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Design, synthesis, and biological activity of novel PPAR γ ligands based on rosiglitazone and 15d-PGJ₂

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Abstract—To develop novel PPAR γ ligands, we synthesized thirteen 3-{4-(2-aminoethoxy)phenyl}propanoic acid derivatives, which are designed based on the structures of rosiglitazone and 15d-PGJ₂. Among these compounds, compound **9** was found to be as potent as rosiglitazone in a binding assay and a preadipocyte differentiation test. Molecular modeling suggested that the nonyl group of **9** interacted with hydrophobic amino acid residues constructing the hydrophobic region of PPAR γ protein where the alkyl chain of 15d-PGJ₂ is expected to be located.

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Peroxisome proliferator-activated receptors (PPAR α , PPAR γ , and PPAR δ) belong to the nuclear receptor superfamily and act as ligand-activated transcription factors.^{1–3} These receptors play a pivotal roles in regulating the expression of a large number of genes involved in lipid metabolism and energy balance.⁴ Many studies on PPARs have been performed, and these efforts led to the discovery of the clinically useful thiazolidinedione (TZD) class of insulin sensitizers such as rosiglitazone⁵ and pioglitazone⁶ (Fig. 1), which are potent PPAR γ agonists used in the treatment of Type 2 diabetes. However, the use of TZDs has been limited because of their poor safety profiles. For example, troglitazone, which



Figure 1. Structures of rosiglitazone (GSK) and pioglitazone (Takeda).

Keywords: PPARy ligand; 15d-PGJ₂; Insulin sensitizer; Agonist.

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came out to the market first, disappeared from the market due to its severe hepatic toxicity in 1999,⁷ and rosiglitazone is reported to be associated with liver, cardiovascular, and hematological toxicities.⁸ We therefore initiated a search for non-TZD PPAR γ ligands with the goal of finding novel insulin sensitizers. In this letter, we report the design, synthesis, and biological activity of non-TZD PPAR γ ligands based on the structure of rosiglitazone and 15-deoxy- Δ -12,14-prostaglandin J₂ (15d-PGJ₂).

The compounds prepared for this study are shown in Figure 2, and the routes used for their synthesis are illustrated in Schemes 1–4. Scheme 1 shows the preparation of N-(pyridin-2-yl)-N-alkyl derivatives 1-3 bearing a methyl, ethyl, and propyl group, respectively, on their nitrogen atom as an alkyl chain.⁹ The protection of dialkylamine 14a-c by (Boc)₂O gave 15a-c.¹⁰ The Mitsunobu reaction¹¹ was applied to the conversion of 15a-c into 3-{4-(2-aminoethoxy)phenyl}propanoic acid derivatives 16a-c: treatment of 15a-c with diethylazodicarboxylate, PPh₃, and 3-(4-hydroxyphenyl)propanoic acid methyl ester 21 gave ethers 16a-c. The N-Boc groups of 16a-c were removed with trifluoroacetic acid to give amines 17a-c. Treatment of 17a-c with 2-fluoropyridine, or 2-chloropyridine gave N-(pyridin-2-yl)-N-alkyl compounds 18a-c via nucleophilic aromatic substitution, and subsequent hydrolysis afforded carboxylic acids 1-3.

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Figure 2. Structures of compounds 1–13.



Scheme 1. Reagents and conditions: (a) Boc_2O , CH_2Cl_2 , 0 °C to rt, 91–100%; (b) DEAD, PPh₃, 3-(4-hydroxyphenyl)propanoic acid methyl ester 21, THF, 0 °C to rt, 49–63%; (c) TFA, CH_2Cl_2 , 0 °C to rt, 81–94%; (d) 2-fluoropyridine or 2-chloropyridine, DMF, reflux, 7–38%; (e) aq NaOH, THF/MeOH, rt, 78–92%.

The preparation of the other *N*-(pyridin-2-yl)-*N*-alkyl derivatives **4–10** is outlined in Scheme 2. The preparation of 2-alkylamino pyridine **20a–g** was achieved by the method of Buchwald:¹² treatment of **19** with *n*-alkylamine, $Pd_2(DBA)_3$, BINAP, and *t*-BuONa in toluene under reflux. Propanoic acid methyl ester **21** was allowed to react with 1,2-dibromoethane to give ether **22**. Coupling between amines **20a–g** and ether **22** afforded *N*-(pyridin-2-yl)-*N*-alkyl compounds **23a–g**, and subsequent hydrolysis afforded carboxylic acids **4–10**.

N-(2-Pyridin-2-yl)-*N*-aryl derivatives **11**–**13** were prepared by the procedure outlined in Schemes 3 and 4.



Scheme 2. Reagents and conditions: (a) $CH_3(CH_2)_nNH_2$, $Pd_2(DBA)_3$, BINAP, *t*-BuOH, toluene, 80 °C, 7–53%; (b) 1,2-dibromoethane, K₂CO₃, THF, 115 °C, 25%; (c) **20a**–g, Et₃N, KI, THF, 120 °C, 2– 25%; (d) aq NaOH, THF, rt, 81–96%.



Scheme 3. Reagents and conditions: (a) (i) NaH, DMF, rt; (ii) 22, KI, 90 °C, 72%; (b) aq NaOH, THF, rt, 89%.



Scheme 4. Reagents and conditions: (a) 2-aminopyridine, Pd₂(DBA)₃, BINAP, *t*-BuONa, toluene, 80 °C, 70–88%; (b) (i) NaH, DMF, rt, (ii) 22, KI, 90 °C, 18–30%; (c) aq NaOH, THF, rt, 70–80%.

Norharman 24 was reacted with bromide 22 in the presence of sodium hydride in DMF to give 9H- β -carboline compound 25, and subsequent hydrolysis gave compound 11 (Scheme 3). Compounds 27a and b were prepared in the same way as 2-alkylamino pyridines 20a-g (Scheme 4). Compounds 27a and b were allowed to react with bromide 22 in the presence of sodium hydride in DMF to give compounds 28a and b. Treatment of 28a and b with aqueous NaOH gave *N*-(pyridin-2-yl)-*N*-phenyl derivative 12 and dipyridinyl derivative 13.

The binding affinity of the compounds for PPAR γ was evaluated with a CoA–BAP system (Microsystems).¹³ In this system, the alkaline phosphatase (AP) activity is directly proportional to the PPAR γ -binding affinity of the ligands.

Since it has been revealed that the TZD ring can be replaced by a carboxyl group,¹⁴ we initially examined the binding affinity for PPAR γ of compound 1, in which the TZD group of rosiglitazone is replaced by a carboxyl group. Although compound 1 did not show any activity at 0.1 and 1 μ M, a certain level of activity was observed at $10 \,\mu\text{M}$ (Table 1, line 1). For the further design of PPAR γ ligands, we focused on the alkyl chain of 15d- PGJ_2 ,^{15,16} an endogenous ligand of PPAR γ . Since certain fatty acids with a long alkyl chain are known to be natural PPAR γ ligands,¹⁷ the hydrophobic moiety is assumed to be critical for the binding affinity for PPAR γ . Our study regarding the binding mode of 15d-PGJ₂ in PPAR γ protein (PDB code 1FM6) by computer calculation (Macromodel 8.1)¹⁸ also suggested that the alkyl chain of 15d-PGJ₂ is located in the wide hydrophobic region of the PPAR γ ligand-binding cavity (Fig. 3). However, the crystal structure of a PPAR γ /rosiglitazone complex¹⁹ revealed that rosiglitazone does not have any hydrophobic groups interacting with the hydrophobic amino acid residues of PPARy. We hypothesized that the introduction of a hydrophobic group into compound 1 may increase the affinity for PPAR γ (Fig. 4). We therefore designed compounds 2– 10 in which alkyl groups of various lengths were intro-

Table 1. Binding affinity for PPAR γ of compounds 1–13 at 0.1, 1.0, and 10 $\mu M.^a$



^a Values are means of at least three experiments.



Figure 3. View of the conformation of 15d-PGJ₂ (tube) docked in PPAR γ . The hydrophobic and hydrophilic regions are shown in yellow and blue, respectively.

duced at the 2-aminopyridinyl moiety of compound 1, and evaluated their ability to bind PPAR γ . It was found that the affinity of compounds 1–10 was closely related to chain length, and the most potent compounds were heptyl 7, octyl 8, and nonyl 9. In addition, *N*,*N*-diaryl compounds 11–13 exhibited weak activity compared with compounds 7–9 (Table 1, lines 11–13). We next compared the binding affinity of compounds 7–9 with that of rosiglitazone at lower concentrations. As shown in Figure 5, compound 9 showed the highest activity among the three, and had only slightly less affinity for PPAR γ than did rosiglitazone.

As compound 9 was most active in our study, we used it for further evaluation. Since it has been reported that activation of PPAR γ enhances adipocyte differentiation²⁰ and increases insulin sensitivity, compound 9 was subjected to a rat abdominal preadipocyte differentiation test.^{21,22} The accumulation of neutral fat in the cells was observed after the administration of compound 9 at concentrations of 1, 2.5, and 5 μ M, and the activity of compound 9 was found to be comparable to that of rosiglitazone (Fig. 6).

Since *N*-nonyl carboxylic acid **9** had a high level of activity, we studied its mode of binding to PPAR γ . A low energy conformation was calculated when **9** was docked in a model based on the crystal structure of PPAR γ using Macromodel 8.1 software.¹⁸ An inspection of the simulated PPAR γ /**9** complex suggested that oxygen atoms of compound **9** form hydrogen bonds with Ser 289, Tyr 327, and Tyr 473 (Fig. 7). In addition, it was shown that the nonyl group of **9** is located in the hydrophobic region formed by Phe 287, Gly 284, Ile 281, Ile 341, and Met 348 (Fig. 8) where the alkyl chain of 15d-PGJ₂ is calculated to be located (Fig. 3).

In summary, in order to explore novel PPAR γ ligands, we prepared several 3-{4-(2-aminoethoxy)phenyl} propanoic acid derivatives designed based on the structures of rosiglitazone and 15d-PGJ₂. Among them, *N*-(pyridin-2-yl)-*N*-nonyl compound **9** was found to be as



Figure 4. Structures of compounds 2-10 designed on the basis of the structure of 15d-PGJ₂ and rosiglitazone.



Figure 5. Binding affinity for PPAR γ of rosiglitazone and compounds 7–9 at 0.001, 0.01, 0.1, and 1.0 μ M. Values are means of at least three experiments.



Figure 6. Accumulation of fatty acid in rat preadipocytes by rosiglitazone and compound 9. Values are means of at least three experiments.

potent as rosiglitazone in the binding assay and the preadipocyte differentiation test. Molecular modeling suggested that the carboxylate anion of **9** forms hydrogen



Figure 7. View of the conformation of 9 (tube) docked in PPAR γ . Residues around compound 9 and hydrogen bonds are displayed as wires, and dotted lines, respectively. Figures represent distances in angstroms.



Figure 8. View of the conformation of 9 (tube) docked in PPAR γ . The hydrophobic and hydrophilic regions are shown in yellow and blue, respectively.

bonds with some hydrophilic amino acid residues, and the nonyl group appropriately interacts with hydrophobic amino acid residues. The findings of this study will help provide an effective agent for Type 2 diabetes. Currently, further detailed studies on compound 9 are under way.

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