of high-density cholesterol, gangliosides, and sphingolipids, referred to as caveolae or lipid rafts (Galbiati et al., 2001). Many GPCRs have been shown to localize to these structures, often aided by C-terminal palmitoylation. A striking example of how localization of a GPCR within lipid microdomains dictates signal selectivity is the oxytocin receptor. When present in caveolae, the receptor exerts a proliferative effect upon human embryonic kidney 293 cells through a Gq-mediated mechanism involving cross-talk with epidermal growth factor (EGF) receptors that also concentrate in caveoli. Oxytocin-stimulated EGF receptor “transactivation” is independent of phospholipase C, c-Src, or phosphoinositide-3 kinase activity. In contrast, activation of oxytocin receptors outside of rafts produces the exact opposite effect, an inhibition of cell proliferation that is Gi-, phospholipase C-, c-Src-, and phosphoinositide-3 kinase-dependent (Rimoldi et al., 2003). In addition to lipid rafts, other regions of the plasma membrane where signaling proteins are aggregated, such as focal adhesion complexes and clathrin-coated pits, seem to serve as sites of GPCR signal integration and specificity.

Scaffolding and Preorganization as Determinants of Signal Specificity

It is now clear that the intracellular domains of GPCRs participate in numerous interactions with cellular proteins that serve to organize the partners in a signaling cascade (Brady and Limbird, 2002). In essence, these scaffolds assemble GPCRs, G proteins, effectors, and downstream elements into prearranged “solid-state” signaling devices that impose crucial spatial resolution and signaling compartmentalization on GPCR-mediated signaling systems. For example, β_2 -adrenergic receptors have a well documented association with plasma membrane A kinase anchoring proteins (Malbon et al., 2004). A kinase anchoring proteins act as dynamic platforms that orchestrate the interactions of protein kinases, including tyrosine kinases, protein phosphatases (e.g., calcineurin), and cytoskeletal elements with β_2 -adrenoceptor. Other preformed complexes between the β_2 -adrenoceptor and potential effectors have been reported, including association with the EGF receptor, a target for GPCR-stimulated transactivation (Maudsley et al., 2000), and recently with the BKCa large-conductance Ca^{2+} -dependent potassium channel (Liu et al., 2004).

Several PDZ domain-containing proteins, in addition to Na^+/H^+ exchanger regulatory factor/ezrin binding protein 50, interact with the distal C terminus of select GPCRs and direct the assembly of functional protein networks (Bockaert et al., 2003). This preorganization of GPCRs into signalsomes seems to be particularly prevalent within the central nervous system, where signaling efficiency and spatial constraint are at a premium. Postsynaptic density protein of 95 kDa, membrane-associated guanylate kinase inverted-2, SH3 multiple ankyrin domain-containing protein/somatostatin receptor-interacting protein, protein interacting with C kinase 1, multi-PDZ domain protein 1, and spinophilin contain between 1 and 13 PDZ domains, and all can associate with GPCRs. Their binding to receptors has been reported to modulate such diverse properties as receptor dimerization, sub-cellular localization, effector coupling, and trafficking.

Other GPCR protein-protein interactions seem to influence receptor localization and trafficking or dictate the specificity of the GPCR-G protein-effector interaction (Bockaert et al., 2003). The Homer proteins, which are involved in the control of actin filament dynamics, interact with polyproline sequences found in mGluR1a, mGluR5 metabotropic glutamate receptor, SH3 multiple ankyrin domain-containing protein/somatostatin receptor-interacting protein, inositol 1,4,5-trisphosphate receptors, ryanodine receptors, and P/Q-type calcium channels. Homer proteins function in the organization of postsynaptic glutaminergic sites, and

excitation-dependent expression of Homer isoforms affects mGluR trafficking and targeting to axons and dendrites. The dopamine receptor-interacting protein of 78 kDa binds to a C-terminal hydrophobic motif in D1 dopamine receptors and controls post-translational processing of the receptor, whereas binding of the t-complex testis-expressed 1 protein to the C terminus of rhodopsin targets the receptor to the rod outer segment. The angiotensin receptor-associated protein binds to the C terminus of the angiotensin AT1a receptor and modulates receptor coupling to phospholipase C and Ang II-stimulated transcriptional activation and cell proliferation. Actin-binding protein 280 (filamin A) interacts with the third intracellular loop of the D2 and 3 dopamine receptors. Actin-binding protein 280 binding fosters D2 receptor clustering at the plasma membrane and enhances the ability of D2 receptors to inhibit adenylate cyclase. The 14-3-3 proteins, a family of at least seven acidic brain proteins that bind to phosphorylated serine/threonine motifs, interact with the third intracellular loops of α_2 -adrenergic and GABA_BR1 receptors and seem to regulate GPCR dimerization, activation of the Ras/Raf cascade, and the localization of regulator of G protein signaling proteins. Collectively, these examples illustrate the extent to which scaffolding protein interactions preorganize GPCR signals and ensure signal fidelity.

Therapeutic Implications

Pharmacologic agents acting via GPCRs have traditionally been classified as agonists, partial agonists, or antagonists based on the two-state model of receptor function embodied in the ternary complex model. Agonists and partial agonists are assumed to differ only in intrinsic efficacy, the ability to stabilize a receptor in the R* conformation. The active conformation of the receptor is presumed to be the same wherever the receptor is expressed and irrespective of the stimulus-response element being activated. However, as data continue to emerge indicating that GPCR signal transduction is both more diverse and more specific than originally imagined, these fundamental concepts of receptor biology are being refined. The existence of multiple active receptor states, receptor-receptor and receptor-scaffold interactions that modify receptor pharmacology, possible G protein-independent signaling, and tissue-selective preorganization of signals presents the opportunity to develop drugs that induce only a subset of the GPCR response profile. At the same time, signaling complexity implies the existence of pitfalls arising from unintended drug action.

The potential therapeutic implications of agonist-selective signal trafficking extend beyond regulation of receptor-G protein coupling. For example, ligands that selectively induce receptor internalization could be beneficial in the treatment of tolerance (Yu et al., 1997). Similarly, selective GPCR internalization may prevent HIV-1 infection through chemo-kine receptor fusion. Ligands that cause internalization of CXCR4 (Amara et al., 1997) or CCR5 (Simmons et al., 1997) have been shown to protect against HIV-1 infection in vitro. Selective removal of chemokine receptors from the cell surface could be superior to blocking chemokine receptor interaction with HIV viral coat proteins because it would prevent the possible rapid emergence of resistant HIV variants through therapeutic pressure and mutation (Domingo et al., 1997). Receptor dimerization may also generate therapeutic targets with unique pharmacology and signaling characteristics. Receptor dimers have been implicated in numerous areas, including HIV-1 infection (Kuhmann et al., 2000) and the function of cannabinoid receptors (Mukhopadhyay et al., 2000), GABA_B receptors (Jones et al., 1998), adenosine A1 receptors (Ciruela et al., 1997), δ -opioid receptors (Cvejic and Devi, 1997), β_2 -adrenoreceptors (Hebert et al., 1996), and calcium-sensing receptors (Bai et al., 1998). Drugs that selectively target unique ligand-binding pockets generated through dimerization may produce effects not associated with monomeric receptor signaling. Finally, the ability of ligands to selectively activate non-G protein-mediated signaling through GPCRs may prove therapeutically relevant. In this context, the finding that antagonist or inverse agonist ligands of the β_2 -adrenergic and AT1a receptors can stimulate MAP kinase signaling through β -arrestin-mediated pathways

(Azzi et al., 2003; Wei et al., 2003) interjects a note of caution, in that antagonists that provide benefit in heart failure by antagonizing G protein activation could act counterproductively if they also stimulate pathways involved in cardiomyocyte hypertrophy and vascular smooth muscle hyperplasia.

The concept of agonist-selective trafficking of receptor signaling has received much attention because it prompts the search for drugs that can change the quality as well as the quantity of efficacy (Kenakin, 2002). It is now clear that even the terms “agonist” and “antagonist” are strictly context-dependent. If a ligand can discriminate between multiple active receptor conformations to preferentially activate a subset of effector pathways, then agonist efficacy needs to be defined in terms of the assay used to measure receptor activation. In the broadest sense, all ligands that productively engage a GPCR have the potential to be “pluriprotean”, acting as both agonist and antagonist depending on the signaling function and the nature of the cellular environment. In some cases, it may be useful to reclassify compounds based on a full profile of stimulus-response coupling. Separating agonists in this manner could offer insights into preferred profiles of agonism as compounds progress from screening assays into therapeutically oriented secondary assays. In situations where an original screening program was limited to measuring a single signaling pathway, consideration should be given to reexamining the properties of some compounds that were initially disregarded on the basis of apparently poor efficacy. As ongoing work provides greater insights into the multitude of factors that give texture to GPCR signaling, the challenge will be to exploit the complex behavior of these receptors for therapeutic advantage while minimizing the pitfalls associated with too narrow a vision of receptor function.

Conclusions

For most of its experimental lifetime, information flow through GPCRs has been envisioned as unidirectional; i.e., changes in receptor conformation produced by agonist binding promote the transfer of information from outside the cell inwards. Recent experimentation, however, has demonstrated that receptor conformation is also controlled by protein-protein interactions occurring inside the cell. Receptor dimerization and interactions with scaffolding and signaling proteins can modify ligand selectivity and predetermine, from a menu of available options, which intracellular responses will predominate. In essence, the influences on receptor conformation are bidirectional; internal factors change the conformation of the receptor to reflect the status of the intracellular milieu while extracellular factors, i.e., agonists, convey information to the cell about the external environment. This concept has critical implications for receptor theory.

If one accepts the premise that the association of GPCRs with intracellular proteins places a constraint on the array of active conformations that the receptor can adopt, then even within a single cell there may exist different “flavors” of the same receptor that are prewired to produce specific responses to preferred ligands. In the limit case of one cell expressing multiple copies of the same receptor, it seems unlikely that every copy of the receptor would be coupled to the same signal transduction machinery at all times. This is certainly true if the receptor is susceptible to G protein switching induced by heterologous desensitization Daaka et al., 1997) or capable of signaling through β -arrestins (Luttrell and Lefkowitz, 2002). These various receptor flavors could preferentially interact with different ligands, e.g., CRLR-RAMP1-recognizing calcitonin gene-related peptides and CRLR-RAMP2-RCP-binding adrenomedullin (McLatchie et al., 1998; Evans et al., 2000), or activate different down-stream effectors in response to the same ligand. We have recently invoked the latter scenario with respect to tissue-specific differences in GnRH receptor signaling (Maudsley et al., 2004).

An interesting corollary of this postulate is that GPCRs may not be “truly” promiscuous in the sense of a single receptor interacting with multiple effector pathways in a random manner. If GPCRs can be preassembled with their downstream transduction machinery, it may be biophysically more efficient to generate a variety of receptor flavors that are hard-wired to specific transduction pathways than to switch a single receptor between different pathways. Such a model could accommodate experimentally observed promiscuity if the primary response pathway is defined as that mediated by the receptor flavor with the highest affinity for a given agonist, whereas promiscuous coupling results from the activation of alternative receptor flavors that have lower affinity for the ligand and therefore are only activated by higher agonist concentrations. Reversal of agonist efficacy could similarly result from altered ligand selectivity imposed from inside the cell through protein-protein interactions affecting ligand affinity. Although selective examples of each of these phenomena exist, additional experimentation will be required to determine whether these mechanisms have broad applicability to models of GPCR signaling.

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ABBREVIATIONS

GPCR, G protein-coupled receptor
 GEF, guanine nucleotide exchange factor
 5-HT, 5-hydroxytryptamine
 NK, neurokinin
 CCK, cholecystokinin
 GnRH, gonadotropin-releasing hormone
 ICI-118-551, ($\pm$)-1-[2,3-(dihydro-7-methyl-1*H*-inden-4-yl)oxy]-3-[(1-methylethyl)-amino]-2-butanol hydrochloride
 Ang, angiotensin
 MAP, mitogen-activated protein
 ERK1/2, extracellular signal-regulated kinases 1 and 2
 RAMP, receptor activity modifying protein
 RCP, receptor component protein
 CRLR, calcitonin receptor-like receptor
 GRK, G protein-coupled receptor kinase
 mGluR, metabotropic glutamate receptor
 PDZ, postsynaptic density protein of 95 kDa/disc-large/zona occludens-1
 EGF, epidermal growth factor
 HIV, human immunodeficiency virus
 Ant135-25, Ac-D-Nal(2)-D-4-CIPhe-D-Pal-Ser-1-MePal-D-IsopropylLys-Leu-IsopropylLys-Pro-D-AlaNH₂.

References

- Ahn S, Shenoy SK, Wei H, Lefkowitz RJ. Differential kinetic and spatial patterns of β -arrestin and G protein-mediated ERK activation by the angiotensin II receptor. *J Biol Chem* 2004;279:3551–3558.
- Ali MS, Sayeski PP, Dirksen LB, Hayzer DJ, Marrero MB, Bernstein KE. Dependence on the motif YIPP for the physical association of Jak2 kinase with the intracellular carboxyl tail of the angiotensin II AT1 receptor. *J Biol Chem* 1997;272:23382–23388. [PubMed: 9287353]

- Amara A, Gall SL, Schwartz O, Salamero J, Montes M, Loetscher P, Baggiolini M, Virelizier JL, Arenzana-Seisdedos F. HIV coreceptor downregulation as antiviral principle: SDF-1 α -dependent internalization of the chemokine receptor CXCR4 contributes to inhibition of HIV replication. *J Exp Med* 1997;186:139–146. [PubMed: 9207008]
- Angers S, Salahpour A, Bouvier M. Dimerization: an emerging concept for G protein-coupled receptor ontogeny and function. *Annu Rev Pharmacol Toxicol* 2002;42:409–435. [PubMed: 11807178]
- Arey BJ, Stevis PE, Deecher DC, Shen ES, Frail DE, Negro-Vilar A, Lopez FJ. Induction of promiscuous G protein coupling of the follicle-stimulating hormone (FSH) receptor: a novel mechanism for transducing pleiotropic actions of FSH isoforms. *Mol Endocrinol* 1997;11:517–526. [PubMed: 9139796]
- Azzi M, Charest PG, Angers S, Rousseau G, Kohout T, Bouvier M, Pinyero G. β -Arrestin-mediated activation of MAPK by inverse agonists reveals distinct active conformations for G protein-coupled receptors. *Proc Natl Acad Sci USA* 2003;100:11406–11411. [PubMed: 13679574]
- Bai M, Trivedi S, Brown EM. Dimerization of the extracellular calcium-sensing receptor (CaR) on the cell surface of CaR-transfected HEK293 cells. *J Biol Chem* 1998;273:23605–23610. [PubMed: 9722601]
- Berg KA, Maayani S, Goldfarb J, Scaramellini C, Leff P, Clarke WP. Effector pathway-dependent relative efficacy at serotonin type 2A and 2C receptors: evidence for agonist-directed trafficking of receptor stimulus. *Mol Pharmacol* 1998;54:94–104. [PubMed: 9658194]
- Bockaert J, Marin P, Dumuis A, Fagni L. The 'magic tail' of G protein-coupled receptors: an anchorage for functional protein networks. *FEBS Lett* 2003;546:65–72. [PubMed: 12829238]
- Brady AE, Limbird LE. G protein-coupled receptor interacting proteins: emerging roles in localization and signal transduction. *Cell Signal* 2002;14:297–309. [PubMed: 11858937]
- Brink CB, Harvey BH, Bodenstein J, Venter DP, Oliver DW. Recent advances in drug action and therapeutics: relevance of novel concepts in G-protein-coupled receptor and signal transduction pharmacology. *Br J Clin Pharmacol* 2004;57:373–387. [PubMed: 15025734]
- Chakrabarti S, Prather PL, Yu L, Law PY, Loh HH. Expression of the μ -opioid receptor in CHO cells: ability of μ -opioid ligands to promote α -azidoanilido[32P]GTP labeling of multiple G protein alpha subunits. *J Neurochem* 1995;64:2534–2543. [PubMed: 7760033]
- Ciruela F, Saura C, Canela EI, Mallol J, Lluís C, Franco R. Ligand-induced phosphorylation, clustering and desensitization of A1 adenosine receptors. *Mol Pharmacol* 1997;52:788–797. [PubMed: 9351969]
- Clark JD, Lin LL, Kriz RW, Ramesha CS, Sultzman LA, Lin AY, Milona N, Knopf JL. A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-dependent translocation domain with homology to PKC and GAP. *Cell* 1991;65:1043–1051. [PubMed: 1904318]
- Cordeaux Y, Briddon SJ, Megson AE, McDonnell J, Dickenson JM, Hill SJ. Influence of receptor number on functional responses elicited by agonists acting at the human adenosine A(1) receptor: evidence for signaling pathway-dependent changes in agonist potency and relative intrinsic activity. *Mol Pharmacol* 2000;58:1075–1084. [PubMed: 11040056]
- Cvejic S, Devi LA. Dimerization of the delta opioid receptor: implication for a role in receptor internalization. *J Biol Chem* 1997;272:26959–26964. [PubMed: 9341132]
- Daaka Y, Luttrell LM, Lefkowitz RJ. Switching of the coupling of the β 2-adrenergic receptor to different G proteins by protein kinase A. *Nature (Lond)* 1997;390:88–91. [PubMed: 9363896]
- DeFea KA, Zalevsky J, Thoma MS, Dery O, Mullins RD, Bunnett NW. β -Arrestin-dependent endocytosis of proteinase-activated receptor 2 is required for intracellular targeting of activated ERK1/2. *J Cell Biol* 2000;148:1267–1281. [PubMed: 10725339]
- DeLean A, Stadel JM, Lefkowitz RJ. A ternary complex model explains the agonist specific binding properties of the adenylate cyclase-coupled beta-adrenergic receptor. *J Biol Chem* 1980;255:7108–7117. [PubMed: 6248546]
- Domingo E, Menendez-Arias L, Quinones-Mateu ME, Holguin A, Gutierrez-Rivas M, Martinez MA, Quer J, Novella IS, Holland JJ. Viral quasispecies and the problem of vaccine-escape and drug-resistant mutants. *Prog Drug Res* 1997;48:99–128. [PubMed: 9204684]

- Evans BN, Rosenblatt MI, Mnayer LO, Oliver KR, Dickerson IM. CGRP-RCP, a novel protein required for signal transduction at calcitonin gene-related peptide and adrenomedullin receptors. *J Biol Chem* 2000;275:31438–31443. [PubMed: 10903324]
- Exton JH. Regulation of phosphoinositide phospholipases by hormones, neurotransmitters and other agonists linked to G proteins. *Annu Rev Pharmacol Toxicol* 1996;36:481–509. [PubMed: 8725399]
- Ferguson SS. Evolving concepts in G protein-coupled receptor endocytosis: the role in receptor desensitization and signaling. *Pharm Rev* 2001;53:1–24. [PubMed: 11171937]
- Ferre S, Torvinen M, Antoniou K, Irenius E, Civelli O, Arenas E, Fredholm BB, Fuxe K. Adenosine A1 receptor-mediated modulation of dopamine D1 receptors in stably cotransfected fibroblast cells. *J Biol Chem* 1998;273:4718–4724. [PubMed: 9468534]
- Franco R, Ferre S, Agnati L, Torvinen M, Gines S, Hillion J, Casado V, Lledo P, Zoli M, Lluís C, Fuxe K. Evidence for adenosine/dopamine receptor interactions: indications for heteromerization. *Neuropsychopharmacology* 2000;23:S50–S59. [PubMed: 11008067]
- Galbiati F, Razani B, Lisanti MP. Emerging themes in lipid rafts and caveolae. *Cell* 2001;106:403–411. [PubMed: 11525727]
- George SR, Fan T, Xie Z, Tse R, Tam V, Varghese G, O'Dowd BF. Oligomerization of μ - and δ -opioid receptors. Generation of novel functional properties. *J Biol Chem* 2000;275:26128–26135. [PubMed: 10842167]
- Ghanouni P, Gryczynski Z, Steenhuis JJ, Lee TW, Farrens DL, Lakowicz JR, Kobilka BK. Functionally different agonists induce distinct conformations in the G protein coupling domain of the β_2 adrenergic receptor. *J Biol Chem* 2001;276:24433–24436. [PubMed: 11320077]
- Gong H, Sun H, Koch WJ, Rau T, Eschenhagen T, Ravens U, Heubach JF, Adamson DL, Harding SE. Specific $\beta(2)$ AR blocker ICI 118,551 actively decreases contraction through a G(i)-coupled form of the $\beta(2)$ AR in myocytes from failing human heart. *Circulation* 2002;105:2497–2503. [PubMed: 12034656]
- Gurevich VV, Pals-Rylaarsdam R, Benovic JL, Hosey MM, Onorato JJ. Agonist-receptor-arrestin, an alternative ternary complex with high agonist affinity. *J Biol Chem* 1997;272:28849–28852. [PubMed: 9360951]
- Hall RA, Premont RT, Chow CW, Blitzer JT, Pitcher JA, Claing A, Stoffel RH, Barak LS, Shenolikar S, Weinman EJ, Grinstein S, Lefkowitz RJ. The β_2 -adrenergic receptor interacts with the Na^+/H^+ -exchanger regulatory factor to control Na^+/H^+ exchange. *Nature (Lond)* 1998;392:626–630. [PubMed: 9560162]
- Harper JF, Haddox MK, Johanson RA, Hanley RM, Steiner AL. Compartmentation of second messenger action: immunocytochemical and biochemical evidence. *Vitam Horm* 1985;42:197–252. [PubMed: 3006347]
- Hebert TE, Moffett S, Morello JP, Loisel TP, Bichet DG, Barret C, Bouvier M. A peptide derived from a β_2 -adrenergic receptor transmembrane domain inhibits both receptor dimerization and activation. *J Biol Chem* 1996;271:16384–16392. [PubMed: 8663163]
- Herrero I, Miras-Portugal MT, Sanchez-Prieto J. Functional switch from facilitation to inhibition in the control of glutamate release by metabotropic glutamate receptors. *J Biol Chem* 1998;273:1951–1958. [PubMed: 9442030]
- Holloway AC, Qian H, Pipolo L, Ziogas J, Miura S-I, Karnik S, Southwell BR, Lew MJ, Thomas WG. Side-chain substitutions within angiotensin II reveal different requirements for signaling, internalization, and phosphorylation of type 1A angiotensin receptors. *Mol Pharmacol* 2002;61:768–777. [PubMed: 11901215]
- Jin LQ, Wang HY, Friedman E. Stimulated D(1) dopamine receptors couple to multiple $G\alpha$ proteins in different brain regions. *J Neurochem* 2001;78:981–990. [PubMed: 11553672]
- Jones KA, Borowsky B, Tamm JA, Craig DA, Durkin MM, Dai M, Yao WJ, Johnson M, Gunwaldsen C, Huang LY, et al. GABA(B) receptors function as a heteromeric assembly of the subunits GABA(B)R1 and GABA(B)R2. *Nature (Lond)* 1998;396:674–679. [PubMed: 9872315]
- Jones SB, Halenda SP, Bylund DB. Alpha 2-adrenergic receptor stimulation of phospholipase A2 and of adenylate cyclase in transfected Chinese hamster ovary cells is mediated by different mechanisms. *Mol Pharmacol* 1991;39:239–245. [PubMed: 1847497]

- Jordan BA, Devi LA. G-protein-coupled receptor heterodimerization modulates receptor function. *Nature (Lond)* 1999;399:697–700. [PubMed: 10385123]
- Karlin A. On the application of “a plausible model” of allosteric proteins to the receptor for acetylcholine. *J Theor Biol* 1967;16:306–320. [PubMed: 6048545]
- Keith DE, Murray SR, Zaki PA, Chu PC, Lissin DV, Kang L, Evans CJ, von Zastrow M. Morphine activates opioid receptors without causing their rapid internalization. *J Biol Chem* 1996;271:19021–19024. [PubMed: 8702570]
- Kenakin T. Agonist-receptor efficacy. I: Mechanisms of efficacy and receptor promiscuity. *Trends Pharmacol Sci* 1995a;16:188–192. [PubMed: 7652927]
- Kenakin T. Agonist-receptor efficacy. II. Agonist trafficking of receptor signals. *Trends Pharmacol Sci* 1995b;16:232–238. [PubMed: 7667897]
- Kenakin T. Drug efficacy at G protein-coupled receptors. *Annu Rev Pharmacol Toxicol* 2002;42:349–379. [PubMed: 11807176]
- Kenakin TP. Pharmacological proteus? *Trends Pharmacol Sci* 1995c;16:256–258. [PubMed: 7482982]
- Kjelsberg MA, Cotecchia S, Ostrowski J, Caron MG, Lefkowitz RJ. Constitutive activation of the $\alpha 1B$ -adrenergic receptor by all amino acid substitutions at a single site. Evidence for a region which constrains receptor activation. *J Biol Chem* 1992;267:1430–1433. [PubMed: 1346134]
- Kohout TA, Nicholas SL, Perry SJ, Reinhart G, Junger S, Struthers RS. Differential desensitization, receptor phosphorylation, β -arrestin recruitment and ERK1/2 activation by the two endogenous ligands for the CC chemokine receptor 7. *J Biol Chem* 2004;279:23214–23222. [PubMed: 15054093]
- Kuhmann SE, Platt EJ, Kozak SL, Kabat D. Cooperation of multiple CCR5 coreceptors is required for infections by human immunodeficiency virus type 1. *J Virol* 2000;74:7005–7015. [PubMed: 10888639]
- Laugwitz KL, Allgeier A, Offermanns S, Spicher K, Van Sande J, Dumont JE, Schultz G. The human thyrotropin receptor: a heptahelical receptor capable of stimulating members of all four G protein families. *Proc Natl Acad Sci USA* 1996;93:116–120. [PubMed: 8552586]
- Lawler OA, Miggin SM, Kinsella BT. Protein kinase A-mediated phosphorylation of serine 357 of the mouse prostacyclin receptor regulates its coupling to G(s)-, to G(i)- and to G(q)-coupled effector signaling. *J Biol Chem* 2001;276:33596–33607. [PubMed: 11443126]
- Lefkowitz RJ, Cotecchia S, Samama P, Costa T. Constitutive activity of receptors coupled to guanine nucleotide regulatory proteins. *Trends Pharmacol Sci* 1993;14:303–307. [PubMed: 8249148]
- Liu G, Shi J, Yang L, Cao L, Park SM, Cui J, Marx SO. Assembly of a Ca^{2+} -dependent BK channel signaling complex by binding to $\beta 2$ adrenergic receptor. *EMBO (Eur Mol Biol Organ) J* 2004;23:2196–2205.
- Luttrell LM, Ferguson SSG, Daaka Y, Miller WE, Maudsley S, Della Rocca GJ, Lin F-T, Kawakatsu H, Owada K, Luttrell DK, et al. β -Arrestin-dependent formation of $\beta 2$ adrenergic receptor/Src protein kinase complexes. *Science (Wash DC)* 1999;283:655–661.
- Luttrell LM, Lefkowitz RJ. The role of β -arrestins in the termination and transduction of G-protein-coupled receptor signals. *J Cell Sci* 2002;115:455–465. [PubMed: 11861753]
- MacKinnon AC, Waters C, Jodrell D, Haslett C, Sethi T. Bombesin and substance P analogues differentially regulate G-protein coupling to the bombesin receptor. Direct evidence for biased agonism. *J Biol Chem* 2001;276:28083–28091. [PubMed: 11323408]
- Mahon MJ, Donowitz M, Yun CC, Segre GV. Na^{+}/H^{+} exchanger regulatory factor 2 directs parathyroid hormone 1 receptor signalling. *Nature (Lond)* 2002;417:858–861. [PubMed: 12075354]
- Malbon CC, Tao J, Wang HY. AKAPs (A-kinase anchoring proteins) and molecules that compose their G-protein-coupled receptor signalling complexes. *Biochem J* 2004;379:1–9. [PubMed: 14715081]
- Maudsley S, Davidson L, Pawson AJ, Chan R, de Maturana RL, Millar RP. Gonadotropin-releasing hormone (GnRH) antagonists promote proapoptotic signaling in peripheral reproductive tumor cells by activating a $G_{\alpha i}$ -coupling state of the type I GnRH receptor. *Cancer Res* 2004;64:7533–7544. [PubMed: 15492280]
- Maudsley S, Gent JP, Findlay JB, Donnelly D. The relationship between the agonist-induced activation and desensitization of the human tachykinin NK2 receptor expressed in *Xenopus* oocytes. *Br J Pharmacol* 1998;124:675–684. [PubMed: 9690859]

- Maudsley S, Pierce KL, Zamah AM, Miller WE, Ahn S, Daaka Y, Lefkowitz RJ, Luttrell LM. The $\beta(2)$ -adrenergic receptor mediates extracellular signal-regulated kinase activation via assembly of a multi-receptor complex with the epidermal growth factor receptor. *J Biol Chem* 2000;275:9572–9580. [PubMed: 10734107]
- McDonald PH, Chow C-W, Miller WE, LaPorte SA, Field ME, Lin F-T, Davis RJ, Lefkowitz RJ. β -Arrestin 2: A receptor-regulated MAPK scaffold for the activation of JNK3. *Science (Wash DC)* 2000;290:1574–1577.
- McLatchie LM, Fraser NJ, Main MJ, Wise A, Brown J, Thompson N, Solari R, Lee MG, Foord SM. RAMPs regulate the transport and ligand specificity of the calcitonin-receptor-like receptor. *Nature (Lond)* 1998;393:333–339. [PubMed: 9620797]
- Meller E, Puza T, Diamond J, Lieu HD, Bohmaker K. Comparative effects of receptor inactivation, 17 β -estradiol and pertussis toxin on dopaminergic inhibition of prolactin secretion in vitro. *J Pharmacol Exp Ther* 1992;263:462–469. [PubMed: 1359107]
- Mukhopadhyay S, McIntosh HH, Houston DB, Howlett AC. The CB(1) cannabinoid receptor juxtamembrane C-terminal peptide confers activation to specific G proteins in brain. *Mol Pharmacol* 2000;57:162–170. [PubMed: 10617691]
- Nasman J, Kukkonen JP, Ammoun S, Akerman KE. Role of G-protein availability in differential signaling by $\alpha 2$ -adrenoceptors. *Biochem Pharmacol* 2001;62:913–922. [PubMed: 11543726]
- Neubig RR. Membrane organization in G-protein mechanisms. *FASEB J* 1994;8:939–946. [PubMed: 8088459]
- Offermanns S, Wieland T, Homann D, Sandmann J, Bombien E, Spicher K, Schultz G, Jakobs KH. Transfected muscarinic acetylcholine receptors selectively couple to Gi-type G proteins and Gq/11. *Mol Pharmacol* 1994;45:890–898. [PubMed: 8190105]
- Ostrom RS, Post SR, Insel PA. Stoichiometry and compartmentation in G protein-coupled receptor signaling: implications for therapeutic interventions involving G(s). *J Pharmacol Exp Ther* 2000;294:407–412. [PubMed: 10900212]
- Paasche JD, Attramadal T, Sandberg C, Johansen HK, Attramadal H. Mechanisms of endothelin receptor subtype-specific targeting to distinct intracellular trafficking pathways. *J Biol Chem* 2001;276:34041–34050. [PubMed: 11382773]
- Pak Y, Pham N, Rotin D. Direct binding of the beta1 adrenergic receptor to the cyclic AMP-dependent guanine nucleotide exchange factor CNrasGEF leads to Ras activation. *Mol Cell Biol* 2002;22:7942–7952. [PubMed: 12391161]
- Perez DM, Hwa J, Gaivin R, Mathur M, Brown F, Graham RM. Constitutive activation of a single effector pathway: evidence for multiple activation states of a G protein-coupled receptor. *Mol Pharmacol* 1996;49:112–122. [PubMed: 8569696]
- Perry SJ, Baillie GS, Kohout TA, McPhee I, Magiera MM, Ang KL, Miller WE, McLean AJ, Conti M, Houslay MD, Lefkowitz RJ. Targeting of cyclic AMP degradation to $\beta 2$ -adrenergic receptors by β -arrestins. *Science (Wash DC)* 2002;298:834–836.
- Pommier B, Da Nascimento S, Dumont S, Bellier B, Million E, Garbay C, Roques BP, Noble F. The cholecystokinin B receptor is coupled to two effector pathways through pertussis toxin-sensitive and -insensitive G proteins. *J Neurochem* 1999;73:281–288. [PubMed: 10386981]
- Rimoldi V, Reversi A, Taverna E, Rosa P, Francolini M, Cassoni P, Parenti M, Chini B. Oxytocin receptor elicits different EGFR/MAPK activation patterns depending on its localization in caveolin-1 enriched domains. *Oncogene* 2003;22:6054–6060. [PubMed: 12955084]
- Rocheville M, Lange DC, Kumar U, Sasi R, Patel RC, Patel YC. Subtypes of the somatostatin receptor assemble as functional homo- and heterodimers. *J Biol Chem* 2000;275:7862–7869. [PubMed: 10713101]
- Roettger BF, Ghanekar D, Rao R, Toledo C, Yingling J, Pinon D, Miller LJ. Antagonist-stimulated internalization of the G protein-coupled cholecystokinin receptor. *Mol Pharmacol* 1997;51:357–362. [PubMed: 9058588]
- Sagan S, Chassaing G, Pradier L, Lavielle S. Tachykinin peptides affect differently the second messenger pathways after binding to CHO-expressed human NK-1 receptors. *J Pharmacol Exp Ther* 1996;276:1039–1048. [PubMed: 8786533]

- Sagan S, Karoyan P, Chassaing G, Lavielle S. Further delineation of the two binding sites (R*(n)) associated with tachykinin neurokinin-1 receptors using [3-prolinomethionine(11)]SP analogues. *J Biol Chem* 1999;274:23770–23776. [PubMed: 10446137]
- Samama P, Cotecchia S, Costa T, Lefkowitz RJ. A mutation-induced activated state of the β 2-adrenergic receptor. Extending the ternary complex model. *J Biol Chem* 1993;268:4625–4636. [PubMed: 8095262]
- Samama P, Pei G, Costa T, Cotecchia S, Lefkowitz RJ. Negative antagonists promote an inactive conformation of the β 2-adrenergic receptor. *Mol Pharmacol* 1994;45:390–394. [PubMed: 7908404]
- Seifert R, Gether U, Wenzel-Seifert K, Kobilka BK. Effects of guanine, inosine and xanthine nucleotides on β (2)-adrenergic receptor/G(s) interactions: evidence for multiple receptor conformations. *Mol Pharmacol* 1999;56:348–358. [PubMed: 10419554]
- Shenoy SK, McDonald PH, Kohout TA, Lefkowitz RJ. Regulation of receptor fate by ubiquitination of activated β 2-adrenergic receptor and β -arrestin. *Science (Wash DC)* 2001;294:1307–1313.
- Simmons G, Clapham PR, Picard L, Offord RE, Rosenkilde MM, Schwartz TW, Buser R, Wells TN, Proudfoot AE. Potent inhibition of HIV-1 infectivity in macrophages and lymphocytes by a novel CCR5 antagonist. *Science (Wash DC)* 1997;276:276–279.
- Spengler D, Waeber C, Pantaloni C, Holsboer F, Bockaert J, Seeburg PH, Journot L. Differential signal transduction by five splice variants of the PACAP receptor. *Nature (Lond)* 1993;365:170–175. [PubMed: 8396727]
- Steinberg SF, Brunton LL. Compartmentation of G protein-coupled signaling pathways in cardiac myocytes. *Annu Rev Pharmacol Toxicol* 2001;41:751–773. [PubMed: 11264475]
- Stoffel RH 3rd, Pitcher JA, Lefkowitz RJ. Targeting G protein-coupled receptor kinases to their receptor substrates. *J Membr Biol* 1997;157:1–8. [PubMed: 9141353]
- Stout BD, Clarke WP, Berg KA. Rapid desensitization of the serotonin(2C) receptor system: effector pathway and agonist dependence. *J Pharmacol Exp Ther* 2002;302:957–962. [PubMed: 12183652]
- Takeda S, Kadowaki S, Haga T, Takaesu H, Mitaku S. Identification of G protein-coupled receptor genes from the human genome sequence. *FEBS Lett* 2002;520:97–101. [PubMed: 12044878]
- Tohgo A, Pierce KL, Choy EW, Lefkowitz RJ, Luttrell LM. β -Arrestin scaffolding of the ERK cascade enhances cytosolic ERK activity but inhibits ERK-mediated transcription following angiotensin AT1a receptor stimulation. *J Biol Chem* 2002;277:9429–9436. [PubMed: 11777902]
- van Hooft JA, Vijverberg HP. Selection of distinct conformational states of the 5-HT3 receptor by full and partial agonists. *Br J Pharmacol* 1996;117:839–846. [PubMed: 8851499]
- Wade SM, Lim WK, Lan KL, Chung DA, Nanamori M, Neubig RR. G(i) activator region of α (2A)-adrenergic receptors: distinct basic residues mediate G(i) versus G(s) activation. *Mol Pharmacol* 1999;56:1005–1013. [PubMed: 10531407]
- Wei H, Ahn S, Shenoy SK, Karnik SS, Hunyady L, Luttrell LM, Lefkowitz RJ. Independent β -arrestin 2 and G protein-mediated pathways for angiotensin II activation of extracellular signal-regulated kinases 1 and 2. *Proc Natl Acad Sci USA* 2003;100:10782–10787. [PubMed: 12949261]
- Yu Y, Zhang L, Yin X, Sun H, Uhl GR, Wang JB. μ -Opioid receptor phosphorylation, desensitization and ligand efficacy. *J Biol Chem* 1997;272:28869–28874. [PubMed: 9360954]
- Zamah AM, Delahunty M, Luttrell LM, Lefkowitz RJ. Protein kinase A-mediated phosphorylation of the β 2-adrenergic receptor regulates its coupling to Gs and Gi. Demonstration in a reconstituted system. *J Biol Chem* 2002;277:31249–31256. [PubMed: 12063255]
- Zhu X, Gilbert S, Birnbaumer M, Birnbaumer L. Dual signaling potential is common among Gs-coupled receptors and dependent on receptor density. *Mol Pharmacol* 1994;46:460–469. [PubMed: 7935326]