

Coupling of Metabotropic Glutamate Receptors 2 and 4 to $G_{\alpha 15}$, $G_{\alpha 16}$, and Chimeric $G_{\alpha q/i}$ Proteins: Characterization of New Antagonists

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SUMMARY

Together with the calcium-sensing receptor, the metabotropic glutamate receptors (mGluRs) share no sequence homology with the other G protein-coupled receptors (GPCRs) and therefore constitute a new family of receptors. Recently, it was reported that $G_{\alpha 15}$ and $G_{\alpha 16}$ subunits allow many GPCRs to activate phospholipase C (PLC). Furthermore, the exchange of a few carboxyl-terminal residues of $G_{\alpha q}$ by those of $G_{\alpha 12}$ or $G_{\alpha o}$ allows the resulting chimeric G_{α} subunits ($G_{\alpha qi}$ and $G_{\alpha qo}$, respectively) to couple G_i-coupled receptors to PLC. We report that mGluR2 and mGluR4, two receptors negatively coupled to adenylyl cyclase, activate PLC when coexpressed with $G_{\alpha 15}$, $G_{\alpha qi}$, or $G_{\alpha qo}$. This indicates that the carboxyl-terminal end of the G_{α} subunit also plays an important role in the specific interaction between mGluRs and the G proteins. In addition, the measurement of PLC activation by G_i-coupled mGluRs coex-

pressed with these G_{α} subunits constitutes an easy functional assay for the pharmacological characterization of these receptors. The rank order of potency of antagonists was found to be (2S,3S,4S)-2-methyl-2-(carboxycyclopropyl)glycine \sim (R,S)- α -methyl-4-phosphonophenylglycine > (R,S)- α -methyl-4-sulfonophenylglycine > (R,S)- α -methyl-4-tetrazolylphenylglycine = (S)-2-amino-2-methyl-4-phosphonobutyrate for mGluR2 and to be (R,S)- α -methyl-4-phosphonophenylglycine \geq (S)-2-amino-2-methyl-4-phosphonobutyrate \gg (R,S)- α -methyl-4-sulfonophenylglycine [(R,S)- α -methyl-4-tetrazolylphenylglycine and (2S,3S,4S)-2-methyl-2-(carboxycyclopropyl)glycine being inactive at 1 mM] for mGluR4. Using this functional assay, (R,S)- α -methyl-4-phosphonophenylglycine was found to have a similar K_d value for mGluR2 and mGluR4.

The major excitatory neurotransmitter in the brain, glutamate, activates ionotropic and metabotropic (G protein-coupled) receptors (1). These latter receptors modulate the activity of many synapses and play important roles in glutamate-mediated effects, including neurotoxicity, brain development, and memory formation (2-4). Eight genes encoding mGluRs have been identified. Based on their sequence

homology, transduction mechanism, and pharmacology, they can be classified into three groups (2-4). The first one is composed of mGluR1 and mGluR5, which are coupled to PLC. The second group is composed of mGluR2 and mGluR3, both of which negatively coupled to AC. The other mGluRs (mGluR4, mGluR6, mGluR7, and mGluR8) constitute the third group. They are negatively coupled to AC in heterologous expression systems and are selectively activated by L-AP4 (5-8). Although the pharmacology of PLC-coupled mGluRs has been studied extensively, the pharmacology of many AC-coupled mGluRs is not well characterized, probably because of the difficulty in developing simple functional assays for these receptors.

mGluRs possess seven TMDs but share no sequence homology with other GPCRs except the recently identified cal-

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ABBREVIATIONS: mGluR, metabotropic glutamate receptor; AC, adenylyl cyclase; ACPD, 1-amino-1,3-cyclopentane dicarboxylate; 4C3HPG, (S)-4-carboxy-3-hydroxyphenylglycine; 4CPG, (S)-4-carboxyphenylglycine; 3,5-DHPG, (R,S)-3,5-dihydroxyphenylglycine; DMEM, Dulbecco's modified Eagle's medium; GPCR, G protein-coupled receptor; IP, inositol phosphates; HEK, human embryonic kidney; L-AP4, L-2-amino-4-phosphonobutyrate; L-CCGI, (2S,3S,4S)- α -(carboxycyclopropyl)glycine; L-SOP, L-serine-O-phosphate; MAP4, (S)-2-amino-2-methyl-4-phosphonobutyrate; MCCGI, (2S,3S,4S)-2-methyl-2-(carboxycyclopropyl)glycine; MCPG, (R,S)- α -methyl-4-carboxyphenylglycine; MPPG, (R,S)- α -methyl-4-phosphonophenylglycine; MSPG, (R,S)- α -methyl-4-sulfonophenylglycine; MTPG, (R,S)- α -methyl-4-tetrazolylphenylglycine; PLC, phospholipase C; PTX, pertussis toxin; t-ADA, trans-azetidine diacid; TMD, transmembrane domain; HEPES, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid.

cium-sensing receptor (9). This absence of homology prevents the construction of a three-dimensional model for the seven-TMD region of mGluRs based on the known structure of bacteriorhodopsin or on other GPCR models (10). In contrast to many GPCRs, the agonist binding site of mGluRs is located in a large extracellular domain homologous to bacterial periplasmic binding proteins (11, 12). Finally, most of the structural and sequence requirements for G protein coupling in GPCRs are not fulfilled by mGluR intracellular sequences (4). We recently proposed that the second intracellular loop of mGluRs plays a role equivalent to that of the third intracellular loop of the other GPCRs (13, 14).

Recently, $G_{\alpha 15}$ and $G_{\alpha 16}$, which activate PLC, have been reported to be activated by many different GPCRs, including those recognized not to stimulate PLC (15). It has also been reported that the carboxyl-terminal end of the α subunit of G proteins plays an important role in the specific interaction between the G protein and the receptor. Accordingly, the exchange of the five carboxyl-terminal residues of the PLC activating G_{α} subunit, $G_{\alpha q}$, by those of either $G_{\alpha 12}$ or $G_{\alpha o}$ is sufficient to allow these chimeric $G_{\alpha q}$ and $G_{\alpha qo}$ subunits to be activated by receptors coupled to $G_{\alpha i}$ or $G_{\alpha o}$ (16).

In the current study, we show that despite the absence of sequence homology between mGluRs and the other GPCRs, the representative members of group II and III mGluRs (i.e., mGluR2 and mGluR4, respectively) activate $G_{\alpha 15}$ and the chimeric $G_{\alpha q}$ and $G_{\alpha qo}$ subunits. We also show that these wild-type and chimeric α subunits can be used to develop simple functional assays for the pharmacological characterization of group II and group III mGluRs. This is of particular interest because of the difficulty of maintaining stable cell lines expressing these receptors and because such an assay will prove to be useful for the functional characterization of a large number of chimeric or mutated mGluRs negatively coupled to AC. Such an assay allowed us to further characterize the pharmacological profiles of mGluR2 and mGluR4.

Experimental Procedures

Materials. MCPG, 4CPG, 4C3HPG, 3,5-DHPG, L-AP4, L-SOP, L-CCGI, MAP4, MCCGI, MTPG, MSPG, and MPPG were obtained from Tocris Cookson (Essex, UK). The four different stereoisomers of ACPD were a generous gift of Dr. K. Curry (University of British Columbia, Vancouver, Canada). (\pm) -t-ADA was a gift from A. P. Kozikowski (Trophic Pharmaceuticals, Inc., South Plainfield, NJ), $(+)$ -t-ADA (CGP-61919) and $(-)$ -t-ADA (CGP-61920) were gifts from Dr. T. Knöpfel (Ciba, Basle, Switzerland).

For the transient expression of mGluRs, the cDNA of mGluR1a (17), mGluR2 (isolated like mGluR3; 13), and mGluR4a (a generous gift from Prof. S. Nakanishi, University of Kyoto, Kyoto, Japan) were subcloned into the eukaryotic expression vector pRK5 containing a cytomegalovirus immediate-early promoter. The plasmids pcDNA- $G_{\alpha wt}$, pcDNA- $G_{\alpha 15}$, pcDNA- $G_{\alpha 16}$, and pcDNA- $G_{\alpha qo}$ were gifts from Dr. B. Conklin and H. Bourne (University of California, San Francisco, San Francisco, CA). The plasmids pCIS- $G_{\alpha 15}$ and pCIS- $G_{\alpha 16}$ were kindly provided by Dr. M. Simon (California Institute of Technology, Los Angeles, CA).

Culture and transfection of HEK 293 cells. HEK 293 cells were cultured in DMEM (GIBCO BRL, Baltimore, MD) supplemented with 10% fetal calf serum and antibiotics (final concentration of penicillin and streptomycin, 100 units/ml). Electroporation was performed in a total volume of 300 μ l with 10 μ g of carrier DNA, 4 μ g of mGluR2 plasmid DNA, 10 μ g of mGluR4 plasmid DNA, 4 μ g of wild-type or mutated G_{α} subunit plasmid DNA when indicated, and

10 million cells in electroporation buffer (50 mM K_2HPO_4 , 20 mM CH_3COOK , 20 mM KOH). After electroporation [260 V, 960 μ F; BioRad gene pulser electroporator (Hercules, CA)], cells were resuspended in DMEM supplemented with 10% fetal calf serum and antibiotics and split into 12-well clusters (Falcon Plastics, Oxnard, CA) (10 million cells/cluster) previously coated with poly-L-ornithine (15 μ g/ml; molecular weight, 40,000; Sigma Chemical, St. Louis, MO) to favor adhesion of the cells.

Determination of IP accumulation. Determination of IP accumulation in transfected cells was performed as described previously (18). At 3–4 hr after electroporation, cells were washed and incubated for 12 hr in DMEM/Glutamax-I (GIBCO) containing 1 μ Ci/ml myo -[3H]inositol (23.4 Ci/mol, Dupont-New England Nuclear, Les Ulis, France). Cells were then washed three times and incubated for 1–2 hr at 37° in 1 ml of HEPES buffer saline (146 mM NaCl, 4.2 mM KCl, 0.5 mM $MgCl_2$, 0.1% glucose, 20 mM HEPES, pH 7.4) supplemented with 1 unit/ml glutamate pyruvate transaminase (Boehringer-Mannheim, Meylan, France) and 2 mM pyruvate (Sigma, Lisle d'Abeau, France). Cells were then washed again twice with the same medium and preincubated for 5 min in medium containing 10 mM LiCl. The agonist was then added for a period of 30 min. The reaction was stopped by replacing the incubation medium with 1 ml of perchloric acid (5%) on ice. The total IP were then extracted and purified on Dowex columns as described previously (18). Total radioactivity remaining in the membrane fraction was counted after solubilization in 10% Triton X-100 and 0.1 N NaOH and used as standard. Results are expressed as the amount of IP produced over the radioactivity present in the membranes. The dose-response curves were fitted using the equation $y = [(y_{max} - y_{min}) / (1 + (x/EC_{50})^n)] + y_{min}$ and the Kaleidagraph program.

Results

To examine whether group II and III mGluRs that are negatively coupled to AC could activate the promiscuous G protein α subunits $G_{\alpha 15}$ and $G_{\alpha 16}$, these α subunits were expressed alone or in combination with either mGluR2 or mGluR4 in HEK-293 cells. As shown in Fig. 1, glutamate stimulated IP formation in cells coexpressing mGluR2 and either $G_{\alpha 15}$ or $G_{\alpha 16}$. The glutamate-stimulated IP formation was higher in cells expressing mGluR2 and $G_{\alpha 15}$ than in cells expressing mGluR2 and $G_{\alpha 16}$. When coexpressed with

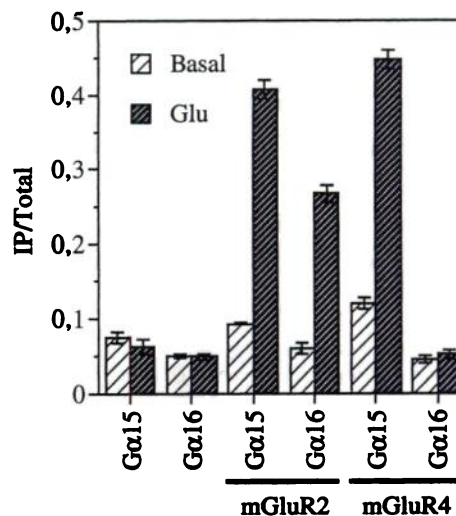


Fig. 1. Basal and 1 mM glutamate (Glu)-stimulated IP formation in cells expressing $G_{\alpha 15}$ or $G_{\alpha 16}$ alone or in combination with mGluR2 or mGluR4. Values are mean \pm standard error of triplicate determinations from a typical experiment. Similar data were obtained in at least five other experiments.

mGluR4, G_{α15} allowed glutamate to stimulate PLC, whereas G_{α16} did not. No glutamate stimulation of IP formation was observed in cells expressing G_{α15}, G_{α16} (Fig. 1), mGluR2, or mGluR4 (Fig. 2) alone.

We next examined whether the carboxyl-terminal domain of the G_α subunit plays a critical role in the specific interaction with mGluRs, as already observed with the other GPCRs. mGluR2 and mGluR4 were therefore coexpressed with the chimeric G_{αq} subunits in which the five or nine carboxyl-terminal residues of G_{αq} have been replaced by those of G_{α12} (G_{αqi5} and G_{αqi9}, respectively) or G_{αo} (G_{αqu5}). As shown in Fig. 2, glutamate stimulated IP formation in cells coexpressing mGluR2 or mGluR4 with any of these three chimeric G_α subunits. The larger glutamate stimulation of IP formation was observed when mGluR2 or mGluR4 was coexpressed with either G_{αqi9} or G_{αqu5}. No stimulation of IP formation was observed in cells expressing mGluR2 or mGluR4 alone or in combination with the wild-type G_{αq}, indicating that the activation of PLC did not result from an overexpression of the G_{αq}-like subunit but that the exchange of the carboxyl-terminal end was indeed necessary for this glutamate-induced response.

To confirm that the chimeric G_α subunits were responsible for the coupling of mGluR2 and mGluR4 to PLC, we examined the sensitivity of the glutamate-stimulated IP formation to PTX. This toxin is known to block the activation of G_{αi} and G_{αo} subunits by ADP-ribosylating a cysteine residue located

three residues from their carboxyl terminus (19). This cysteine residue is therefore in the carboxyl-terminal end of the chimeric G_{αqi5}, G_{αqi9}, and G_{αqu5} subunits, making these subunits possible targets for PTX. Accordingly, the glutamate-stimulated IP formation in cells coexpressing mGluR2 and G_{αqi9} was inhibited dose-dependently by PTX (Fig. 3). Similar data were obtained in cells expressing mGluR4 (data not shown). Although high concentrations of PTX are necessary for the complete inhibition of the glutamate-induced IP formation, no effect of such high PTX concentrations were observed on the activation of PLC by mGluR1a (Fig. 3).

Full dose-response curves for glutamate were constructed by measuring IP formation in cells coexpressing mGluR2 or mGluR4 with the promiscuous and chimeric α subunits (Fig. 4). For mGluR2, the EC₅₀ values (mean ± standard error from more than two experiments) were 3.7 ± 1.2, 11.5 ± 1.7, 8.4 ± 0.9, 7.6 ± 1.5, and 11.1 ± 0.6 μM with G_{α15}, G_{α16}, G_{αqi5}, G_{αqu5}, and G_{αqi9} respectively. For mGluR4, these values were 9.9 ± 2.3, 20.7 ± 3.7, 16.1 ± 1.3, and 19.1 ± 2.7 μM when determined with G_{α15}, G_{αqi5}, G_{αqu5}, and G_{αqi9} respectively.

The effects of well-characterized agonists of mGluR2 and mGluR4 were examined in cells coexpressing G_{αqi9} and G_{αqu5}, respectively. Glutamate, L-CCGI, 1S,3R-ACPD, and 4C3HPG stimulated IP formation in mGluR2 expressing cells with EC₅₀ values very similar to those reported by measuring the inhibition of forskolin-stimulated cAMP formation in Chinese hamster ovary cells stably expressing mGluR2 (Fig. 5a and Table 1) (20, 21). Furthermore, quisqualate and L-AP4, the potent agonists of group I and group III mGluRs, respectively, had no effects (Table 1). Similarly, the specific and potent agonists of group III mGluRs, L-AP4 and L-SOP, potently stimulated IP formation in cells coexpressing mGluR4 and G_{αqu5} (Fig. 5b and Table 1). The EC₅₀ values were very similar to those reported using cell lines stably expressing mGluR4 (22–25). Taken together, these results indicate that mGluR2 and mGluR4 couple to chimeric G_{αqi/o} subunits and activate PLC and indicate that the few last carboxyl-terminal residues of the G_α subunits play an important role in the specific recognition of mGluRs.

As shown in Fig. 6, the pharmacological profiles of mGluR2 and mGluR4 determined by measuring PLC activation after coexpression with the chimeric G_{αqi9} or G_{αqu5} subunits per-

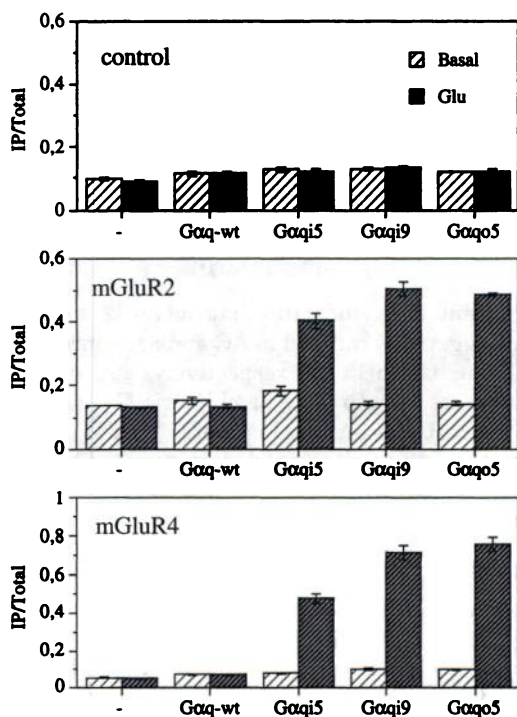


Fig. 2. PLC activation by mGluR2 or mGluR4 coexpressed with chimeric G_{αq} subunits. *Top*, basal and 1 mM glutamate (Glu)-stimulated IP formation in mock-transfected cells or cells expressing the wild-type G_{αq} (G_{αqw}) or the chimeric G_{αq} subunits in which the carboxyl-terminal five amino acid residues have been replaced by those of G_{α12} (G_{αqi5}) or G_{αo} (G_{αqu5}) or in which the nine carboxyl-terminal residues have been replaced by those of G_{α12} (G_{αqi9}). *Middle*, same as *top* except that cells also expressed mGluR2. *Bottom*, same as *top* except that cells also expressed mGluR4. Values are mean ± standard error of triplicate determinations from typical experiments. Similar data were obtained in at least five other experiments.

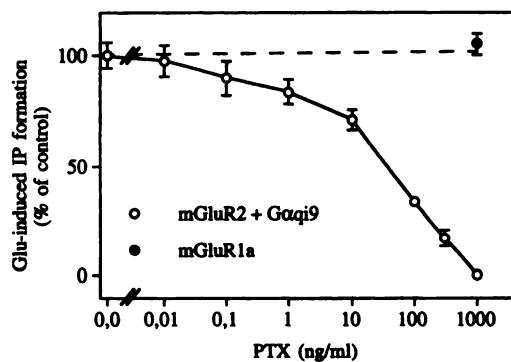


Fig. 3. Effect of PTX treatment on IP formation stimulated by 1 mM glutamate (Glu) in cells expressing mGluR1a or mGluR2 plus G_{αqi9}. After electroporation, cells were incubated for 16 hr in the presence of the indicated concentration of PTX. Basal and 1 mM glutamate-induced IP formations were determined as described in the text. Values are mean ± standard error of triplicate determinations from a typical experiment and are expressed as a percentage of the effect of glutamate in cells not treated with PTX.

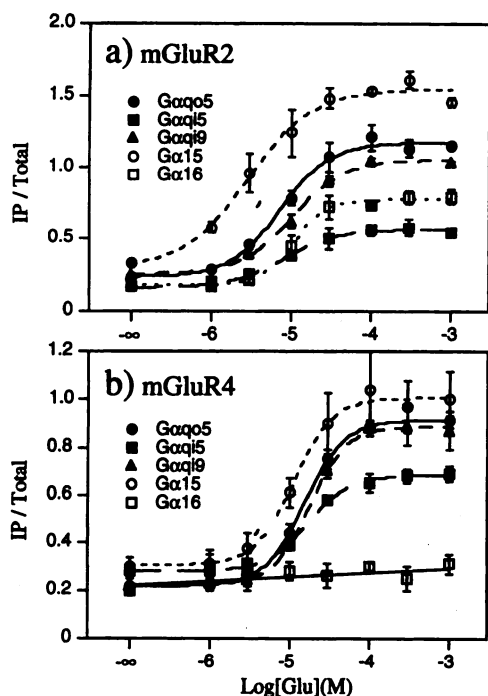


Fig. 4. Dose-response curves for glutamate (Glu) on the IP production in cells coexpressing mGluR2 (a) or mGluR4 (b) with $G_{\alpha qo5}$, $G_{\alpha qi5}$, $G_{\alpha qi9}$, $G_{\alpha 15}$, or $G_{\alpha 16}$. Results are mean \pm standard error of at least three independent experiments performed in triplicate.

fectly correlate with those previously reported by others measuring inhibition of cAMP formation in cells stably expressing these receptors. The use of the chimeric G_{α} subunits therefore seems to be a simple functional assay for the pharmacological characterization of these receptors. We took advantage of this system to study further the effects of recently described drugs on these two cloned receptors. 3,5-DHPG and (-)-t-ADA, which have been described as potent agonists at mGluR1a and mGluR5a (26–29), were inactive at either mGluR2 or mGluR4 (Table 1). Among the four stereoisomers of ACPD, none were potent agonists at mGluR4, but both 1S,3S-ACPD and 1S,3R-ACPD were potent agonists at mGluR2 (Table 1).

Recently, the α -methyl derivatives of L-AP4 (MAP4) and of L-CCGI (MCCGI) (30) and a series of new derivatives of phenylglycine, MPPG, MSPG, and MTPG (31, 32), were described as putative specific antagonists of group II and group III mGluRs. None of these compounds tested at 300 μ M inhibited the effect of 3 μ M glutamate in cells expressing mGluR1a (data not shown). A significant inhibition was observed with MPPG and MTPG when used at 1 mM ($46 \pm 4\%$ and $65 \pm 5\%$ inhibition, respectively). The effect of these drugs was therefore examined on mGluR2 and mGluR4 and compared with the other antagonist, MCPG. The rank order of potency of these antagonists was MCCGI \sim MPPG $>$ MSPG $>$ MCPG = MTPG = MAP4 at mGluR2 and MPPG $>$ MAP4 \gg MSPG at mGluR4, with MCPG, MTPG, and MCCGI being inactive at this receptor (Fig. 7 and Table 1). The Schild plot analysis of MPPG and MCCGI on mGluR2 revealed K_B values of 54.4 ± 2.8 and 69.5 ± 8.1 μ M with a slope of 0.98 ± 0.08 and 1.09 ± 0.06 , respectively ($n = 3$), as expected for competitive antagonists (Fig. 8). The Schild plot analysis of MAP4 and MPPG also revealed that these compounds behave as competitive antagonists of mGluR4 ($K_B =$

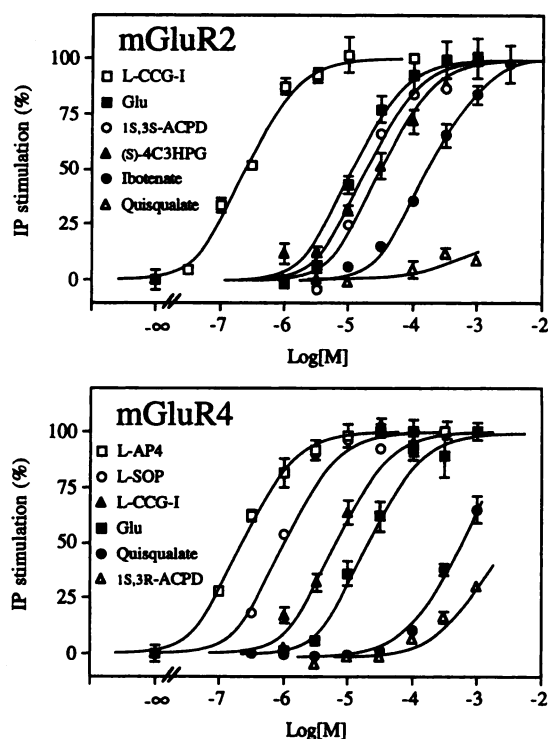


Fig. 5. Effect of various agonists on IP formation in cells expressing mGluR2 plus $G_{\alpha qi9}$ (a) or cells expressing mGluR4 plus $G_{\alpha qo5}$ (b). Transfected cells were washed, preincubated for 10 min with 10 mM LiCl in Krebs' buffer, and then stimulated for 30 min with the agonist at the indicated concentration. IP formation was then determined as described in the text. Values are mean \pm standard error of triplicate determinations from typical experiments and are expressed as a percentage of the maximal effect of glutamate.

69.6 ± 13.3 and 50.3 ± 16.0 μ M, slope = 1.29 ± 0.10 and 1.12 ± 0.07 , $n = 3$, respectively; Fig. 9).

Discussion

The current data indicate that mGluR2 and mGluR4, which are negatively coupled to AC and are representative of group II and III mGluRs, respectively, can activate PLC when coexpressed with $G_{\alpha 15}$ or chimeric $G_{\alpha q}$ subunits that possess the carboxyl-terminal end of $G_{\alpha i2}$ or $G_{\alpha o}$.

$G_{\alpha 15}$ and $G_{\alpha 16}$ subunits cloned from mice and human cDNA libraries, respectively, are specifically expressed in hematopoietic cells (33, 34). They have been recently shown to couple many receptor types to PLC, even receptors that usually stimulate or inhibit AC (15). These proteins share 85% amino acid sequence identity, so $G_{\alpha 16}$ is often considered the human homolog of $G_{\alpha 15}$. According to their high homology, these two G_{α} subunits are equally able to couple many different receptors to PLC (15). However, although $G_{\alpha 15}$ can couple both mGluR2 and mGluR4 to PLC, $G_{\alpha 16}$ was found to be activated only by mGluR2, suggesting that the region of low homology between $G_{\alpha 15}$ and $G_{\alpha 16}$ found 30–50 residues from the carboxyl terminus affects the interaction of these G_{α} subunits with the receptor. Accordingly, it has recently been reported that the 100 carboxyl-terminal residues of $G_{\alpha 16}$ play a role in the coupling specificity to the C5a receptor (35), and the equivalent region in transducin has been shown to contact rhodopsin (19, 36). Although mGluR2 and mGluR4 are unlikely to couple to $G_{\alpha 15}$ and $G_{\alpha 16}$ *in vivo* because these G_{α}

TABLE 1

Pharmacological profile of mGluR2 and mGluR4 as determined by stimulation of IP formation after coexpression of these receptors with G_{αq15} and G_{αq11}, respectively

Each dose-response curve was fitted, and the EC₅₀ and IC₅₀ values were determined using the Kaleidagraph program as described in the text. The antagonists were tested using 20 and 30 μM Glu for mGluR2 and mGluR4, respectively. Values represent mean ± standard error of three or four independent experiments performed in triplicate.

	EC ₅₀	
	mGluR2	mGluR4
μM		
Agonist		
Glu	11.1 ± 0.6	16 ± 1
1S,3S-ACPD	12.9 ± 2.9	48 ± 3
1S,3R-ACPD	18.1 ± 0.3	>1000
1R,3S-ACPD	111 ± 11	>1000
1R,3R-ACPD	≥1000	NE
Ibotenate	272 ± 72	1000
L-CCGI	0.49 ± 0.10	8.9 ± 3.4
4C3HPG	51 ± 19	NE
L-Quisqualate	≥1000	≥1000
L-AP4	NE	0.4 ± 0.2
L-SOP	ND	2.3 ± 1.5
(S)3-hydroxyphenylglycine	NE	NE
3,5-DHPG	NE	NE
4CPG	24 ± 2	NE
(+)-t-ADA	>1000	NE
(-)-t-ADA	NE	NE
IC ₅₀		
Antagonist		
(±)-MCPG	671	NE
MCCG-I	84 ± 8	NE
MPPG	100 ± 9	54 ± 14
MSPG	250 ± 50	>1000
MTPG	453 ± 71	NE
MAP4	447 ± 72	88 ± 10

NE, no effect; ND, not determined.

subunits are expressed at very low levels in the brain, our results indicate that these two mGluRs do not couple with the same potency to different G proteins, reinforcing their classification into two different groups of mGluRs.

The carboxyl-terminal end of the α subunit of G proteins has been shown to play an important role in the interaction with GPCRs (19). A synthetic peptide corresponding to the carboxyl terminus of transducin stabilizes rhodopsin in its active state (36, 37), and chimeric G_{αq} subunits that possess the carboxyl-terminal end of G_{α12} or G_{αo} can be activated by G_i- or G_o-coupled receptors (16). These latter results indicate that the carboxyl-terminal end of the G_α subunit is critical for the specific interaction between GPCRs and the G protein. Our results indicate that glutamate stimulates PLC in cells coexpressing mGluR2 or mGluR4 with the chimeric G_{αq15}, G_{αq19}, or G_{αq11} subunits. This glutamate effect results from the activation of mGluR2 or mGluR4, as indicated by the use of specific mGluR2 and mGluR4 agonists. Furthermore, two observations indicate that the chimeric G_α subunits are responsible for the coupling of these mGluRs to PLC. First, coexpression of mGluR2 or mGluR4 with the wild-type G_{αq} did not allow glutamate to stimulate PLC. Second, as expected by the presence of the PTX ADP-ribosylating site in the chimeric G proteins, the coupling to PLC of mGluR2 and mGluR4 was inhibited after PTX treatment of the cells. Although a high concentration of PTX was required, such a concentration did not affect the stimulation of IP production

by the PLC-coupled mGluR1a. That a high concentration of PTX was necessary for the inhibition of these chimeric G proteins in HEK 293 cells has been reported by others (16). This may be due either to the overexpression of this G_α subunit (so that more PTX is required for a complete ADP-ribosylation) or to a lower efficacy of PTX to ADP-ribosylate such a chimeric G_α subunit. Taken together, these results indicate that even though mGluRs and the other GPCRs constitute two distinct families of receptors, the carboxyl-terminal end of the G_α subunit directs its coupling to receptors of both families.

Determination of the potency of glutamate on stimulating IP formation in cells coexpressing mGluR2 or mGluR4 with the promiscuous or chimeric G protein α subunits revealed that the higher is the efficacy of glutamate in stimulating IP production, the lower is the EC₅₀ value, as expected for a more efficient coupling to PLC. For both mGluR2 and mGluR4, the best coupling to PLC is obtained with G_{α15}. This may result either from better coupling of these receptors to this particular G protein or from a higher level of expression of this α subunit.

The pharmacological profiles of mGluR2 and mGluR4 determined using G_{αq19} and G_{αq11}, respectively, correlates perfectly with those reported by measuring inhibition of cAMP formation in cells stably expressing these receptors (20–25). Measurement of PLC activation in cells transiently expressing G_i-coupled mGluRs and chimeric G proteins therefore seems to be a useful functional assay for the characterization of a large number of wild-types or mutated G_i-coupled mGluRs. Such an assay also seems to be useful for the pharmacological characterization of these receptors. Although the potencies measured using this assay may be slightly different from those on native receptors due to the difference in the transduction pathways analyzed, the rank order of potency of a series of agonists or antagonists may be maintained. Indeed, among the multiple GPCRs studied, only one has been reported to have a slightly different rank order of potency for agonists depending on the transduction mechanism examined (38).

With the limitations mentioned above, this assay was used to further analyze the pharmacological profiles of mGluR2 and mGluR4. Although t-ADA has been reported to be inactive on human mGluR1 and human mGluR5 (39), it has, together with the phenylglycine derivative 3,5-DHPG, a potent agonist action on rat mGluR1 and rat mGluR5 (26–29). Both t-ADA and 3,5-DHPG have therefore been proposed to be specific agonists of group I mGluRs (27, 40), although their action on rat group II and group III cloned mGluRs has not been examined. We show that 3,5-DHPG has no effect on mGluR2 and mGluR4 at 1 mM and that (–)-t-ADA is a very weak agonist of rat mGluR2, as reported for the human mGluR2 (39). The 1S,3S isomer of ACPD has been shown to activate G_i-coupled mGluRs in brain slices (41, 42) and to be a very weak agonist at group I mGluRs (18). Accordingly, it is often used as a selective agonist of group II mGluRs (30, 32, 43–46), but its effect on cloned group II and group III mGluRs has not been reported. A potent agonist action of 1S,3S-ACPD on mGluR3 can, however, be proposed based on its effect on chimeric mGluRs (13). We report here that 1S,3S-ACPD is a potent agonist of mGluR2, being even more potent than 1S,3R-ACPD. However, 1S,3S-ACPD is also an agonist at mGluR4, with a 4-fold lower potency only, suggest-

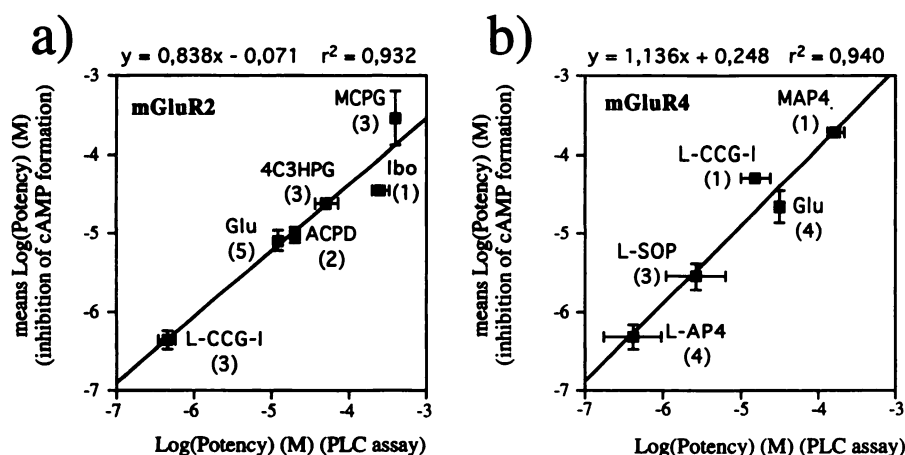


Fig. 6. Correlation between the potencies of several drugs on mGluR2 (a) and mGluR4 (b) determined via the PLC stimulation mediated by $G_{\alpha q19}$ and $G_{\alpha q15}$ respectively, and those reported in the literature by measuring inhibition of forskolin-stimulated cAMP formation. For the antagonists MCPG and MAP4, published K_B values or K_B values estimated using the Cheng and Prusoff equation were used. Numbers in parentheses, number of values found in the literature and used for the analysis. Glu, glutamate. Values are mean \pm standard error.

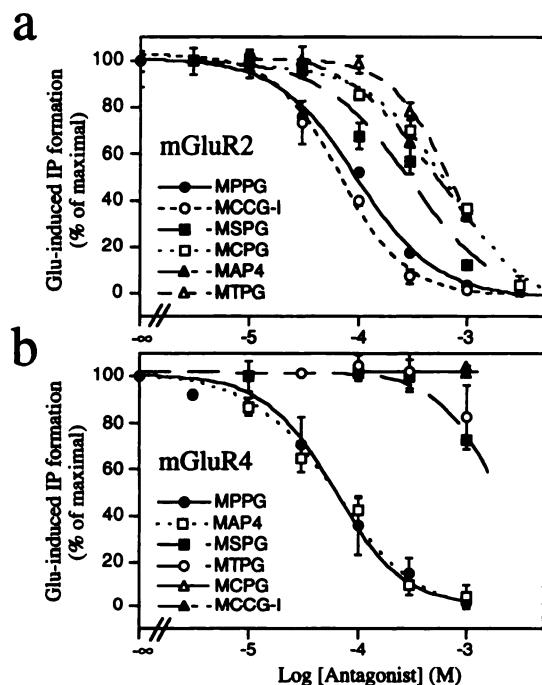


Fig. 7. Effect of various antagonists on IP formation in cells coexpressing mGluR2 and $G_{\alpha q19}$ (a) or cells coexpressing mGluR4 and $G_{\alpha q15}$ (b). Transfected cells were washed, preincubated for 10 min with 10 mM LiCl in Krebs' buffer, and then stimulated for 30 min with 20 μ M glutamate (Glu) (a) or 30 μ M glutamate (b) and the indicated concentration of antagonist. IP formation was then determined as described in the text. Values are mean \pm standard error of triplicate determinations from typical experiments and are expressed as a percentage of the effect of glutamate alone.

ing that its action in the brain will not be exclusively mediated by group II mGluRs.

Although specific agonists will be useful for the characterization of the physiological roles of the different mGluR subtypes, much will be discovered as a result of the specific antagonists. Recently, several compounds have been synthesized and proposed to be specific antagonists of group II and group III mGluRs; these include MCCGI, MAP4, and the phenylglycine derivatives MSPG, MPPG, and MTPG (30–32). Among these, only the effect of MAP4 has been carefully examined on cloned rat receptors (47), and this was performed on mGluR4 only, so that the specificity of this drug is not known. Furthermore, MAP4 has been reported to have L-AP4-like actions in rat adult cortical slices (31). In agree-

ment with Johansen *et al.* (47), we found MAP4 to be a potent and competitive antagonist of mGluR4, being inactive at mGluR1a. However, MAP4 is also an antagonist of mGluR2, with a 5-fold lower potency only, indicating that care should be taken before attributing a physiological role to a specific mGluR subtype based on the effect of MAP4. MCCGI was found to be inactive at mGluR1a and mGluR4 and to be a potent and competitive antagonist of mGluR2. Although its effect on other group I and III mGluRs remains to be determined, MCCGI seems to be a useful drug to characterize the effect of group II mGluRs. Recently, the new phenylglycine derivatives MSPG, MPPG, and MTPG have been proposed as antagonists of group II and group III mGluRs expressed in the spinal cord and responsible for the depressant action of 1S,3S-ACPD and L-AP4, respectively (31, 32). The rank order of potency of these antagonists is MTPG > MPPG > MSPG > MCCGI > MCPG for 1S,3S-ACPD-activated receptors and MPPG > MAP4 > MSPG > MTPG for L-AP4 activated receptors. Here, we show that the rank order of potency of these antagonists is MCCGI \sim MPPG > MSPG > MCPG = MTPG = MAP4 at mGluR2 and MPPG \geq MAP4 \gg MSPG at mGluR4 receptors, suggesting that mGluR2 is not responsible for the 1S,3S-ACPD presynaptic action in the spinal cord. It is, however, possible that differences in the diffusion properties of these molecules affect their apparent potencies determined in the spinal cord preparation.

These results indicate that despite the sequence and structural differences between mGluRs and the other GPCRs, the carboxyl-terminal end of the α subunit of G proteins plays an important role in the specific interaction with mGluRs. The total absence of homology between the mGluR seven-TMD region and the other GPCRs and the observation that the second intracellular loop of mGluRs plays a role equivalent to that of the third intracellular loop of the other GPCRs suggest a convergent evolution of these two receptor families. Interestingly, during evolution, different domains of these two families of proteins have been selected for the interaction with the same domains of the G_α subunits. This further suggests that the interaction of these regions of the α subunit with the receptor is important for the G protein activation (19, 37, 48). In addition, our results indicate that the promiscuous G protein α subunit $G_{\alpha 15}$ or the chimeric $G_{\alpha q15/o}$ proteins can be used to develop simple functional assays for the pharmacological characterization of group II and group III mGluRs.

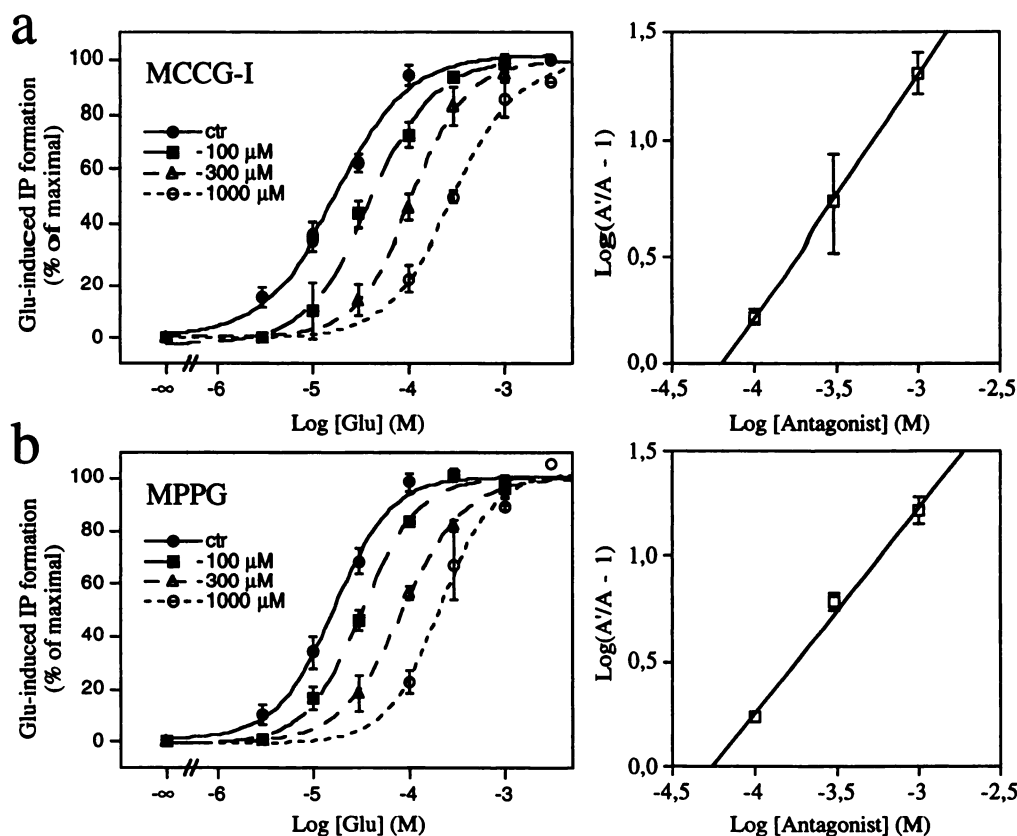


Fig. 8. Dose-response curves of glutamate for Schild plot determination of the antagonist potencies of MCCGI (a) and MPPG (b) on mGluR2. IP formation in cells expressing mGluR2 and $G_{\alpha q19}$ was determined after 30-min stimulation with the indicated concentrations of glutamate alone (ctr) or in the presence of 100 μ M, 300 μ M, or 1000 μ M antagonist. *Right*, Schild plots obtained from the EC_{50} values. Values are mean \pm standard error of three independent experiments performed in triplicates. The K_B values and slopes were determined in individual experiments by linear regression analysis.

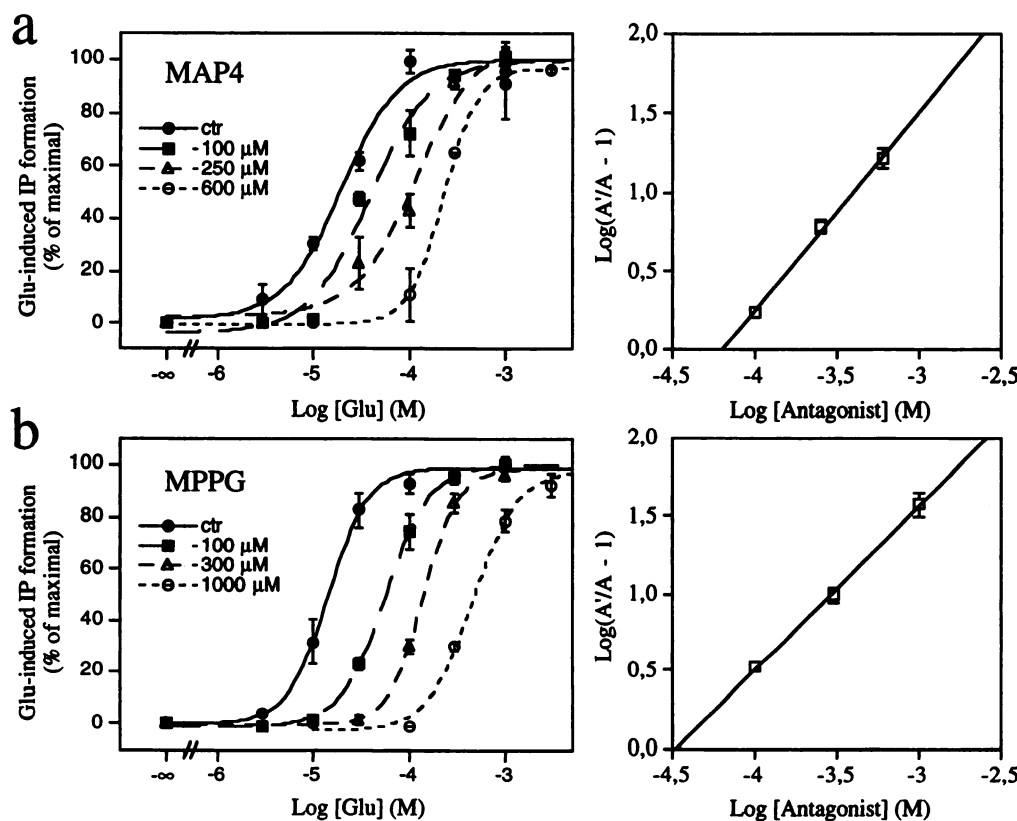


Fig. 9. Dose-response curves of glutamate for Schild plot determination of the antagonist potencies of MAP4 (a) and MPPG (b) on mGluR4. IP formation in cells expressing mGluR4 and $G_{\alpha q15}$ was determined after 30-min stimulation with the indicated concentrations of glutamate alone (ctr) or in the presence of 100 μ M, 250 μ M, or 600 μ M MAP4 (a) or in the presence of 100 μ M, 300 μ M, or 1000 μ M MPPG (b). *Right*, Schild plots obtained from the EC_{50} values. Values are mean \pm standard error of three independent experiments performed in triplicate. The K_B values and slopes were determined in individual experiments by linear regression analysis.

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