

Regulation of the avidity of ternary complexes containing the human 5-HT_{1A} receptor by mutation of a receptor contact site on the interacting G protein α subunit

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1 Fusion proteins were constructed between the human 5-HT_{1A} receptor and pertussis toxin-resistant forms of both G_{i1} α and G_{o1} α mutated at residue³⁵¹ from cysteine to either glycine or isoleucine. Each of these was expressed stably in HEK293 cells.

2 Increasing concentrations of GDP inhibited binding of the agonist [³H]-8-OH-DPAT but not the antagonist [³H]-MPPF to each construct.

3 The IC₅₀ for GDP was greater for constructs containing isoleucine at residue³⁵¹ of the G proteins compared to those with glycine at this position.

4 The G protein antagonist suramin had similar effects to GDP on the binding of [³H]-8-OH-DPAT.

5 The proportion of 5-HT_{1A} receptor binding sites detected by [³H]-MPPF that displayed high affinity for 8-OH-DPAT was significantly greater when the interacting G protein contained isoleucine rather than glycine at residue³⁵¹.

6 The 5-HT_{1A} receptor displayed similar avidity of interaction with G_{i1} α and G_{o1} α .

7 These results indicate that a higher avidity ternary complex is formed between 8-OH-DPAT, the 5-HT_{1A} receptor and G proteins when isoleucine rather than glycine is located at residue³⁵¹ of the interacting G protein.

British Journal of Pharmacology (2002) 137, 345–352. doi:10.1038/sj.bjp.0704880

Keywords: 5-HT_{1A} receptor; G protein; ternary complex; adenylyl cyclase; suramin

Abbreviations: DMEM, Dulbecco's modified Eagle's medium; GPCR, G protein-coupled receptor; MPPF, 4-(2'-methoxy)-phenyl-1-[2'-(N''-pyridinyl)-p-fluorobenzamido]ethyl-piperazine

Introduction

The 5-HT_{1A} receptor plays important roles in the regulation of anxiety and depression (Heisler *et al.*, 1998; Ramboz *et al.*, 1998; Middlemiss *et al.*, 2002). This has resulted in it being one of the most studied G protein-coupled receptors (GPCRs) that interacts selectively with the G_i-family of pertussis toxin-sensitive G proteins.

The ternary complex model (Wreggett and De Lean, 1984) and extensions of it (Samama *et al.*, 1993; Weiss *et al.*, 1996) is central to our understanding of interactions between GPCRs and G proteins and to analysis of signal transduction *via* these proteins. Predictions based on these models have been robust (Kenakin *et al.*, 2000). However, simulations of the behaviour of such models are based on circumstances in which GPCR and G protein concentrations are equivalent. This is generally not the situation in cell membranes where levels of G proteins are routinely in marked excess over any given GPCR (Milligan, 2000a). It is also well appreciated that the characteristics of ligand

binding and agonist efficacy can vary markedly with alterations in GPCR-G protein stoichiometry (Kenakin, 1997). Although designed predominantly to allow detailed enzyme kinetic analysis of agonist activation of G proteins (Wise *et al.*, 1997a) and its regulation by interacting proteins (Cavalli *et al.*, 2000) GPCR-G protein fusion proteins offer attractive models for detailed pharmacological analysis (Seifert *et al.*, 1999; Milligan, 2000b; Wurch & Pauwels, 2001). This reflects their defined 1:1 stoichiometry that is unchanged by mutation of the protein sequence or exposure to ligands. However, when such constructs are generated using wild type forms of the G proteins it is at least possible that the signal measured reflects GPCR-mediated activation of endogenously expressed G proteins as well as the G protein physically linked to the receptor. Indeed, in certain cases this has been demonstrated directly (Burt *et al.*, 1998; Holst *et al.*, 2001). As pertussis toxin-catalysed ADP-ribosylation eliminates functional contacts between GPCRs and G_i-family G proteins, such fusions are frequently generated using variant forms of the G protein mutated to be resistant to the actions of this toxin (Milligan, 2002c). Thus, following pertussis toxin treatment of cells, signals generated must reflect only activation of the GPCR-linked G protein. However, the identity of the amino acid used to

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replace the cysteine that is the target for pertussis toxin can alter the effectiveness of information transfer between GPCR and G proteins as it is located within a key contact interface (Moon *et al.*, 2001a, b). For example, fusion proteins between the 5-HT_{1A} receptor and G_{i1} α display substantially higher levels of constitutive activity when cysteine³⁵¹ of the G protein is replaced with isoleucine than when it is replaced by glycine (Kellett *et al.*, 1999). The implication is that, even in the absence of agonist, the avidity of interaction between the 5-HT_{1A} receptor and G_{i1} α is greater with a more hydrophobic amino acid at this site. Agonists, but not antagonists, bind with higher affinity to a GPCR associated with a G protein than following their dissociation. Furthermore, agonist occupation of a GPCR results in reduction in the affinity of binding of GDP to the G protein α subunit to allow guanine nucleotide exchange and G protein activation (Gilman, 1987). It should thus also be expected that increasing concentrations of GDP reduce the binding affinity of agonists but not antagonists for the GPCR (see Birnbaumer *et al.*, 1990 for review) and limit the potency of agonists to stabilize the ternary complex and produce guanine nucleotide exchange (McLoughlin & Strange, 2000). Thus, herein we have used measurements of the regulation of [³H]-agonist binding to fusion proteins incorporating the 5-HT_{1A} receptor and glycine and isoleucine containing forms of both G_{i1} α and G_{o1} α to gain direct information on the relative stability of such ternary complexes that differ simply in a single amino acid. The interactions between the GPCR and the forms of the G protein with isoleucine at residue³⁵¹ are noted to be of substantially higher avidity than for the equivalent G proteins with glycine at this location. It is thus not surprising that the 5-HT_{1A} receptor-G protein fusions containing the isoleucine mutation displays significantly greater information transfer in the absence of agonist, i.e. constitutive activity, than those containing the glycine mutation (Kellett *et al.*, 1999; Welsby *et al.*, 2002). A similar approach has recently been adopted to monitor interactions between the A1 adenosine receptor and various G proteins (Waldhoer *et al.*, 1999; Kudlacek *et al.*, 2002).

Methods

All materials for tissue culture were supplied by Life Technologies Inc. (Paisley, Strathclyde, U.K.). The 5-HT_{1A} receptor antagonist [³H]-MPPF (70.5 Ci/mmol) was obtained from DuPont/NEN and the agonist [³H]8-OH-DPAT (221 Ci/mmol) from Amersham Pharmacia Biotech. Pertussis toxin was purchased from Sigma. Oligonucleotides were purchased from Cruachem (Glasgow, Strathclyde, U.K.). All other chemicals were from Sigma or Boehringer Mannheim.

Construction of plasmids encoding 5-HT_{1A}-G_{i1} α and 5-HT_{1A}-G_{o1} α fusion proteins

The human 5-HT_{1A} receptor clone in pSP64 (a gift from Glaxo SmithKline, Stevenage, U.K.) was digested with *Xba*I/*Bam*HI and the resulting 1.5 Kb fragment ligated to pcDNA3. To obtain the reading frame of 1.3 Kb PCR was carried out using the following primers to introduce a *Hind*III restriction site at the 5' end and to remove the stop codon and introduce a *Bam*HI restriction site at the 3' end

respectively: 5'-CTGAAGCTTATGGATGTGCTCAGCCC-TGGTC-3'; 5'-CTGGGATCCCTGGCGGCAGAAGTTA-CACCTAATG-3' (restriction enzyme sites underlined). The PCR fragment was digested with *Hind*III and *Bam*HI and ligated into pcDNA3 to make the plasmid p5HT. To link the G_{i1} α wild type (Cys³⁵¹) cDNA to the 5HT_{1A} receptor sequence PCR was carried out on G_{i1} α to produce compatible restriction sites. The oligonucleotides used to do this were 5'-CTGGGATCCGGCTGCACACTGAGCGCT-GAG-3' at the 5' end and 5'-GAGAATTCTTAGAAAGA-GACCACAGTC-3' for the 3' end. The plasmid p5HT was digested with *Bam*HI/*Eco*RI as was the G_{i1} α PCR fragment and the two were ligated to give the plasmid p5HTG_{i1}. To construct the 5-HT_{1A}-(Gly³⁵¹) and (Ile³⁵¹)G_{i1} α fusion proteins plasmid (Gly or Ile³⁵¹)G_{i1} α in pBS (Bahia *et al.*, 1998) was digested with *Sac*II/*Eco*RI and the 730 bp fragment used to replace the corresponding fragment in p5HTG_{i1}. Equivalent strategies were used to produce the 5-HT_{1A}-(Gly or Ile³⁵¹)G_{o1} α fusions using pertussis toxin-resistant forms of G_{o1} α (Moon *et al.*, 2001a). The constructs were then sequenced to verify the DNA sequence.

Cell culture and stable expression

HEK293 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% (v v⁻¹) newborn calf serum, 2 mM L-glutamine. Cells were seeded into 100 mm culture dishes and grown to 60–80% confluency (18–24 h) before transfection with 5 μ g of appropriate cDNAs using DOTAP reagent (Boehringer Mannheim). Forty-eight hours after transfection, the cells were split 1 : 4 into 800 μ g ml⁻¹ G418 sulphate (Calbiochem) containing medium. A 100 mm dish of untransfected HEK293 cells was also split into the same medium as a control dish. About one week later, after all the cells in the control dish had died, G418-resistant cells in the transfected dishes were picked and transferred into 24 well plates using autoclaved pipette tips. About 20 clones of each cDNA were picked and grown in 1 ml well⁻¹ of G418 medium (400 μ g ml⁻¹). Clones were amplified, membrane preparations made and their binding of [³H]-MPPF determined (Kellett *et al.*, 1999).

Preparation of membranes

Plasma membrane-containing P2 particulate fractions were prepared from cell pastes that had been stored at -80°C after harvesting. Cell pellets were resuspended in TE buffer (10 mM Tris HCl (pH 7.5)/0.1 mM EDTA) and rupture of the cells was achieved with 25 strokes of a hand-held Teflon-on-glass homogenizer. Unbroken cells and nuclei were removed by centrifugation at low speed (1600 r.p.m.) in a refrigerated microcentrifuge. The supernatant fraction was then centrifuged at 50 000 r.p.m. for 30 min in a Beckman Optima TLX Ultracentrifuge with a TLA100.2 rotor. The pellets were resuspended in TE buffer to a final protein concentration of 1 mg/ml⁻¹ and stored at -80°C until required.

[³H]-MPPF binding studies

Binding assays were performed by adding 5 μ g membrane protein to an assay buffer (20 mM HEPES, 10 mM MgCl₂, 0.2% ascorbic acid, 10 μ M pargyline, pH 7.4) containing [³H]-

4-(2'-methoxy)-phenyl-1-2'-[N-2''-pyridinyl]-p-fluorobenzamidoethyl-piperazine. [³H]-MPPF (0.25–9 nM). Non-specific binding was determined in parallel in the presence of 100 μ M 5-HT. Samples were incubated at 30°C for 40 min and then terminated by rapid filtration through GF/C filters. The filters were washed three times with 5 ml ice-cold wash buffer (20 mM HEPES, 10 mM MgCl₂, 0.1% ascorbic acid, pH 7.4) and then counted. In competition binding assays [³H]-MPPF was present at 1 nM.

[³H]-8-OH DPAT binding studies

Binding in triplicate reaction mixtures containing 2.5 μ g membrane protein and either suramin or GDP (1 nM–1 mM) was initiated by the addition of [³H]-8-OH-DPAT (0.6 nM) and incubated at 30°C for 30 min in binding buffer (20 mM HEPES, 10 mM MgCl₂, 0.1% ascorbic acid, 10 μ M pargyline, pH 7.4). Reaction was terminated by rapid filtration through GF/C filters subsequently washed three times with 5 ml ice-cold wash buffer (20 mM HEPES, 10 mM MgCl₂, 0.1% ascorbic acid, pH 7.4) and then counted. Non-specific binding was determined in parallel in the presence of 100 μ M 5-HT.

Adenylyl cyclase

Intact cell adenylyl cyclase assays were performed essentially as described by Wong (1994) and Merkouris *et al.* (1997). Cells were split into wells of a 24-well plate and incubated in medium containing [³H]-adenine at 0.5 μ Ci well⁻¹ for 24 h. The generation of [³H]-cAMP in response to forskolin or 5-HT was assessed in the presence of the non-selective cAMP phosphodiesterase inhibitor isobutylmethylxanthine (1 mM).

Results

Fusion proteins between the human 5-HT_{1A} receptor and forms of both G_{i1} α and G_{o1} α that are insensitive to the ADP-ribosyltransferase activity of pertussis toxin because cysteine³⁵¹ had been mutated to either glycine or isoleucine (Welsby *et al.*, 2002) were each expressed stably in HEK293 cells. Clones expressing similar levels (some 6 pmol mg⁻¹ membrane protein) of each construct as measured by the specific binding of the antagonist [³H]-MPPF were expanded and used in these studies. The K_d for [³H]-MPPF (1.5–2.0 nM) was similar for each construct and for the wild type 5-HT_{1A} receptor and this was not altered by pertussis toxin pre-treatment of the cells (data not shown). In all cases the binding isotherms were consistent with this ligand interacting with a single population of sites.

The binding of a single concentration (1 nM) of the agonist [³H]-8-OH-DPAT to membranes of HEK293 cells expressing the isolated 5-HT_{1A} receptor was reduced by some 90% by pre-treatment of the cells with pertussis toxin (Figure 1). Addition of increasing concentrations of GDP to membranes of untreated cells also resulted in a reduction in the binding of [³H]-8-OH-DPAT to the 5-HT_{1A} receptor (Figure 1) with an EC₅₀ for GDP of 13.7 ± 2.4 μ M (mean \pm s.e.m., $n = 4$). By contrast no further reduction in [³H]-8-OH-DPAT binding was produced by adding GDP to membranes from pertussis toxin-treated cells (Figure 1). When equivalent experiments

were performed on membranes expressing the 5-HT_{1A} receptor-Gly³⁵¹G_{i1} α fusion protein increasing concentrations of GDP again reduced the specific binding of [³H]-8-OH-DPAT (Figure 2 and Table 1). However, pertussis toxin pre-treatment altered neither the binding of [³H]-8-OH-DPAT in the absence of GDP nor the potency of GDP to reduce binding of [³H]-8-OH-DPAT to this construct (Figure 2).

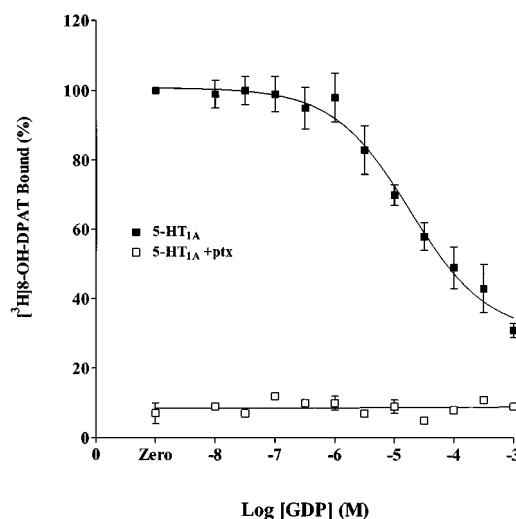


Figure 1 GDP and pertussis toxin pre-treatment reduces the binding of [³H]-8-OH-DPAT to the 5-HT_{1A} receptor. Membranes were prepared from untreated and pertussis toxin-pre-treated (25 ng ml⁻¹, 16 h) HEK293 cells stably expressing the human 5-HT_{1A} receptor. The specific binding of [³H]-8-OH-DPAT (1 nM) was then assessed in the presence of increasing concentrations of GDP.

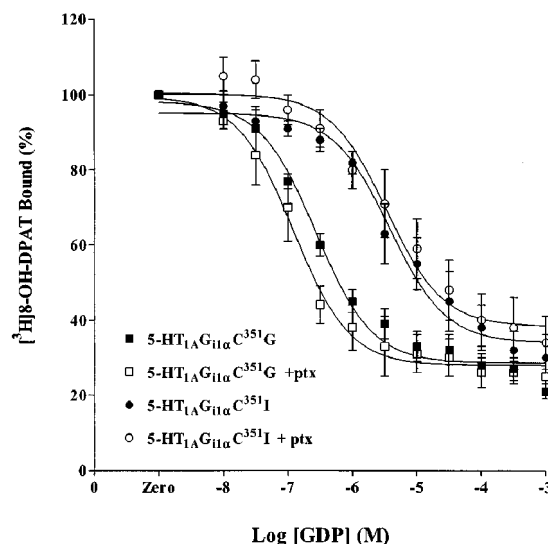


Figure 2 GDP but not pertussis toxin pre-treatment reduces the binding of [³H]-8-OH-DPAT to pertussis toxin-resistant 5-HT_{1A} receptor-G_{i1} α fusion proteins. Membranes were prepared from untreated and pertussis toxin-pre-treated (25 ng ml⁻¹, 16 h) HEK293 cells stably expressing 5-HT_{1A} receptor-G_{i1} α fusion proteins in which the pertussis toxin-sensitive cysteine was replaced by either glycine or isoleucine. The specific binding of [³H]-8-OH-DPAT was assessed in the presence of varying concentrations of GDP as in Figure 1.

Although the same was true when membranes were generated from cells expressing the 5-HT_{1A} receptor-Ile³⁵¹G_{i1}α fusion protein the potency of GDP to reduce the binding of [³H]-8-OH-DPAT was markedly lower than for the 5-HT_{1A} receptor-Gly³⁵¹G_{i1}α construct (Table 1 and Figure 2). Exactly the same was observed for the fusion proteins incorporating the Gly³⁵¹ and Ile³⁵¹ forms of G_{o1}α (Figure 3 and Table 1). Although pertussis toxin treatment was without effect, the potency of GDP to limit binding of [³H]-8-OH-DPAT was significantly lower ($P < 0.05$) for the Ile³⁵¹ containing constructs. In contrast to these results, GDP had little effect on the binding of [³H]-MPPF to any of these constructs (data not shown).

Suramin is sometimes described as a 'G protein antagonist' (Freissmuth *et al.*, 1999). Addition of increasing concentrations of suramin to [³H]-8-OH-DPAT binding assays employing membranes expressing the isolated 5-HT_{1A} receptor also

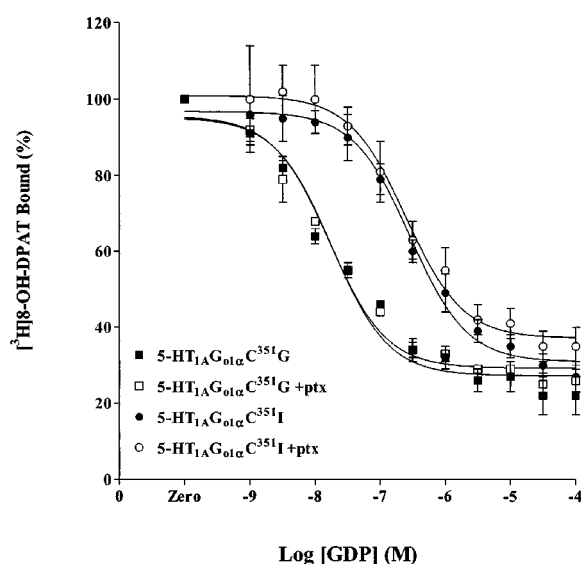


Figure 3 The nature of the pertussis toxin-insensitive mutation alters the potency of GDP to reduce the binding of [³H]-8-OH-DPAT to pertussis toxin-resistant 5-HT_{1A} receptor-G_{o1}α fusion proteins. Membranes were prepared from untreated and pertussis toxin-pretreated (25 ng ml⁻¹, 16 h) HEK293 cells stably expressing 5-HT_{1A} receptor-G_{o1}α fusion proteins in which the pertussis toxin-sensitive cysteine was replaced by either glycine or isoleucine. The specific binding of [³H]-8-OH-DPAT was assessed in the presence of varying concentrations of GDP as in Figure 2.

Table 1 GDP inhibits the binding of [³H]-8-OH-DPAT to pertussis toxin-resistant 5-HT_{1A} receptor-G_{i1}α and G_{o1}α fusion proteins

	EC ₅₀ GDP (μM)	
	5-HT _{1A} -G _{i1} α	5-HT _{1A} -G _{o1} α
Gly ³⁵¹	0.3 ± 0.05 (3)	0.10 ± 0.04 (3)
Ile ³⁵¹	10.0 ± 3.1 (5)	3.0 ± 0.6 (3)

The ability of GDP to inhibit the specific binding of [³H]-8-OH-DPAT to fusion proteins between the 5-HT_{1A} receptor and pertussis toxin-resistant forms of G_{i1}α or G_{o1}α in which Cys³⁵¹ was replaced by Gly or Ile is recorded. Data represent means ± s.e.m. Numbers in parentheses indicate the number of experiments performed.

resulted in reduction of agonist binding (Figure 4). Suramin did not produce this effect by acting as a competitive inhibitor at the ligand binding site as it did not reduce the binding of [³H]-MPPF (Figure 4). Increasing concentrations of suramin also reduced the binding of [³H]-8-OH-DPAT to the 5-HT_{1A} receptor-G_{i1}α fusion proteins (Figure 5). The concentrations of suramin required to reduce binding of [³H]-8-OH-DPAT to the 5-HT_{1A} receptor-Ile³⁵¹G_{i1}α construct were significantly greater than for the 5-HT_{1A} receptor-Gly³⁵¹G_{i1}α fusion protein in membranes from both untreated ($P = 0.012$) and pertussis toxin treated ($P = 0.002$) cells (Figure 5a). An equivalent significant difference ($P = 0.002$) in the potency of suramin to reduce binding of [³H]-8-OH-DPAT to the fusion proteins containing Ile³⁵¹ and Gly³⁵¹G_{o1}α was also observed (Figure 5b).

Competition for the specific binding of [³H]-MPPF to the 5-HT_{1A} receptor-Gly³⁵¹G_{i1}α fusion protein by increasing concentrations of 8-OH-DPAT was unaffected by prior pertussis toxin treatment of cells (Figure 6 and data not shown) and was best described by a 2-site model in which the high affinity sites for the agonist comprised 30.9 ± 0.1% and the low affinity sites 69.1 ± 0.2% of the total. This was also true when the 5-HT_{1A} receptor-Ile³⁵¹G_{i1}α construct was examined, except that the proportion of high affinity sites for agonist represented 60.3 ± 11.0% of the binding sites and those with low affinity 39.7 ± 5.5% (Figure 6). This difference was highly significant ($P = 0.004$). To explore whether the 5-HT_{1A} receptor displayed different affinities of interaction with G_{i1}α and G_{o1}α we constructed fusion proteins between the receptor and the wild type (Cys³⁵¹) version of these G proteins. As anticipated, 5-HT_{1A} was able to mediate inhibition of forskolin-stimulated adenylyl cyclase activity in cells expressing either of these constructs (data not shown). However, as these constructs are sensitive to pertussis toxin-catalysed ADP-ribosylation, such treatment largely eliminated agonist regulation of cAMP levels (data not shown). This is distinct from the fusion proteins containing the

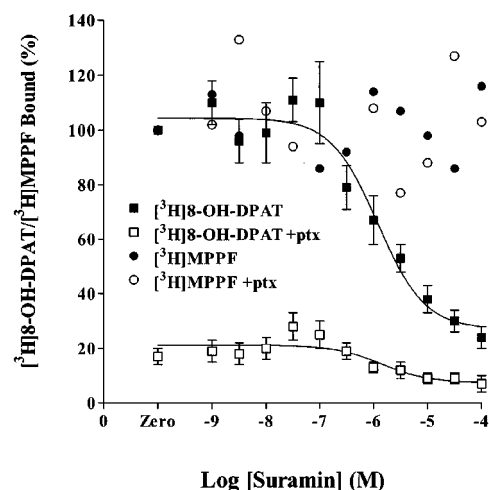


Figure 4 Suramin reduces the binding of [³H]-8-OH-DPAT but not [³H]-MPPF to the 5HT_{1A} receptor. Membranes were prepared from untreated and pertussis toxin pre-treated (25 mg ml⁻¹, 16 h) HEK293 cells stably expressing the human 5-HT_{1A} receptor. The specific binding of [³H]-8-OH-DPAT (1 nM) or [³H]-MPPF (1 nM) was then assessed in the presence of increasing concentrations of suramin.

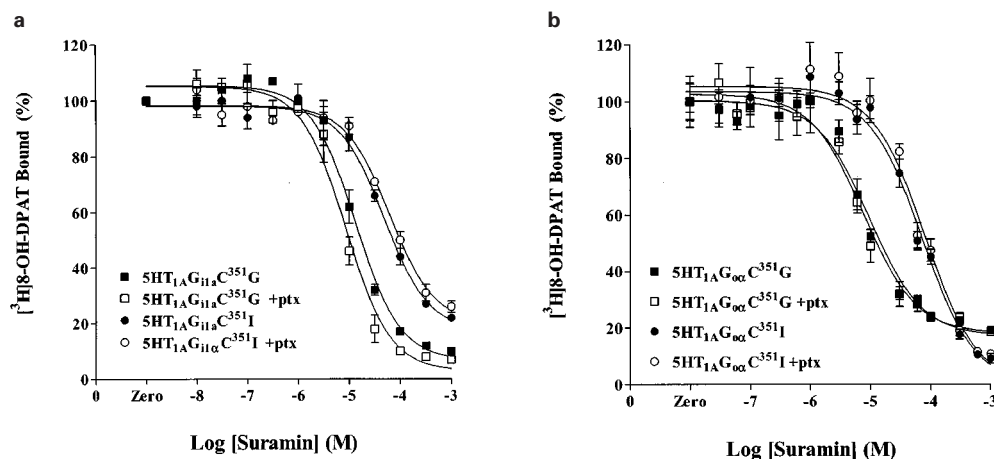


Figure 5 The nature of the pertussis toxin-insensitive mutation alters the potency of suramin to reduce the binding of [³H]-8-OH-DPAT to pertussis toxin-resistant 5-HT_{1A} receptor-G_{i1α} and -G_{o1α} fusion proteins. Membranes were prepared from untreated and pertussis toxin-pre-treated (25 ng ml⁻¹, 16 h) HEK293 cells stably expressing 5-HT_{1A} receptor-G_{i1α} (a) or 5-HT_{1A} receptor-G_{o1α} (b) fusion proteins in which the pertussis toxin sensitive cysteine was replaced by either glycine or isoleucine. The specific binding of [³H]-8-OH-DPAT was assessed in the presence of varying concentrations of suramin as in Figure 4.

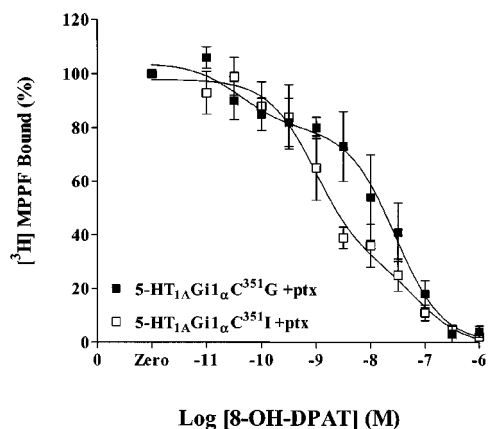


Figure 6 A 5HT_{1A}-(Cys³⁵¹Ile)G_{i1α} fusion protein displays a greater proportion of high affinity binding sites for 8-OH-DPAT than a 5HT_{1A}-(Cys³⁵¹Gly)G_{i1α} fusion protein. Membranes were prepared from pertussis toxin pre-treated HEK293 cells expressing either the 5HT_{1A}-(Cys³⁵¹Ile)G_{i1α} fusion protein or the 5HT_{1A}-(Cys³⁵¹Gly)G_{i1α} fusion protein. The ability of varying concentrations of 8-OH-DPAT to compete with [³H]-MPPF (1 nM) for the binding site was then assessed.

pertussis toxin-resistant forms of the G proteins where agonist-inhibition of adenylyl cyclase activity is unaffected by pertussis toxin treatment (Kellett *et al.*, 1999). The binding of [³H]-8-OH-DPAT to both of the constructs containing the wild type G proteins was also reduced by increasing concentrations of either GDP or suramin. However, there were no significant differences in the IC₅₀ values for these two compounds when examining 5-HT_{1A} receptor-Cys³⁵¹G_{i1} (GDP 2.2 ± 0.5 μM, suramin 1.7 ± 0.5 μM, means ± s.e.m., n = 4) and 5-HT_{1A} receptor-Cys³⁵¹G_{o1} (GDP 5.9 ± 3.8 μM, suramin 1.3 ± 0.6 μM, means ± s.e.m., n = 4). This indicates that the avidity of ternary complexes between 8-OH-DPAT, the 5-HT_{1A} receptor and the wild type forms of these two G proteins is similar.

Discussion

GPCR agonists function by reducing the affinity and hence enhancing the dissociation of GDP from the nucleotide binding pocket of the G protein α subunit. This increases guanine nucleotide exchange (Gilman, 1987). Thus, a corollary is that increasing concentrations of GDP should reduce the affinity of agonist binding to a receptor. Indeed, previous studies on the 5-HT_{1A} receptor expressed in CHO cells has shown the capacity of GDP to reduce the potency of agonists at this receptor to cause activation of endogenously expressed G proteins. This was modelled to reflect a reduced ability of agonist to stabilize the ternary complex in the presence of GDP (McLoughlin & Strange, 2000). As the complex with high affinity for agonist is between GPCR and G protein denuded of guanine nucleotide, increasing concentration of GDP must limit production of this state. In initial studies the binding of a single concentration of the agonist [³H]-8-OH-DPAT to the isolated human 5-HT_{1A} receptor was assessed in membranes of HEK293 cells. Binding was reduced by GDP in a concentration-dependent manner and the extent of binding remaining in the presence of a maximally effective concentration of GDP was similar to that observed following pertussis toxin pre-treatment of the cells to eliminate interactions with G proteins. When equivalent experiments were performed on cell membranes expressing fusion proteins between the 5-HT_{1A} receptor and pertussis toxin-resistant forms of either G_{i1α} and G_{o1α} increasing concentrations of GDP again reduced binding of the agonist ligand. By contrast with the isolated receptor, however, pertussis toxin pre-treatment had no effect on ligand binding and did not alter the effectiveness of GDP to reduce binding of the agonist. Such results clearly indicated that [³H]-8-OH-DPAT binding was a useful monitor of the 1 : 1 : 1 ternary complex of agonist, receptor and G protein. A substantial difference in potency of GDP to reduce the binding of [³H]-8-OH-DPAT to fusion proteins containing the single isoleucine or glycine substitutions at position 351 of the G proteins was observed. The IC₅₀ for GDP was

significantly higher for the fusions containing the isoleucine substitution in the G proteins and this was true for both G_{i1} α and G_{o1} α . These differences must indicate that the 8-OH-DPAT-5-HT_{1A} receptor-G protein ternary complex is of significantly higher avidity when the isoleucine substituted G protein is present. By contrast, antagonists do not modulate GDP release and guanine nucleotide exchange and thus the binding of [³H]-MPPF to the fusion proteins was unaffected by the presence of GDP or the nature of amino acid³⁵¹ of the G protein.

We also wished to address whether there were marked differences in the avidity of interactions between the 5-HT_{1A} receptor and G_{i1} α and G_{o1} α . As we could not be certain that the glycine and isoleucine substitutions functioned equivalently for the two G proteins we also constructed fusion proteins between the wild type forms of each G protein and the 5-HT_{1A} receptor. As we did not observe large differences in the effectiveness and potency of GDP to limit the binding of [³H]-8-OH-DPAT to these two constructs we conclude that interactions between the 5-HT_{1A} receptor- and G_{i1} α and G_{o1} α are of similar affinity. Similar conclusions have been reached using co-expression studies in insect Sf9 cells (Butkerait *et al.*, 1995).

We extended these studies by the use of suramin. Although suramin is a polyanion with a wide range of pharmacological functions it has been used as a G protein antagonist (Freissmuth *et al.*, 1999) as it is able to interfere with G protein activation by GPCRs, at least partially by interacting directly with G protein. As concentrations up to 10 μ M did not interfere with the binding of [³H]-MPPF to the pertussis toxin-resistant fusion proteins suramin is thus not a direct competitor at the ligand binding pocket. Despite this, increasing concentrations of suramin were able to reduce the binding of [³H]-8-OH-DPAT and this effect of suramin was also unaffected by prior pertussis toxin pre-treatment of cells. Suramin was again less potent in limiting agonist binding to the fusion proteins containing the isoleucine replacement G proteins than to those with glycine at this position. Such data is also consistent with the ternary complexes containing the isoleucine containing G proteins possessing higher avidity. Suramin did not display marked differences in potency to disrupt binding of [³H]-8-OH-DPAT to fusion proteins in which the receptor was linked to either wild type G_{i1} α or G_{o1} α . However, it is interesting to note that an analogue of suramin has recently been shown to selectively interfere with interactions between the A1 adenosine receptor and G_{i1} α but not between this receptor and G_{o1} α (Kudlacek *et al.*, 2002). It thus appears that the detailed contacts between GPCRs and closely related G proteins can differ and thus may be an interface that can be targeted effectively by ligands with therapeutic potential.

As a further test of the hypothesis that the avidity of GPCR-G proteins contacts can be altered significantly by single point mutations we compared the ability of non-radioactive 8-OH-DPAT to compete with [³H]-MPPF for binding to fusion proteins containing the pertussis toxin-resistant forms of G_{i1} α . The competition curves were clearly biphasic demonstrating both high and low affinity sites for the agonist. Although this was expected from the ability of GDP to reduce the binding of [³H]-8-OH-DPAT it is important to note that, given the physical link between GPCR and G protein imbued by the fusion, one hypothesis is

that this would create a single set of non-interconverting binding sites. However, such fusion proteins display both low and high affinity binding sites for agonists, a feature that has also been noted for fusions incorporating, amongst others, the β_2 -adrenoceptor (Seifert *et al.*, 1999) and the δ -opioid receptor (Moon *et al.*, 2001b). They thus function in the manner expected for separated but co-expressed polypeptides. Given that GDP was less potent in reducing agonist binding to the isoleucine containing G proteins it was gratifying to note that the 5-HT_{1A} receptor-G_{i1} α fusion protein containing isoleucine displayed a significantly greater proportion of high affinity agonist binding sites than the variant incorporating the glycine containing form of G_{i1} α . These data are entirely in accord with the results from the other approaches and further support the contention that introduction of isoleucine at this position in the G protein results in the interaction with the 5-HT_{1A} receptor being of greater avidity than when glycine is present.

Since their initial introduction by Bertin *et al.* (1994) GPCR-G protein fusions have become increasingly popular tools to study details of the interactions between these two classes of proteins. They have proved to be ideal reagents to study aspects of ligand efficacy (Wise *et al.*, 1997b; Dupuis *et al.*, 1999), the selectivity of interactions of GPCRs with different G proteins (Fong & Milligan, 1999; Wenzel-Seifert & Seifert, 2000; Holst *et al.*, 2001), the concept that different ligands induce distinct receptor conformations (Seifert *et al.*, 2001), the role and regulation of post-translational acylation of both GPCRs and G proteins (Loisel *et al.*, 1999; Stevens *et al.*, 2001) and the role of G protein β/γ subunits in information transfer between GPCRs and G proteins (Liu *et al.*, 2002). In recent times they have also been used effectively in drug discovery programmes, both to overcome the widespread distribution pattern of Edg receptor subtypes (McAllister *et al.*, 2000), to help identify ligands for orphan GPCRs (Hosoi *et al.*, 2002) and to screen for inverse agonists (Carrillo *et al.*, 2002). In all these cases, the defined 1:1 stoichiometry of the partner polypeptides has provided distinct advantages. This has been of particular value as saturation ligand binding studies thus provide a direct measure of the expression level of not only the GPCR but also the G protein. In concert with measures of agonist stimulated GTPase activity this has allowed measurement of the turnover member for GTP induced by agonists (Wise *et al.*, 1997a) and the regulation of the lifetime of activated G proteins by Regulators of G protein Signalling (Cavalli *et al.*, 2000). Because mutation of either GPCR or G protein does not alter the stoichiometry of the two polypeptides this has also allowed quantitative analysis of the effects of such mutations on signal initiation (Ward & Milligan, 2002) and the extent of constitutive activity imbued by such mutations (Carrillo *et al.*, 2002). The current data further define the usefulness of GPCR-G protein fusions in allowing analysis of pharmacological details inherent in the ternary complex model.

Financial support was provided by the Medical Research Council. P.J. Welsby thanks the Biotechnology and Biosciences for provision of a CASE studentship.

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(Received May 30, 2002

Revised July 10, 2002

Accepted July 19, 2002)