Proceedings of the British Pharmacological Society at http://www.pA2online.org/abstracts/Vol12Issue3abst233P.pdf

Allosteric and Orthosteric Modulation of the Free Fatty Acid Receptor FFA2 by **Bitopic Ligands**

AJ Brown, F Chowdhury, N Faucher, SJ Dowell. GlaxoSmithKline R&D Ltd, Stevenage, UK

FFA2 is a G-protein-coupled receptor activated by propionate and other short-chain fatty acids. 4-CMTB is a synthetic agonist selective for FFA2 that lacks a carboxylate group and binds to a site different from propionate, acting allosterically (1). Here, we study bitopic FFA2 ligands containing both carboxylate and N-thiazolylamide, which is the characteristic chemical feature of 4-CMTB. By investigating the allosteric and orthosteric nature of interaction between ligand pairs, we characterise the mode of binding of bitopic ligands to FFA2. [³⁵S]GTPyS-incorporation and yeast reporter assays were used to measure FFA2 activation. Bitopic compounds showed systemdependent efficacy, in contrast to propionate and 4-CMTB (Table 1). Compound 14 ((R)-3-benzyl-4-((4-(2-chlorophenyl)thiazol-2-yl)(methyl)amino)-4-oxobutanoic acid) weakly activated FFA2 in yeast, and showed allosteric cooperativity with 4-CMTB (Fig.1) but not with propionate (not shown). Compound 9 ((S)-4-(4-(2chlorophenyl)thiazol-2-ylamino)-4-oxo-3-phenylbutanoic acid) acted as an FFA2 inverse agonist in yeast (Table 1). Schild analysis indicated antagonism of propionate by 9 was competitive ($n_H = 1$; $pA_2 = 6.64 \pm 0.17$, n=2) but antagonism of 4-CMTB by 9 was allosteric (pK_B = 6.88 ± 0.17 and cooperativity factor $\alpha = 0.01\pm0.004$ (n=3) using an operational model; Fig.2). Thus, bitopic FFA2 ligands engage the orthosteric site, but appear not to compete at the site of 4-CMTB binding on an FFA2 receptor molecule. It seems paradoxical for two different FFA2 sites to bind the same chemical structure (N-thiazolylamide), and an alternative possibility is that FFA2 has a single *N*-thiazolylamide site but functions as a homodimer (or higher-order oligomer). This mode of action has recently been proposed to explain allosteric behaviour of a bitopic dopamine D_2 antagonist (2), and may be a common mechanism for allosteric interaction between GPCR ligands.

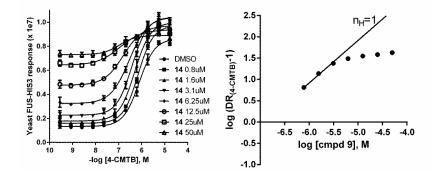
	[³⁵ S]-GTPγS	Yeast
Propionate	4.5±0.08 (n=2)	3.4±0.11 (n=2)
4-CMTB	6.9±0.12 (n=3)	6.4±0.25 (n=45)
Cmpd 9	7.0±0.08 (n=2)	6.74±0.15 (n=3)
Cmpd 14	8.2±0.23 (n=4)	5.1±0.16 (n=4)

Table 1: Activity of FFA2 ligands (pEC₅₀, *pIC*₅₀ in italic, mean±SD)

Fig.1 Allosterism of 14 and 4-CMTB

Fig.2 Allosterism of 9 and 4-

CMTB



(1) Lee T et al. (2008) Mol Pharmacol 74:1599-1609.

(2) Lane IR et al. (2014) Nat Chem Biol 10:745-752