Bioorganic & Medicinal Chemistry Letters 26 (2016) 3632-3635

Contents lists available at ScienceDirect

Bioorganic & Medicinal Chemistry Letters

journal homepage: www.elsevier.com/locate/bmcl

Synthesis and bioactivity of pyrazole and triazole derivatives as potential PDE4 inhibitors

Ya-Sheng Li^{a,†}, Hao Tian^{a,†}, Dong-Sheng Zhao^{b,†}, De-Kun Hu^a, Xing-Yu Liu^a, Hong-Wei Jin^c, Gao-Peng Song^{d,*}, Zi-Ning Cui^{a,*}

^a State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, Integrative Microbiology Research Centre, Guangdong Province Key Laboratory of Microbial Signals and Disease Control, South China Agricultural University, Guangzhou 510642, China

^b Department of Pharmacy, Quanzhou Medical College, Quanzhou 362100, China

^c State Key Laboratory of Natural and Biomimetic Drugs, School of Pharmaceutical Sciences, Peking University, Beijing 100191, China

^d College of Materials and Energy, South China Agricultural University, Guangzhou 510642, China

ARTICLE INFO

Article history: Received 29 January 2016 Revised 18 May 2016 Accepted 2 June 2016 Available online 2 June 2016

Keywords: Synthesis 5-Phenyl-2-furan Pyrazole and triazole derivatives PDE4 inhibitor Molecular simulation

ABSTRACT

A series of pyrazole and triazole derivatives containing 5-phenyl-2-furan functionality were designed and synthesized as phosphodiesterase type 4 (PDE4) inhibitors. The bioassay results showed that title compounds exhibited considerable inhibitory activity against PDE4B and blockade of LPS-induced $TNF\alpha$ release. Meanwhile, the activity of compounds containing 1,2,4-triazole (series II) was higher than that of pyrazole-attached derivatives (series I). The primary structure-activity relationship study and docking results showed that the 1,2,4-triazole moiety of compound **IIk** played a key role to form integral hydrogen bonds and π - π stacking interaction with PDE4B protein while the rest part of the molecule extended into the catalytic domain to block the access of cAMP and formed the foundation for inhibition of PDE4. Compound **IIk** would be great promise as a hit compound for further study based on the preliminary structure-activity relationship and molecular modeling studies.

© 2016 Elsevier Ltd. All rights reserved.

Phosphodiesterases (PDEs) play a key role in catalyzing the hydrolysis of the secondary signal messengers, cyclic adenosine monophosphate (cAMP) and cyclic guanosine monophosphate (cGMP), which are able to regulate the function of airway smooth muscle, inflammatory cells, and immune cells.^{1–3} The PDE4, as one of the 11-membered PDEs, specifically targets the second messenger cAMP and is expressed predominantly in inflammatory and immune cells including eosinophils, lymphocytes, macrophages, and neutrophils.^{4,5} When PDE4 is inhibited, the resultant elevation of intracellular cAMP levels leads to an activation of specific protein phosphorylation cascades, which elicit a variety of functional responses in the inflammatory cells such as suppression of $TNF\alpha$ production.^{6–8} Therefore, the development of PDE4 inhibitors as anti-inflammatory drugs for the treatment of asthma and chronic obstructive pulmonary disease (COPD) has made a long standing research effort.9-14

PDE4 inhibitors have been extensively studied as anti-inflammatory drugs since the discovery of rolipram (Fig.1) and piclamilast was found to be a highly versatile linker and the derivatives exhibited significantly potent PDE4 inhibitory activity.^{20–22} In this study, the oxazole was replaced by furan ring, and pyrazole and triazole were introduced to form a new combination as PDE4-inhibitor pharmacophores (Fig.1). The synthetic route of title compounds I and II was shown in

(Fig.1) in the 1990s. A detailed structure-activity relationship (SAR)

study revealed that the 4-(3,4-dialkoxyphenyl) moiety of catechol

(Fig.1) was important for PDE4 inhibition where two alkoxy groups

occupied each different lipophilic pocket and the catechol ether

oxygens constructed H-bond to the purine-selective glutamine residue, which is surrounded by the P-clamp.^{15,16} Further structural

modification suggested that the 8-methoxyquinoline-5-carboxam-

ides (such as SCH 365351) showed excellent PDE4 inhibitory activ-

ity. Modeling studies on the 8-methoxyquinoline-5-carboxamide

related compounds demonstrated that the quinoline moiety binds

to the adenosine recognition site, while the amide portion served

as a linker to anchor a group containing a polar atom which pro-

vided favorable interactions with the metal ion binding site of PDE4.^{17–19} Five-membered heterocyclic oxazole moiety was

explored as possible linker to replace the amide portion, which

Scheme 1. The key intermediate 2 was synthesized from substituted aniline by Meerwein arylation reaction according to the







^{*} Corresponding authors. Tel./fax: +86 20 85288229.

E-mail addresses: vinsin1021@126.com (G.-P. Song), ziningcui@scau.edu.cn (Z.-N. Cui).

[†] These authors contributed equally to this Letter.



Figure 1. The designed strategy for the title compounds.



Scheme 1. The synthetic route of the title compounds I and II. Reagents and conditions: (a) NaNO₂, hydrochloric acid, 0–5 °C, 3 h; (b) furoic acid, CuCl₂ (cat.), acetone–H₂O, rt, 5 h; (40–65%, two steps) (c) SOCl₂, anhydrous toluene, reflux, 3 h; (d) pyrazole or 1,2,4-triazole, anhydrous dichloromethane, reflux, 4 h (75–91%, two steps). R¹ = Ia: 4-Cl; Ib: 2-NO₂; Ic: 2-Cl; Id: 3-Cl; Ie: 3-F; If: 4-F; Ig: 2.4-di-F; Ih: 2.6-di-F; Ii: H; Ij: 4-CH₃; Ik: 4-OCH₃; II: 3-NO₂; Im: 2-F; IIa: 4-Cl; IIb: 2-NO₂; IIC: 2-Cl; IId: 3-Cl; IIE: 3-F; If: 4-F; Ig: 2.4-di-F; IIh: 2.6-di-F; IIh: 2.6-di-

reported procedure.^{23,24} A mixture of 5-substituted phenyl-2furancarboxylic acid **2** and thionyl chloride was refluxed in anhydrous toluene for 3 h to afford the 5-phenyl-2-furancarbonyl chloride, which was added into pyrazole or 1,2,4-triazole in anhydrous dichloromethane to react and obtain the title compounds **I** and **II** as solid (see the Supplementary data for the details).

In vitro data for the inhibition of PDE4B and blockade of LPSinduced TNF α release were listed in Table 1. Rolipram was chosen as the positive control. Generally, the activity of title compounds containing 1,2,4-triazole (series II) was better than that of compounds containing pyrazole (series I), except compounds e and h. Among the title compounds, the IC₅₀ value of **IIk** was $1.2 \pm 0.1 \,\mu\text{M}$ and $9.8 \pm 0.7 \,\mu\text{M}$ respectively against PDE4B and TNF α , which showed comparable or better activity than rolipram $(1.5 \pm 0.1 \,\mu\text{M} \text{ and } 12.5 \pm 1.1 \,\mu\text{M})$ (Table 1). Compound Ik displayed comparable IC₅₀ values $(2.8 \pm 0.3 \,\mu\text{M} \text{ against PDE4B} \text{ and}$ $22.7 \pm 2.4 \,\mu\text{M}$ against TNF α) to that of rolipram. In addition, compounds Ia and IIa, Ig and IIg also showed favorable activity. A primary structure-activity relationship study showed that the position of the substituted group played a key role in the bioactivity. Activity with respect to substitution at the benzene ring follows the trend: 4->2,4->3->2,6->2-. The compounds li and lli without any substituted group showed the poorest activity.

Considering the inhibitory activity of title compounds, it was of interest to explore the binding to the PDE4 structure. The bioassay results demonstrated that compounds containing *para*-methoxy group (**Ik** and **IIk**) showed the best activity among all the title

compounds. Therefore docking simulation of compounds Ik and IIk at PDE4B (PDB ID: 1XMY) was conducted using Surflex-Dock in Sybyl 8.0 (see the Supplementary data for the method),^{16,25} and the docking contour maps were shown in Figure 2. The docking orientation demonstrated that the five-membered heterocyclic moiety as the pivotal pharmacophore formed integral hydrogen bonds with the conserved glutamine residue (Gln443) (Fig. 2) and the heterocyclic ring was evidently positioned between the phenylalanine (Phe446) and isoleucine (Ile410) (Fig. 2C and E), which formed the cavity accommodating the hydrophobic moiety of compounds **Ik** and **IIk**. Compared with the pyrazole derivative **Ik**, the 1,2,4-triazole moiety of **IIk** formed obvious π - π stacking interaction with benzene ring (3.26 Å, Fig. 2E and F) in the phenylalanine (Phe446), which could enhance the binding affinity with the enzyme. That could be the reason why the activity of most title compounds containing 1,2,4-triazole (series II) was better than that of compounds containing pyrazole. The remainder of the molecule was displayed to extend into the catalytic domain in close to both the Zn^{2+} and Mg^{2+} cations (Fig. 2D and F), which played important roles in the catalytic mechanism of cAMP hydrolysis. The para-methoxy group formed coordinate bond with the Zn^{2+} (2.23 Å, **Ik**, Fig. 2C and D) and Mg²⁺ (1.92 Å, **IIk**, Fig. 2E and F) cations. Such orientation and interactions would block the access of cAMP to the catalytic domain and formed the foundation for inhibition of PDE4.

In summary, the design and synthesis of pyrazole and triazole derivatives containing 5-phenyl-2-furan moiety were reported in

Download English Version:

https://daneshyari.com/en/article/1368530

Download Persian Version:

https://daneshyari.com/article/1368530

Daneshyari.com