

Signal Transduction by GABA_B Receptor Heterodimers

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GABA_B receptors are G-protein-coupled receptors that mediate inhibition throughout the central and peripheral nervous systems. A single cloned receptor, GABA_BR1, which has at least three alternatively spliced forms, appears to account for the vast majority of binding sites in the brain for high-affinity antagonists. In heterologous expression systems GABA_BR1 is poorly expressed on the plasma membrane and largely fails to couple to ion channels. A second gene, GABA_BR2, which exhibits moderately low homology to GABA_BR1, permits surface expression of GABA_BR1 and the appearance of baclofen-sensitive K⁺ and Ca⁺⁺ currents. We review the data that supports a model of

the native GABA_B receptor as a heterodimer composed of GABA_BR1 and GABA_BR2 proteins. New data from mutagenesis experiments are presented that point to amino acid residues on GABA_BR1 critical for ligand activation of the heterodimer. The possible role of GABA_BR2 in signal transduction is also discussed. The interdependent nature of the two subunits for receptor function makes the GABA_B receptor a useful model to explore the larger significance of GPCR dimerization for G-protein activation.

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Gamma-aminobutyric acid (GABA) is an abundant neurotransmitter that mediates inhibition throughout the nervous system via both ligand-gated channels (GABA_A and GABA_C receptors) and G-protein-coupled receptors (GABA_B receptor). GABA_B receptors have both pre- and postsynaptic actions (Bowery 1993; Price et al. 1984). Postsynaptic inhibition of neuronal firing is mediated primarily by the coupling of GABA_B receptors to the activation of inwardly rectifying K⁺ channels (GIRKs) (North 1989; Gahwiler and Brown 1985; Andrade et al. 1986). Presynaptic inhibition of neurotrans-

mitter release by GABA is thought to occur by suppression of any of a number of identified high-threshold Ca⁺⁺ channels (Harayama et al. 1998; Lambert and Wilson 1996; Mintz and Bean 1993; Dolphin and Scott 1987). The physiological importance of GABA_B receptors has been widely appreciated in humans through the use of baclofen (Bowery et al. 1980), a selective agonist at GABA_B receptors that is used clinically for the treatment of muscle spasticity and trigeminal neuralgia. The widespread distribution of GABA_B receptors in both central and peripheral nervous systems reveals their importance in a variety of physiological processes.

There is now a substantial repertoire of ligands, having agonist or antagonist properties, that display high affinity and selectivity for GABA_B receptors (Froestl and Mickel 1997). Although these chemical tools have been useful for studying the neurophysiology and molecular biology of GABA_B receptors, they have failed for the most part to permit the identification of pharmacological subtypes. For example, using semi-intact tissue preparations it is possible to record robust pre- and postsynaptic responses to ba-

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clofen and high-affinity antagonists block these with roughly equal potency (Bon and Galvan 1996; Pozza et al. 1999; Seabrook et al. 1990). Although measurements of neurotransmitter release have permitted some groups to report selective antagonism (Fassio et al. 1994; Bonanno et al. 1996, 1997; Teoh et al. 1996; but see also Baumann et al. 1990), there is no general consensus about pharmacologically defined receptor subtypes (Bowery 1997). This is perhaps surprising for a receptor system that is both widespread and otherwise well characterized.

The identification of a gene encoding GABA_B receptors proved to be at least as challenging as the pharmacological search for subtypes. Several groups attempted to expression clone a receptor using *Xenopus* oocytes (Uezono et al. 1998), or to biochemically characterize a protein from brain, affinity purified using a monoclonal antibody (Nakayasu et al. 1993). The cloning breakthrough came with the development of the photo affinity radioligand, CGP71872. Using this as a marker, Kaupmann and co-workers (Kaupmann et al. 1997) identified a clone, GABA_BR1, predicted to encode a heptahelical protein composed of 844 amino acids. This clone shares many features of other members of the metabotropic glutamate and Ca⁺⁺-sensing receptor family including a large extracellular, N-terminal domain having homology to bacterial amino acid binding proteins, such as LIVBP (O'Hara et al. 1993). When expressed heterologously in cell lines, the antagonist pharmacology of the cloned receptor was shown to be very similar to that of native receptors. In contrast, the apparent affinity of agonist ligands was about 100-fold less than expected from studies of brain membranes. When challenged with an agonist, GABA_BR1 also did not appear to be able to stimulate the expected cellular responses, such as K⁺ channel activation or robust inhibition of the accumulation of cAMP, which suggested that a necessary component of signal transduction was missing.

The publication of GABA_BR1 set off a search by many groups for other genes having a related sequence. A query of public databases using the GABA_BR1 sequence led to the identification of a second, homologous protein, GABA_BR2 (Jones et al. 1998; Kaupmann et al. 1998a; Kuner et al. 1999; White et al. 1998; Martin et al. 1999; Ng et al. 1999). Like GABA_BR1, GABA_BR2 was found to contain a region homologous to LIVBP within the large N-terminal extracellular domain.

Several groups have shown that when expressed in either oocytes or mammalian cells GABA_BR2 fails to produce the anticipated cellular responses to GABA (Jones et al. 1998; Kaupmann et al. 1998a; White et al. 1998; but see also Kuner et al. 1999; Martin et al. 1999). This deficit in coupling was especially surprising considering the lack of function activity of GABA_BR1. Hinting at a resolution of the functional expression problem was the spatial distribution of the mRNAs for both GABA_BR1 and GABA_BR2. The *in situ* localization patterns of both

transcripts were highly convergent throughout the brain (Jones et al. 1998), suggesting that the two receptors were co-expressed in the same cellular regions. Double labeling of mRNAs and receptor proteins at cellular resolution provided proof that co-expression occurs in multiple cell types, including cerebellar Purkinje cells, hippocampal and cerebral cortical neurons, and the vast majority of neuronal somata within dorsal root ganglia (Jones et al. 1998; Kaupmann et al. 1998a; Durkin et al. 1999). We reasoned that fully functional GABA_B receptors might somehow require the expression of both GABA_BR1 and GABA_BR2.

CO-EXPRESSION STUDIES

Co-expression of GABA_BR1 and GABA_BR2 in *Xenopus* oocytes and mammalian cells leads to the development of large amplitude GABA- and baclofen-sensitive GIRK currents (Jones et al. 1998; Kaupmann et al. 1998a; Kuner et al. 1999; White et al. 1998; Ng et al. 1999). These currents are rarely seen in cells expressing either gene alone (Kaupmann et al. 1998a, 1998b). Co-expression also permits robust inhibition of adenylyl cyclase (Kuner et al. 1999; Ng et al. 1999) as well as stimulation of GTPγS binding in cell membranes (White et al. 1998). The pharmacology of agonists at the GABA_BR1/R2 combination (Jones et al. 1998; Brauner-Osborne and Krogsgaard-Larsen 1999; Lingenhoehl et al. 1999) is comparable to that reported for native receptors (Bon and Galvan 1996; Seabrook et al. 1990). Antagonist affinity estimates for saclofen, CGP54626 and CGP55845 (Jones et al. 1998; Brauner-Osborne and Krogsgaard-Larsen 1999) are similar to values reported in previous electrophysiological studies using brain tissue (Bon and Galvan 1996; Seabrook et al. 1990), as well as to those obtained by measuring displacement of radioligand from cells expressing GABA_BR1 alone (Kaupmann et al. 1997).

Just as striking as the appearance of functional cellular responses is the shift in affinity for agonists. The co-expression of GABA_BR2 with GABA_BR1 now results in an apparent shift (10–30-fold) to a higher affinity state for the agonists GABA and baclofen (Kaupmann et al. 1998a; White et al. 1998). This observation led to the speculation that the two GABA_B gene products might closely associate with one another (Kaupmann et al. 1998a). Additional evidence came from epitope tagging experiments that showed a high coincidence in the intracellular distribution of the two proteins when expressed heterologously (Jones et al. 1998).

PHYSICAL ASSOCIATION BETWEEN GABA_BR1 AND GABA_BR2

Using immunoprecipitation methods, several groups demonstrated that GABA_BR1 and GABA_BR2 specifically

associate in a protein complex, probably as heterodimers (Jones et al. 1998; Kaupmann et al. 1998a; Kuner et al. 1999; White et al. 1998). Furthermore, the heterodimers are concentrated on the plasma membrane, which suggests that the dimer is likely to be important for early events in signal transduction including ligand binding and G-protein activation (Jones et al. 1998). These studies provided the first compelling evidence that native G-protein-coupled receptors (GPCRs) can exist not only as homodimers, as is likely the case for other GPCRs (Gouldson and Reynolds 1997; Hebert and Bouvier 1998; Bai et al. 1998) but also as heterodimers composed of more than one receptor subunit.

Additional groups independently came to the conclusion that GABA_B receptors are formed of heterodimers, and in the process provided a molecular mechanism for the subunit interaction. Experiments with the yeast two-hybrid system for identifying protein partners led to the discovery of domains on the extended C-termini of GABA_BR1 and GABA_BR2 that are responsible for their molecular association (White et al. 1998; Kuner et al. 1999). Both C-termini are predicted to contain coiled-coil motifs based on algorithms that reliably detect such features in the primary amino acid sequences of other more well known proteins that dimerize (Lupas 1997; Lupas et al. 1991). When either of the coiled-coil structures are deleted, the proteins no longer associate (Kuner et al. 1999). The yeast two-hybrid experiments also revealed that the associations are strictly heterophilic; there is no evidence that homodimers form.

The coiled-coil structure provides the first molecular substrate for GPCR dimerization; but among GPCRs this structure is so far unique to GABA_B receptors (Table 1). In contrast, the coiled-coil is well conserved within GABA_B receptors from different species (Figure 1). Additional types of protein-protein interactions must be responsible for dimerization of other GPCRs. In the case of the metabotropic glutamate/Ca⁺⁺ sensor family of GPCRs, cysteine disulfide bridges are at least partly responsible for dimer formation. It is very likely that interactions between

transmembrane alpha helices are also critical for dimer formation or stabilization (Gouldson and Reynolds 1997; Hebert et al. 1996; Maggio et al. 1996; George et al. 1998).

CONSEQUENCES OF HETERODIMERIZATION

The heterodimer model immediately raises a myriad of questions about the roles of the two receptor proteins in signal transduction. Does only GABA_BR1 bind ligand? Do both subunits bind G-protein? Does GABA_BR2 merely serve as a shuttle protein, or does it have an active role signaling? Does any part of the signal transduction cascade involve dissociation of the two subunits?

Answers to some of these questions are beginning to emerge. For example, heterodimerization appears to be important for receptor trafficking to the plasma membrane. Several groups have noted that GABA_BR1, when expressed by itself, does not reach the plasma membrane; instead, it accumulates within the cytoplasm, probably in association with the endoplasmic reticulum (Couve et al. 1998; White et al. 1998). Even when over-expressed in neurons, which might be expected to correctly process and transport neuronal proteins, there is a deficit of plasma membrane labeling (Couve et al. 1998). Using fluorescence activated cell sorting and antibodies that recognize an extracellular epitope of GABA_BR1b, White et al. (1998) observed that the inclusion of GABA_BR2 induces a significant increase in the surface expression of GABA_BR1b, and presumably, the heterodimer. In the absence of GABA_BR2, GABA_BR1 also exhibits an immature pattern of glycosylation (White et al. 1998). Thus, GABA_BR2 has an important role in regulating the expression of the mature, signaling heterodimer. In this regard, the assembly and transport of GABA_B receptors may be similar to that of other proteins having multiple subunits, such as ion channels (Yu and Hall 1991). It is interesting to note that in a subset of neurons, such as hippocampal CA1 pyramidal cells and inhibitory interneurons,

Table 1. Analysis of GPCR Databases Using the COILS^a Algorithm

GPCR Family	No. in Database ^b	Hits ^c	Description ^d
Rhodopsin	432	4	d1dr_fugru, m3dr_human, msr_xenla, opsd_octdo
Olfactory	491	0	
Secretin	29	0	
Chemosensor	8	0	
Frizzled	7	0	
mGluR/CaSR/GABA _B	32	7	GABA _B R1 (hum, rat, drosophila), GABA _B R2 (hum, rat, sponge, nematode)
Total	999	11	

^a Lupas (1997).

^b Search set includes GPCRs from all species in Genbank as of November 1999.

^c Hits include those which show a >90% probability using a window size of 28 and weighting the first and fourth positions in the heptad repeat. Note that hits in the rhodopsin family do not extend to species homologues. Therefore, the significance for these receptors is less certain.

^d Swiss Protein database nomenclature (except for GABA_B receptors).

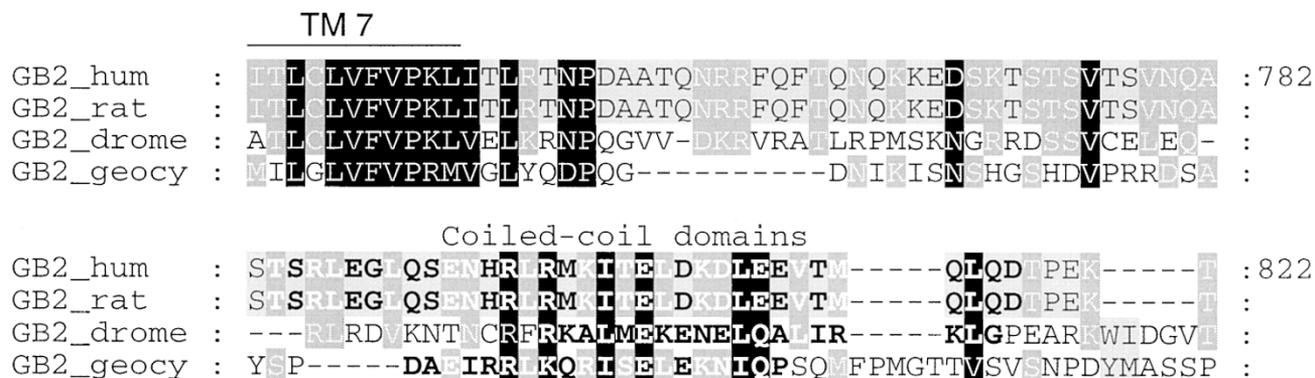


Figure 1. Alignment of portions of the C-terminal regions of GABA_BR2 from four species. Alignment was made using the default settings of Clustal W. Shading shows different levels of amino acid conservation. Residues in bold comprise the coiled-coil domain as predicted using the algorithm "COILS" (Lupas 1997). GB2_drome, GABA_BR2 from *Drosophila melanogaster*; GB2_geocy, *Geodia cydonium* (a marine sponge).

GABA_BR1-immunoreactive protein appears abundantly in the cytoplasm (Sloviter et al. 1999). Although the expression levels of GABA_BR2 protein have not been published for these cells, the CA1 cells do exhibit a much lower level of mRNA encoding this protein as compared to cells in nearby CA3 (Durkin et al. 1999; Kuner et al. 1999). These observations lead to the speculation that GABA_BR2 protein may be constitutively low in certain cell types resulting in an inefficient transport of GABA_BR1 to distal plasma membrane surfaces (Sloviter et al. 1999). The actual extent to which GABA_BR2 protein regulates expression of the functional heterodimer remains to be determined.

Immunochemical methods have demonstrated that native GABA_B receptors in the nervous system exist largely as heterodimers. Throughout the CNS there is a striking degree of overlap of GABA_BR1 and GABA_BR2 immunoreactivity at a gross structural level (Benke et al. 1999). In the cerebellar molecular layer co-localization of GABA_BR1 and GABA_BR2 immunoreactivity has been observed in ultra-thin sections of Purkinje cell spines (Kaupmann et al. 1998a) providing support for co-assembly at particular postsynaptic structures. Since GABA_B receptors are so widespread in the CNS, a useful approach to estimate the overall proportion of receptors that are composed of heterodimers versus homodimers is to perform quantitative immunoprecipitations on fractions containing solubilized receptors. Using this method, Benke and colleagues (Benke et al. 1999) observe that essentially all GABA_BR1 protein is immunoprecipitated with antibodies that recognize GABA_BR2. Thus, the proportion of receptors in the brain that exist either as GABA_BR1 or GABA_BR2 monomers is thought to be quite low.

FUNCTIONS OF THE HETERODIMER SUBUNITS

High-affinity agonists and antagonists bind the GABA_BR1 subunit in a region which exhibits structural homology to

the ligand-binding domain of metabotropic glutamate receptors and bacterial periplasmic amino acid binding proteins (Galvez et al. 1999). And, since the antagonists are capable of completely blocking cellular responses to GABA or baclofen, it is clear that the ligand-binding domain on the N-terminus of GABA_BR1 is essential for initiating signal transduction by the heterodimer. GABA_BR2 does not bind radiolabeled GABA_BR1 antagonists, nor does it appear to bind [³H]-GABA (Jones et al. 1998; Kaupmann et al. 1998; White et al. 1998). There have, however, been reports that GABA_BR2, when expressed alone, can be stimulated by GABA (Kaupmann et al. 1998a; Kuner et al. 1999; Martin et al. 1999). Does GABA_BR2 contribute a binding site for GABA or another ligand? The first possibility explored was sensitivity to Ca⁺⁺ since GABA_BR2 exhibits some sequence similarity to the Ca⁺⁺-sensing receptor (Ruat et al. 1995). In fact, Ca⁺⁺ can be seen to strongly modify the response of the heterodimer to GABA, but this effect can be attributed entirely to specific amino acid residues within the ligand-binding region of GABA_BR1 (Wise et al. 1999; Galvez et al. 2000).

To explore a ligand-binding role for GABA_BR2, we performed mutations within the region of GABA_BR1b that encodes the ligand-binding domain, and then assessed the functional status of the heterodimer by expression with GABA_BR2. The mutations that were performed are described in Figure 2. Using [³H]-CGP54626 as a radiolabel, specific binding was reduced by more than 85% in membranes expressing any of the GABA_BR1b mutants (data not shown). Others have shown that the S246A and Y266A mutations cause a >1000-fold decrease in affinity for antagonists using a different radioligand (Galvez et al. 1999). To determine if the mutations created a parallel decrease in functional activity, receptors were assayed for Ca⁺⁺-mobilization in a fluorescence plate reader using Fluo-3 dye and a chimeric G-protein (Conklin et al. 1993), Gα_{q/i3(5)}, that permits coupling of the heterodimer to activation of phospholipase C. Co-expression of non-

A

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                246                               266 269
GBR1b   . . I L M P G C S S V S T L V A E A A R M W N L I V L S Y G S S S P A L S N R . .
mGluR1  . . V I G P G S S S V A I Q V Q N L L Q L F D I P Q I A Y S A T S I D L S D K . .
LIVPB   . . V I G H L C S S S T Q P A S D I Y E D E G I L M I S P G A T A P E L T Q R . .
CSR1a   . . V V G A T G S G V S T A V A N L L G L F Y I P Q V S Y A S S R L L S N K . .
GBR2    . . M V F G G V C P S V T S I I A E S L Q G W N L V Q L S F A A T T P V L A D . .

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B

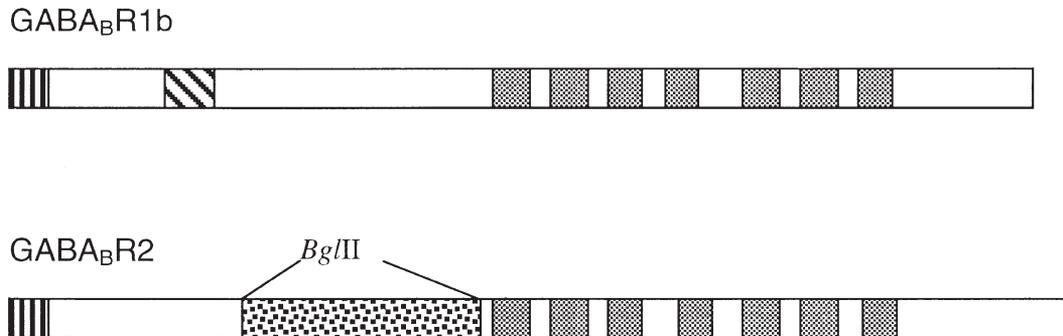


Figure 2. (A) Alignment of a portion of the ligand-binding domains of GABA_BR1b (GBR1b), GABA_BR2 (GBR2), mGluR1, Ca⁺⁺ sensor (CSR1a), and LIVBP. Bold letters in GABA_BR1 indicate residues that were mutated in this study. (B) Schematic of GABA_BR1 and GABA_BR2 showing the approximate locations of the region shown in detail in (A) (diagonals) and the *Bgl*III fragment (stippled region) deleted from GABA_BR2. *Bgl*III digestion of plasmid containing the GABA_BR2 cDNA removes 771 nucleotides encoding amino acids 226–482 in the protein. Signal peptide sequence (vertical stripes) and transmembrane regions (gray boxes) are indicated. All mutant and deletion constructs were verified by sequence analysis.

mutated GABA_BR1b with GABA_BR2 resulted in concentration-dependent increases in liberated Ca⁺⁺ with GABA and baclofen. EC₅₀ values for these agonists were similar to those reported using other methods. In contrast, co-expression of either S246A or Y266A mutants with wild-type GABA_BR2 failed to stimulate Ca⁺⁺ release using concentrations of GABA or baclofen up to 1000-fold above their EC₅₀ values (Figure 3). These mutant receptors appeared to be expressed based on the appearance of cellular immunofluorescence using antibodies directed against the epitope-tagged C-terminus (data not shown). Thus, the most likely explanation for the lack of functional activity even at 1000-fold higher concentrations of agonist is that activation of the heterodimer is absolutely dependent on agonist binding to the GABA_BR1b subunit. Others have shown that the S269A substitution induces a selective reduction in affinity to GABA while sparing baclofen binding (Galvez et al. 1999). When expressed with GABA_BR2, a similar

shift in the EC₅₀ of GABA, but not baclofen, was observed for the Ca⁺⁺ mobilization response (Figure 3). The parallel changes in agonist potency measured either as binding to GABA_BR1b, or as activation of the heterodimer, provides additional support for the view that GABA_BR2 cannot directly contribute to receptor activation by either of these ligands.

The coiled-coil domain on the C-terminus of GABA_BR2 is necessary for binding GABA_BR1 and for formation of functional heterodimers (Kuner et al. 1999; White et al. 1998). Protein assemblies mediated by coiled-coil domains are generally thought to be thermodynamically quite stable. This and the observed predominance of GABA_B receptor heterodimers over monomers (Benke et al. 1999) strongly suggests that the GABA_B receptor is likely to remain as a heterodimer throughout the cycle of agonist binding, receptor activation and G-protein stimulation. What direct role, if any, does GABA_BR2 have in any of these events? The lack of conservation of the agonist-

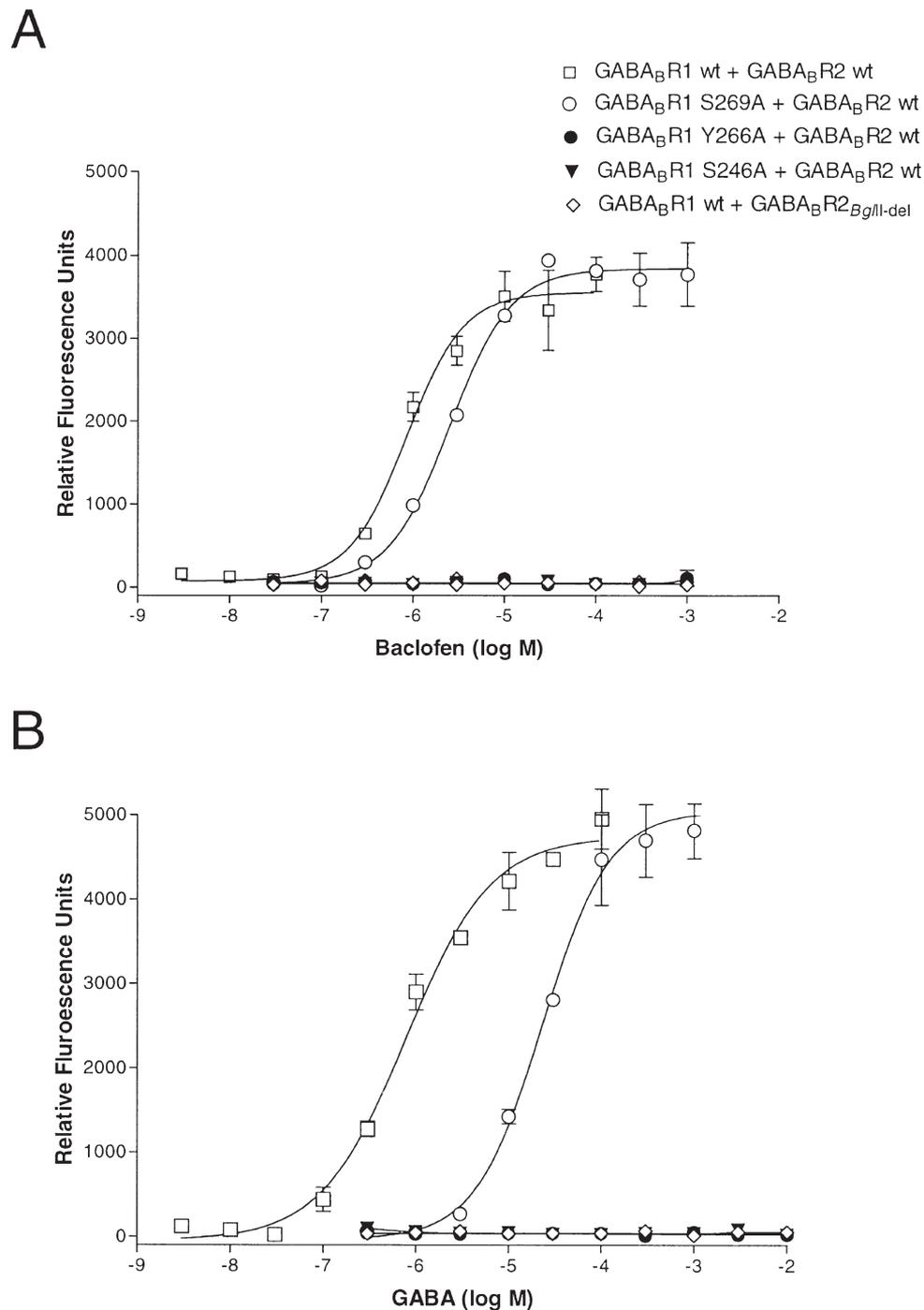


Figure 3. Activation of wild-type and mutant receptors by GABA and baclofen. Intracellular Ca^{++} release was measured by Fluo-3 dye fluorescence using a FLIPR (molecular devices). Cells were transiently transfected with plasmids containing wild-type or mutant GABA_BR1b and wild-type or truncated GABA_BR2 and chimeric $\text{G}\alpha_{q/13(5)}$. Data are expressed as means \pm S.E.M. of a quadruplicate determination from a single experiment. Similar results were obtained in three separate experiments.

binding domain of GABA_BR1 in GABA_BR2 would indicate that point mutations might not be an efficient way to map out domains important for signaling by GABA_BR2.

As a first step toward determining domains on GABA_BR2 important for signal transduction, we performed a deletion of 257 amino acids within the N-ter-

минаl domain of GABA_BR2 (Figure 2B). The expression pattern of this deletion mutant (GABA_BR2_{BgII-del}) was similar to that of wild-type GABA_BR2 as judged by the appearance of cellular immunofluorescence using antibodies directed against the epitope-tagged C-terminus (data not shown). In COS-7 cells co-expressing GABA_BR1b

and GABA_BR2_{Bgl}II-del no evidence was found for receptor activation by either GABA or baclofen using the Ca⁺⁺-mobilization assay (Figure 3). Loss of this region within the N-terminus of GABA_BR2_{Bgl}II-del may prevent heterodimerization, or it may produce a more subtle change in structure of the heterodimer that prevents stimulation of G-protein.

SUMMARY

GABA_B receptors may be thought of as being composed of two subunits, a ligand-binding subunit, GABA_BR1, and a "structural" subunit, GABA_BR2. GABA_BR1 appears to determine the pharmacological properties of the receptor, while GABA_BR2 is important for proper expression of GABA_BR1 on the plasma membrane. Additional deletion and mutagenesis experiments will be required to determine to what extent GABA_BR2 actually participates in signal transduction events.

Suddenly it appears that the field of G-protein-coupled receptors is playing catch-up with its brethren plasma membrane proteins: ion channels, receptor tyrosine kinases and transporters, most of which occur as oligomeric assemblies. GABA_B receptors are now joined by a growing list of GPCRs which are thought to exist as heterodimers, including receptors for endogenous opiates (Jordan and Devi 1999), dopamine and somatostatin (Rocheville et al. 2000) and serotonin (Xie et al. 1999). The recent finding that heterodimerization can change receptor affinities for agonists (Jordan and Devi 1999) indicates that the heteromeric nature of GPCRs is likely to have major implications for drug design in the near future. Given the fact that heterodimerization is now seen to occur in two divergent families of GPCRs, it seems likely that additional examples will become known with further study.

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