Molecular Basis for the Differential Agonist Affinities of Group III Metabotropic Glutamate Receptors

By

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Abbreviations: CaSR, calcium-sensing receptor, mGluR, metabotropic glutamate receptor; HEK, human embryonic kidney 293 cell; L-AP4, L-amino-4-phosphonobutyric acid; L-SOP, L-serine-O-phosphate

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ABSTRACT

Agonist stimulation of Group III metabotropic glutamate receptors (mGluRs) induces an inhibition of neurotransmitter release from neurons. The Group III mGluRs are pharmacologically defined by activation with the glutamate analog L-amino-4-phosphonobutyric acid (L-AP4). The affinities of these receptors for L-AP4 and glutamate vary over approximately a 1500-fold concentration range. The goal of this study was to elucidate the molecular basis for this dispersion of agonist affinities for the Group III receptors mGluR4, mGluR6, and mGluR7. [3H]L-AP4 binding was present in human embryonic kidney cells transfected with the high affinity mGluR4 receptor but not in cells transfected with mGluR6 or the low affinity mGluR7 receptor. Analysis of mGluR4/mGluR6 receptor chimeras revealed that replacement of the first 35 amino acids of mGluR6 with the first 50 amino acids of mGluR4 was sufficient to impart [3H]L-AP4 binding to mGluR6. Homology models of mGluR4 and mGluR7 were employed to predict amino acids that may affect ligand affinity. Mutations were made in mGluR7 to convert selected residues into the equivalent amino acids present in the high affinity mGluR4 receptor. The mGluR7 N74K mutation caused a 12-fold increase in affinity in a functional assay, while the N74K mutation in combination with mutations in residues 258 – 262, which lie outside the binding pocket, caused a 112-fold increase in affinity compared to unmutated mGluR7. Our results demonstrate that the binding site residues at position lysine 74 in mGluR4, glutamine 58 in mGluR6, and asparagine 74 in mGluR7 are key determinants of agonist affinity and that additional residues situated outside of the binding pocket, including those present in the extreme amino terminus, also contribute to agonist affinity and the pharmacological profiles of the Group III mGluRs.
Introduction

The Group III metabotropic glutamate receptors (mGluRs; mGluR4, 6, 7 and 8) share 70-74% amino acid identity and are selectively activated by the synthetic agonist L-amino-4-phosphonobutyric acid (L-AP4), and the endogenous amino acid L-serine-O-phosphate (L-SOP; Fig. 1). The mGluR4, mGluR7, and mGluR8 receptor subtypes are expressed primarily on nerve terminals where they act to inhibit neurotransmitter release in the central and peripheral nervous systems (Macek et al., 1996; Pekhletski et al., 1996; Shigemoto et al., 1996; Lafon-Cazal et al., 1999). mGluR6 expression is restricted to retinal bipolar cells where it acts postsynaptically to regulate visual responses (Nomura et al., 1994). Animal models have suggested mGluR4 as a potential drug target for the treatment of absence epilepsy (Snead et al., 2000), neurodegenerative disorders associated with over-activation of glutamate-gated ion channels (Bruno et al., 2000) and Parkinson’s disease (Marino et al., 2003), while mGluR7 may be a potential target for the development of novel antidepressants (Cryan et al., 2003).

Agonists at mGluRs bind to a site localized within the Venus flytrap domain of the extracellular region and induce a conformational change which results in the closure of the flytrap and propagation of the signal through the transmembrane domain (Bessis et al., 2002; Jingami et al., 2003). Although the Group III receptors have high sequence homology, their affinities for L-AP4, L-SOP, and L-glutamate span a wide concentration range encompassing several orders of magnitude. This large dispersion of affinities for endogenous ligands suggests that the Group III receptors have evolved to operate over a wide range of intensities of synaptic activity.
Biochemical assays measuring receptor activation together with radioligand binding assays using \[^{3}\text{H}]L\text{-AP4}\) have shown that mGluR4 and mGluR8 have similar high affinity for L-AP4 (EC\textsubscript{50} = 0.4 – 1 \(\mu\)M, IC\textsubscript{50} = 0.4 - 0.8 \(\mu\)M; Han and Hampson, 1999; Hampson et al., 1999; Peltekova et al., 2000; Schoepp et al., 1999). As expected based on the reported low affinity of L-AP4 for mGluR7 in functional assays (EC\textsubscript{50} = 160 - 800 \(\mu\)M, Okamoto et al., 1994; Saugstad et al., 1994; Corti et al., 1998), no specific binding of \[^{3}\text{H}]L\text{-AP4}\) was detected in cells expressing mGluR7 (Naples and Hampson, 2001). Surprisingly however, despite reports indicating that mGluR6 has a pharmacological profile similar to mGluR4 and mGluR8 in functional assays, (i.e. high affinity for L-AP4, EC\textsubscript{50} = 0.6 – 0.9 \(\mu\)M; Nakajima et al., 1993; Ahmadian et al., 1997), no specific binding of \[^{3}\text{H}]L\text{-AP4}\) was detected human embryonic kidney (HEK) 293 cells transfected with either rat or human mGluR6 (Naples and Hampson et al., 2001).

Previous studies have determined that the selectivity of L-AP4 and L-SOP for mGluR4 is conferred by several positively charged amino acids within the ligand binding pocket that interact with the negatively charged phosphonate moiety of these compounds (Bertrand et al., 2002; Rosemond et al., 2002; Macchiarulo et al., 2003). In the present study, the molecular basis for the differential affinities and agonist binding properties of mGluR4, mGluR6, and mGluR7 was investigated. Our results demonstrate that a specific subset of residues located within and just outside of the binding pocket is responsible for the wide range of agonist affinities, and that the extreme amino terminal amino acid sequence is critical for imparting high affinity \[^{3}\text{H}]L\text{-AP4}\) binding.
Materials and Methods

Materials. L-AP4, [3H]L-AP4 (specific activity 49 Ci/mmol), and L-SOP were purchased from Tocris Cookson Inc. (Bristol, UK and Ellisville, MO, USA). The anti-mGluR4a and anti-mGluR7a antibodies were purchased from Upstate Group, Inc. (Charlottesville VA, USA). The anti-mGluR6 antibody was purchased from Neuromics Inc. (Northfield, MN, USA).

Expression Constructs and Site-Directed Mutagenesis. The wild-type rat mGluR4a was subcloned into pcDNA3.1/myc-His (Invitrogen, Carlsbad, CA, USA) as previously described (Rosemond et al., 2002). The mGluR4a with a c-myc epitope inserted between amino acids lysine 35 and glycine 36 was subcloned into pcDNA3 (Invitrogen, Carlsbad, CA, USA) as described previously by Han and Hampson, (1999). The rat mGluR6 was subcloned into the HindIII and NotI sites of the pcDNA3 vector and the pcDNA3.1 vector. The wild-type rat mGluR7 was subcloned into pcDNA3.1/myc-His vector. The human CaSR-mGluR7 cDNA construct was generated by replacing the first 44 amino acids of the human mGluR7 with the first 27 amino acids of the human calcium-sensing receptor (CaSR); the cDNA was subcloned into the NheI and NotI sites of the pIREShyg3 vector (BD Biosciences, Clontech Laboratories Inc., Palo Alto, CA, USA).

A series of chimeras between mGluR4 and mGluR6 were produced in the mGluR6-c-myc background (in pcDNA3.1/myc-His). Restriction enzyme sites at equivalent positions in the cDNAs of mGluR4 and mGluR6 were used to construct the chimeric receptors. The restriction enzyme sites either pre-existed within the cDNAs, or were introduced through site-directed mutagenesis. Base pair changes were produced using the QuikChange site-directed mutagenesis strategy (Stratagene, CA, USA).
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4/6A chimera (mGluR41-586/mGluR6579-871) used the SrfI site to exchange the entire amino termini of the two receptors. The introduction of the SrfI site resulted in two amino acid changes in each receptor (P586A and W587R in mGluR4 and P579A and W580R in mGluR6). The 4/6B chimera (mGluR41-110/mGluR695-871) used the XhoI restriction enzyme site and the 4/6C chimera (mGluR41-78/mGluR663-871) used an alternate XhoI restriction enzyme site. The pre-existing XhoI site within mGluR4 was deleted to produce the 4/6C chimera while the 4/6D chimera (mGluR41-50/mGluR635-871) utilized the AvrII restriction enzyme site. A second series of chimeras between mGluR4 and mGluR7 were produced within the mGluR7-c-myc background (pcDNA3.1/myc-His). Restriction enzyme sites at equivalent positions in the cDNAs of mGluR4 and mGluR7 were used to construct the chimeric receptors. The 4/7A chimera (mGluR41-315/mGluR7317-915) used the BamHI site, the 4/7B chimera (mGluR41-286/mGluR7288-915) used the NruI site, the 4/7C chimera (mGluR41-221/mGluR7222-915) used the SalI site and the 4/7D chimera (mGluR41-110/mGluR7109-915) used the XhoI restriction enzyme site. All of the single and multiple point mutations in mGluR7 were made on the modified CaSR-mGluR7 construct described above. All chimeras and mutants were sequenced prior to analysis.

**Cell Culture and transfections.** HEK-293-TSA-201 cells were cultured in minimal essential medium supplemented with 6% fetal bovine serum, 2mM glutamine and penicillin-streptomycin antibiotics (Invitrogen, Carlsbad, CA, USA). For radioligand binding assays, transient transfections of HEK cells were conducted using a calcium phosphate precipitation protocol as described previously (Han and Hampson, 1999). For functional assays, transient transfections of HEK cells were conducted using the
LipofectAMINE 2000 reagent (Invitrogen, CA, USA) in 6-well microtiter plates. Two µg of receptor cDNA were co-transfected with 1 µg of the cDNA coding for Gα15 per well.

**Radioligand Binding.** Membranes were harvested 48 hours post-transfection and prepared as previously described (Naples and Hampson, 2001; Rosemond et al., 2002). Frozen membranes were thawed and homogenized using a Polytron. 125 µg of membrane protein was used for all binding assays in a final volume of 250 µl. All assays were performed on ice using 30 nM [³H]L-AP4. Nonspecific binding of this ligand to cell membranes was defined as binding in the presence of 300 µM L-SOP. Following a 30 min incubation, bound and free radioligand were separated by centrifugation (14,000 X g, 4 min). The membranes were washed with cold (4°C) assay buffer, solubilized overnight in 1M NaOH and dissolved in Ultima Gold liquid scintillation fluid (Packard / PerkinElmer Life and Analytical Sciences Inc., Boston, MA, USA) prior to counting on a Tri-Carb 2100TR liquid scintillation analyzer (Packard / PerkinElmer Life and Analytical Sciences Inc., Boston, MA, USA).

**Functional assay for mGluRs.** Responses to L-AP4 were measured in HEK cells loaded with the calcium-sensitive dye Fluo-4 in a fluorescence-based assay as described previously (Kuang et al., 2003; Yao et al., 2003). The fluorescence-induced calcium release was recorded on a FLEXstation benchtop scanning fluorometer (Molecular Devices Corp., Sunnyvale, CA, USA) at room temperature with settings of 485 nm for excitation and 525 nm for emission. For mGluR7 we found that at L-AP4 concentrations of ≥ 1 mM, responses were seen in mock-transfected HEK cells. Therefore in the calculation of the EC₅₀ value for mGluR7, the responses observed at high L-AP4
concentrations in mock transfected cells were subtracted from the responses obtained in mGluR7 transfected cells. The GraphPad Prism 3.0 software was used to plot fluorescence intensities and calculate EC$_{50}$ values.

**Immunoblotting.** Electrophoresis samples containing 100 mM dithiothreitol were incubated at 37$^\circ$C for 15 minutes prior to gel electrophoresis. The procedure for immunoblotting was conducted as described previously (Pickering et al., 1995).

**Molecular Modeling.** A homology model of the closed form of the extracellular domain of human mGluR7 was generated using the X-ray crystal structure of the extracellular domain of rat mGluR1 as a template (Kunishima et al., 2000, PDB coordinates, 1EWK.pdb). The sequence alignment between the rat mGluR1 and human mGluR7 sequences was adopted from the multiple alignment of the eight mGluRs (Fig. 2). The alignment was checked to avoid gap insertions in the conserved secondary structural motifs. MODELER 6 (Sali and Blundell, 1993) was used to generate the homology model and Sybyl 6.9 (Tripos Incorporated, St Louis, MO) was used to view, analyze and manipulate the structure. The short disordered loop absent in the crystal structure of mGluR1 was excluded from the model. The MODELER and VERIFY 3D server (Luthy et. al., 1992) were used to assess the integrity of the model. The best initial model was subjected to further refinement using energy minimization with AMBER 7.0 (Case et. al., 2001). The force field parameters for the ligands were developed with the aid of the antechamber module in AMBER. The coordinates for the zwitterionic forms of glutamate and L-AP4 were generated in an extended conformation using the Xleap module in AMBER 7.0. The ionization state of the phosphate group of L-AP4 was PO$_3^{2-}$. 

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The mGluR7 homology model was first energy minimized with glutamate docked in the same orientation as in the mGluR1 crystal structure. The complex was solvated in a TIP3P water box (Jorgensen et. al., 1983) so that the box boundaries were at least 10 angstroms away from any protein atom. A water molecule in the crystal structure of mGluR1 between the bound glutamate and arginine 78 was retained in the mGluR7 model because this amino acid is conserved in all mGluRs. Additional water molecules were placed in the binding pocket by solvation using AMBER. Although the placement of the water molecules in the binding pocket causes a negative and thus unfavorable change in entropy, this procedure optimizes the interactions between the ligand and the receptor. Counter ions (Cl\textsuperscript{-}) were added to neutralize the system. The coordinates for the solvated complex were then energy minimized in AMBER 7.0 using the Cornell force field. A dielectric multiplicative constant of 1.0 was used to calculate the electrostatic interactions and a cut off of 12 angstrom was used for nonbonding interactions. The final energy minimization was carried out by restraining the protein backbone and then reducing the constraints gradually to zero. Subsequently, the model was minimized for 5000 steps without constraints. The bound glutamate was replaced by L-AP4 and the mGluR7-L-AP4 complex was energy minimized as described above.

Results

Pharmacological profiles of mGluR4, mGluR6 and mGluR7

In heterologous expression systems the Group III mGluRs are coupled to the inhibition of adenylyl cyclase. To switch the signal transduction system to the stimulation of phosphoinositide turnover and release of intracellular calcium, the receptor cDNAs were transiently co-transfected with the cDNA coding for the promiscuous G\textsubscript{\alpha15}
G-protein subunit to artificially couple the receptor to the phospholipase C pathway (Gomeza et al., 1996). L-AP4-induced responses were monitored by measuring the release of intracellular calcium in HEK cells loaded with the calcium-sensitive dye, Fluo-4. The EC$_{50}$ values for L-AP4 for mGluR4 and mGluR6 were 0.29 ± 0.03 and 1.97 ± 0.59 µM respectively (Fig. 3). In contrast, no responses were observed in cells co-expressing either rat or human mGluR7 and Goα15 (or the chimeric G-protein Gqi9) with concentrations of L-AP4 up to 500 µM. However, responses were consistently obtained in HEK cells co-transfected with Goα15 and a construct in which the first the first 44 amino acids of the human mGluR7 receptor were replaced with the first 27 amino acids of the human CaSR; the EC$_{50}$ value for L-AP4 was 429 ± 134 µM.

**Analysis of chimeras of mGluR4 and mGluR6**

We previously reported that in HEK cells expressing mGluR4, high levels of [³H]L-AP4 binding were observed while [³H]L-AP4 binding was undetectable in HEK cells expressing mGluR6 or mGluR7 (Naples and Hampson, 2001). This experiment was repeated and the results were confirmed in the present study. To identify the region within the mGluR6 receptor responsible for the inhibition of [³H]L-AP4 binding, chimeric receptors containing portions of the extracellular domain of mGluR4 were ligated to the complementary downstream segments of mGluR6 (Fig. 3). Membranes prepared from cells expressing the mGluR4/6 chimeras and the mGluR6 wild-type receptor were probed on immunoblots with a C-terminal anti-mGluR6 antibody; the mGluR6 receptor was highly expressed while the chimeras were expressed at lower levels (Fig. 4).
The mGluR4/6A chimera encompassed the complete extracellular domain of mGluR4 (amino acids 1-586) spliced to the transmembrane and C-terminal regions of mGluR6 (amino acids 579-871). Autocompetition radioligand binding experiments with labeled and unlabeled L-AP4 showed that the mGluR4/6A chimera had an affinity for L-AP4 that was similar that of wild-type mGluR4 (IC$_{50}$ = 0.43 ± 0.04 µM; mGluR4 IC$_{50}$ = 0.35 ± 0.10 µM, Fig. 3). However, in the functional assay the 4/6A chimera was not activated by L-AP4 at concentrations of up to 500 µM. The lack of activity with the m4/6A chimera could have been caused by the two amino acid change at the junction of the extracellular domain and the transmembrane domain region in the construction of this chimera. However, it should be noted that other non-functional chimeras have also been observed in other family C receptors (e.g. mGluR2/mGluR1, Takahashi et al., 1993; mGluR1/DmGluRA, Paramentier et al., 1998; GABA$_B$R1/mGluR1, Malitschek et al., 1999; mGluR1/4, Maj et al., 2003).

The mGluR4/6B chimera contained the first 110 amino acids of mGluR4 spliced to amino acids 95-871 of mGluR6, the mGluR4/6C chimera contains the first 78 amino acids of mGluR4 spliced to amino acids 63-871 of mGluR6, and the mGluR4/6D chimera contains the first 50 amino acids of mGluR4 spliced to amino acids 35-871 of mGluR6. All of these chimeras displayed affinities for L-AP4 similar to the wild-type mGluR4 receptor in the autocompetition binding assay and in the functional assay (Fig. 3). These findings indicate that the region of the mGluR6 receptor responsible for the lack of [$^3$H]L-AP4 binding is located within the first 35 amino acids of the mGluR6 receptor.
The affinity of L-AP4 for activation of mGluR6 is influenced by amino acids within the ligand binding pocket. To explore the ligand binding pocket of mGluR6, amino acids that establish bonds with agonists in the binding pocket were mutated to alanine residues. We previously generated a structural model of mGluR4 with L-SOP docked into the binding pocket (Rosemond et al., 2002) based on the crystal structure of mGluR1 (Kunishima et al., 2000; Tsuchiya et al., 2002). Two amino acids within the binding pockets differ between mGluR4 and mGluR6; lysine 74 and glycine 158 in mGluR4 correspond to glutamine 58 and alanine 159 in mGluR6 (see Fig. 2). The mGluR6 Q58K/A159G double mutant displayed a 7-fold higher affinity for L-AP4 in the functional assay (EC$_{50} = 0.27 \pm 0.14 \mu M$) compared to the wild-type mGluR6 receptor with an affinity that was similar to wild-type mGluR4. Surprisingly however, the Q58K/A159G mutant showed no specific $[^3]$H-L-AP4 binding despite the high level of protein expression observed on immunoblots (data not shown).

Analysis of mGluR7

To identify regions of the extracellular domain of mGluR7 receptor responsible for the low affinity of this receptor for agonists, four chimeras of mGluR4 and mGluR7 were studied (Fig. 6). The mGluR4/7A chimera included the first 315 amino acids of rat mGluR4 spliced to amino acids 317-915 of mGluR7. This chimera displayed a similar affinity for $[^3]$H-L-AP4 in the binding assay and a relatively small 2.5-fold decrease in affinity for L-AP4 in the functional assay compared to wild-type mGluR4. The mGluR4/7B chimera contained the first 286 amino acids of mGluR4 spliced to amino acids 288-915 of mGluR7 and showed a 3-fold lower affinity for L-AP4 compared to
mGluR4 (EC$_{50}$ = 0.94 ± 0.23 μM). The mGluR4/7C chimera contained the first 221 amino acids of mGluR4 spliced to amino acids 222-915 of mGluR7; this construct showed a 10-fold decrease in affinity in the functional assay (EC$_{50}$ = 3.02 ± 0.52 μM) compared to the wild-type mGluR4 receptor and a complete loss of detectable [$^3$H]L-AP4 binding. The mGluR4/7D chimera contained the first 110 amino acids of mGluR4 spliced to amino acids 109-915 of mGluR7. Despite robust expression on immunoblots (Fig. 4B), no specific [$^3$H]L-AP4 binding or activation by L-AP4 was observed in this construct with concentrations of up to 500 μM (Fig. 6).

A homology model of mGluR7 was generated to facilitate further analysis of L-AP4 interactions at this receptor. The degree of amino acid sequence identity between mGluR7 and the template (mGluR1) within the region modeled was 41%. The model indicated that the ligand binding pocket of mGluR7 differs from mGluR4 by two residues; asparagine 74 in mGluR7 is a lysine in mGluR4, and aspartate 289 in mGluR7 is a glutamate in mGluR4 (Figs. 2 and 5). Surprisingly, conservatively mutating aspartate 289 in mGluR7 to glutamate caused a complete loss of detectable protein on immunoblots; however, this mutant was detected when the cells were incubated with the proteosome inhibitor MG-132 prior to analysis on SDS-PAGE (Fig. 4C). In contrast to D289E, converting asparagine 74 in mGluR7 to lysine increased the affinity for L-AP4 by 12-fold (EC$_{50}$ = 35.6 ± 14 μM, Table 1) compared to the unmutated mGluR7 receptor.

In addition to the two residues in the binding pocket, the homology model also indicated that a short segment encompassing amino acids glutamine 258 to aspartate 262 (Q$_{258}$E$_{259}$R$_{260}$K$_{261}$D$_{262}$) in mGluR7 differs between mGluR7 and the other Group III
receptors. This difference is readily apparent when the carbon backbone derived from the mGluR7 model is overlaid onto the structural model of mGluR4 where it can be seen that this stretch of residues forms a small loop in mGluR7 that is not present in the other Group III receptors (Fig. 7). This five amino acid segment in mGluR7 is represented by only three amino acids in the other Group III receptors. We hypothesized that although this section of the polypeptide lies just outside of the binding pocket, it may influence ligand affinity. Therefore, the two extra residues in mGluR7 were deleted (glutamine 258 and glutamate 259, termed the QE deletion mutant) and then further mutants were produced that combined the QE deletion mutant with additional mutations in mGluR7 designed to mimic mGluR4. These included a triple mutant (QE deletion + K261E), a tetra-mutant (QE deletion + K261E and D262P), a penta-mutant (QE deletion + K261E + D262P + N74K) and a hexa-mutant (QE deletion + K261E + D262P + N74K + D289E).

The mutants were analyzed in the fluorescence-based functional assay and the results are summarized in Table 1. All of the mutants in this series displayed affinities that were higher than the unmutated mGluR7 except for the QE deletion mutant where no responses were seen. The highest affinity mutant was the penta-mutant (EC50 = 3.8 ± 0.8 µM) which included the deletion of two residues (Q258 and E259) and the replacement of two residues (K261E + D262P) in the loop region and replacement of one residue in the binding pocket (N74K). The hexa-mutant, which included the five amino acids in the penta-mutant plus the second binding pocket mutation D289E, showed a lower affinity (EC50 = 9.3 ± 0.22 µM) compared to the penta-mutant.

**Discussion**
Glutamate and GABA mediated excitatory and inhibitory synaptic transmission are tightly regulated processes. In the central nervous system, Group III mGluRs are present on both glutamatergic neurons and GABAergic interneurons (Shigemoto et al., 1996; Bradley et al., 1999; Corti et al., 2002), the latter of which are thought to be activated by glutamate “spillover” from nearby glutamatergic terminals (Mitchell and Silver, 2000; Semyanov and Kullmann, 2000). The precise amount of glutamate and GABA released is determined in part by the presence of the different subtypes of presynaptic mGluRs. Thus the affinity of a presynaptic mGluR for glutamate is a critical factor in regulating synaptic neurotransmitter levels.

We previously proposed that the inhibitory properties of mGluR4 on neurotransmitter release are an important parameter in maintaining the appropriate level of neuronal firing during synaptic transmission (Pekhletski et al., 1996). High affinity receptors such as mGluR4 and mGluR8 would be activated at low levels of synaptic activity whereas high frequency neuronal firing would be required to activate the low affinity mGluR7 receptor (Sansig et al., 2001). Results from more recent studies also indicate that some L-AP4 sensitive receptors are tonically activated by resting levels of extracellular glutamate (Xi et al., 2003; Acuna-Goycolea et al., 2004).

The results from the present study provide an explanation for the molecular basis of the differential agonist affinities of the Group III mGluRs. A side by side comparison of mGluR4, mGluR6, and mGluR7 expressed in HEK cells indicated that in the functional assay, wild-type mGluR4 and mGluR6 showed robust activity while no receptor activation was observed with either rat or human mGluR7. The inability to detect responses to mGluR7 was likely not caused by a lack of cell surface expression.
because immunocytochemical analysis showed surface expression in fixed transfected HEK cells (data not shown). However, when the first 35 amino acids of mGluR7 were replaced with the first 44 amino acids of the CaSR, receptor activation was observed at concentrations of L-AP4 at and above 250 µM. Thus the rank order of the EC\textsubscript{50}s values was mGluR4 > mGluR6 >> mGluR7. However as reported previously (Naples and Hampson, 2001), only mGluR4 (and mGluR8) displayed specific [\textsuperscript{3}H]L-AP4 binding.

The absence of [\textsuperscript{3}H]L-AP4 binding in mGluR7 can be explained by its extremely low affinity for agonists. The measured affinity for mGluR6 in the functional assay (EC\textsubscript{50} = 1.9 µM) also suggests the possibility that the affinity of L-AP4 for mGluR6 was below the limit of detection in the binding assay. However the mGluR6 double mutant which mimicked the binding pocket of mGluR4, increased the affinity of L-AP4 in the functional assay to that of mGluR4, yet this mutant still did not display [\textsuperscript{3}H]L-AP4 binding. Surprisingly, high affinity binding could be imparted to mGluR6 by replacing the first 35 amino acids with the first 50 amino acids of mGluR4. Although the homology models did not encompass most of this section of the receptor polypeptide because it is not part of the crystal structure of mGluR1 used as template in the model, it is thought that this region, which includes the predicted signal peptide sequence, lies well outside of the ligand binding pocket.

It is not clear how the amino terminus of the receptor could modulate high affinity agonist binding. It has been reported that the extreme amino terminus of the GluR1 glutamate-gated AMPA receptor channel was required for proper trafficking to the plasma membrane (Xia et al., 2002). However, functional responses were obtained with mGluR6 in live HEK cells and an immunocytochemical analysis showed that mGluR6
was expressed on the surface of transfected cells (data not shown); thus aberrant receptor trafficking does not provide an explanation for the lack of detectable \[^3\text{H}\]L-AP4 binding in mGluR6.

Another possibility is that proper processing and cleavage of the signal peptide may be required for maintaining a high affinity conformation of the receptor, or alternatively, the extreme amino terminus of the mature receptor, excluding the putative cleaved signal peptide sequence may indirectly affect the precise 3-dimensional architecture of the binding pocket and therefore ligand affinity. We note that the importance of the first 30-50 residues in the Group III mGluRs is also reflected in the observation that replacement of this region in mGluR7 with amino acids of the CaSR was required for generating functional responses to mGluR7 in HEK cells. Taken together, these findings indicate that the extreme amino termini contribute to the tertiary structure and pharmacological properties the Group III mGluRs.

The molecular basis for the very low affinity of mGluR7 was first examined in a series of chimeras between mGluR4 and mGluR7. A pharmacological profile roughly similar to mGluR4 was seen in the mGluR4/7A chimera that contained the first 315 amino acids of mGluR4 ligated to the complementary downstream sequence of mGluR7. The mGluR4/7B and mGluR4/7C chimeras had progressively smaller segments of mGluR4 and displayed affinities in the functional assay that were three and ten fold lower than mGluR4 respectively.

The mGluR4/7A chimera included the only two residues in the ligand binding pocket of mGluR4 that differ between the two receptors; asparagine 74 and aspartate 289 in mGluR7 align with lysine 74 and glutamate 287 in mGluR4. To determine the
contribution of these two residues to the affinity of L-AP4, we generated and characterized the mGluR7 mutants N74K and D289E. The N74K mutant displayed a 12-fold increase in affinity over wild-type mGluR7, while the D289E mutant was undetectable on immunoblots unless a proteosome inhibitor was present. This latter observation indicates that the D289E mutant was rapidly degraded.

The largest mutagenesis-induced shift to higher affinity in mGluR7 was seen in the penta-mutant where four residues comprising a small loop outside of the binding pocket and the binding pocket residue asparagine 74 were mutated to the equivalent amino acids in mGluR4. This loop region is situated on the top of lobe II just outside of the pocket containing the docked ligand and protrudes into the cavity formed by the two lobes of the Venus flytrap (Fig. 7). The data suggest that this loop or “bump” in the polypeptide chain contributes to the lower agonist affinity of mGluR7. The residues in this region may perturb the binding pocket residues that make direct contact with the bound ligand such that they establish less favorable contacts with the ligand compared with the high affinity L-AP4 receptors. Alternatively, the protrusion of this loop into the cavity formed by the two lobes may hinder full closure of the lobes in the Venus flytrap domain. This scenario would be consistent with a previous proposal that ligand affinity depends in part on the propensity of the ligand to stabilize the closed conformation of the Venus flytrap (Parmentier et al., 2002).

Our results also clearly demonstrate that a primary contributor to agonist affinity in the Group III mGluRs is the single position occupied by lysine 74 in mGluR4, glutamine 58 in mGluR6, and asparagine 74 in mGluR7 (see Figs. 5 and 8). The amino acids occupying this position are also variable in the other members of the mGluR family.
(i.e. a tyrosine in Group I receptors and an arginine in Group II receptors, Fig. 2). We suggest that the higher affinity of mGluR4 (and mGluR8) is mediated in part by an ion pair formed between lysine 74 in mGluR4 (and lysine 71 in mGluR8) and the phosphonate group of L-AP4 and L-SOP, and that the lower affinity of mGluR6 is caused by the replacement of the charged lysine with polar glutamine which likely establishes a lower energy hydrogen bond with the phosphonate group (Fig. 8). In mGluR7, we propose that a water molecule could link the oxygen atoms of the phosphonate group on L-AP4 and asparagine 74. In the homology model, the distance between these two oxygens is 4.3 angstroms which is sufficient to accommodate a water molecule as shown in Figure 8. Although the longer length of the charged side chain of lysine 74 in this position in mGluR4 precludes the presence of a water molecule, this residue likely establishes a direct interaction with the ligand that may contribute to the higher agonist affinity of this receptor. We predict that the various residues occupying this position in the mGluRs would be good candidates for structure based drug design efforts seeking to optimize ligand selectivity and affinity.

Acknowledgements

We thank Drs. S. Nakanishi and M. Simon for the rat mGluR and G\(\alpha\)15 cDNAs. This work was supported by an operating grant (to DRH) and a PDF Strategic Training grant (to MW) from the Canadian Institutes of Health Research, and an Ontario Graduate Scholarship (to ER). We are also grateful for the support of the supercomputing facility at the Molecular Design and Information Technology Centre in the Dept. of Pharmaceutical Sciences, University of Toronto.
References


Han G and Hampson DR (1999) Ligand binding to the amino-terminal domain of the mGluR4 subtype of metabotropic glutamate receptor. *J Biol Chem* **274**: 10008-10013.


**FIGURE LEGENDS**

**Fig. 1.** *Structures of the Group III mGluR agonists.* The synthetic compound L-AP4 has higher affinity for Group III mGluRs compared to the endogenous amino acids L-
glutamate and L-serine-O-phosphate (L-SOP). The phosphonate functional group on L-AP4 and L-SOP confers selectivity for the Group III mGluRs.

**Fig. 2.** Multiple sequence alignment of a portion of the extracellular domains of mGluRs. The alignment was generated using ClustalX v.1.8. Amino acids in bold are in the glutamate-binding pocket; the numbers above the residues indicate amino acids in mGluR1. Amino acids highlighted with black background represent residues in the ligand binding pocket that differ between mGluR4 and mGluR6 (Q58 and A159 of mGluR6) and mGluR4 and mGluR7 (N74 and D289 of mGluR7). The proposed loop region mGluR7 (encompassing glutamine 258 to aspartate 262) that was mutated is underlined. Ligation sites for the receptor chimeras are indicated by the arrows and the predicted signal peptides are underlined. The sequences shown are the rat sequences except for mGluR7 which is the human sequence. Within the region shown, the human mGluR7 sequence differs from the rat sequence at two amino acids (G5R and V27A, rat to human).

**Fig. 3.** Radioligand binding and functional analysis of mGluR4/mGluR6 receptor chimeras. IC$_{50}$ values were calculated from $[^{3}H]$L-AP4 radioligand binding experiments while EC$_{50}$ values were generated from the fluorescence-based functional assay. All values are the means ± SEM of 3-6 experiments. N.B., no binding detected; N.R, no response with 500 $\mu$M L-AP4.

**Fig. 4.** ImmunobLOTS of Group III mGluR chimeras and point mutations.
A. Immunoblots of wild-type mGluR6 and the mGluR4/6 chimeras probed with an anti-mGluR6 antibody; B. immunoblots of the mGluR4/7 chimeras probed with the anti-mGluR7 antibody; C. immunoblots of mGluR7 mutations.

Fig. 5. Comparative schematic diagrams of the ligand binding pockets of mGluR4 and mGluR7. Schematic diagrams illustrating the differences in the interactions of L-AP4 at mGluR4 and mGluR7. Hydrogen-bonding distances are labelled in angstroms. For clarity, the interactions between the $\alpha$-amino group of L-AP4 and the receptors are omitted. The diagram was produced using LIGPLOT (Wallace et al., 1995).

Fig. 6. Radioligand binding and functional analysis of mGluR4/mGluR7 receptor chimeras. $[^{3}H]$L-AP4 binding and L-AP4 activation studies of wild-type and mGluR4/7 receptor chimeras. All values are the means ± SEM of 3-5 experiments. N.B., no binding detected; N.R. no response at 500 $\mu$M L-AP4.

Fig. 7. 3-Dimensional folds of the extracellular domains of mGluR4 and mGluR7. Ribbon structures of the backbones of the closed forms of mGluR4 (red) and mGluR7 (blue) are superimposed on each other with glutamate docked into the ligand-binding pocket (depicted as a space filled representation). The small loop region mutated in mGluR7 is colored in yellow.

Fig. 8. Close up of the ligand-binding pocket of mGluR7. L-AP4 is docked into the binding pocket. Blue indicates nitrogen atoms, red oxygen, orange, phosphorous and the
purple spheres represent water molecules. Selected hydrogen bonds are depicted as dotted yellow lines. Water molecules link the side chains of arginine 78 and asparagine 74 to the phosphonate side chain of the bound L-AP4; the water linking arginine 78 with the ligand is consistent with its presence in this position in the mGluR1 crystal structure while the water molecule linking asparagine 74 with L-AP4 is hypothetical and is proposed based on the homology model and the mutagenesis data as detailed in the text.
<table>
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<th>Mutant</th>
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<tr>
<td>mGluR7</td>
<td>429 ± 132</td>
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<tr>
<td>N74K</td>
<td>35.6 ± 14</td>
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<tr>
<td>QE del + K261E (Triple)</td>
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<td>QE del + N74K + K261E + D262P + D289E (Hexa)</td>
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Fig. 1

L-SOP

L-AP4

L-Glutamate
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<td>0.25 ± 0.09</td>
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<td>1-78&lt;sub&gt;m4&lt;/sub&gt;/63-871&lt;sub&gt;m6&lt;/sub&gt;</td>
<td>0.33 ± 0.08</td>
<td>0.17 ± 0.07</td>
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<td>0.45 ± 0.21</td>
<td>0.39 ± 0.07</td>
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Fig. 4

A) mGluR6, 4/6A, 4/6B, 4/6C, 4/6D, Mock

B) 4/7D, 4/7C, 4/7B, 4/7A, mGluR4, Mock

C) mGluR7, N74K, m7 triple, m7 tetra, m7 penta, m7 hexa, D289E, D289E+MG, Mock

kD

99

201

99
Fig. 5

mGluR4

LYS405

L-AP4

THR182

TYR230

TYR230

SER159

mGluR7

LYS317

GLU287

LYS74

SER313

LYS319

ASP289

ASN74

SER315

LYS407

L-AP4

THR182

2.51 2.46 2.78 3.02

3.15 3.09

2.50

2.96 2.77 2.52 2.77

2.72 2.81 2.95 2.59 2.90
### Fig. 6

<table>
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<td>CaSR</td>
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<td>mGluR7</td>
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Fig. 8