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Pharmacophore-based design, synthesis, and biological evaluation of novel chloro-pyridazine piperazines as human rhinovirus (HRV-3) inhibitors

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ABSTRACT

A series of chloro-pyridazine piperazines were developed based on the structure of human rhinovirus (HRV) capsid-binding inhibitors with proven activity using a pharmacophore model. A preliminary evaluation demonstrated potent activity against HRV-3 with low cytotoxicity. A docking analysis indicated that **8a** could fit into, and form tight interactions (e.g., H-bonds, σ - π effect) with the active site in VP1. © 2010 Elsevier Ltd. All rights reserved.

Human rhinoviruses (HRV), a genus of Picornaviridae family, is most often associated with common colds. Although rhinovirus infection is self-limited, complications could still occur in patients with asthma, congestive heart failure, bronchiectasis and cystic fibrosis.^{1,2} The fact that the US FDA has not approved a single antiviral agent for the treatment or prevention of HRV infection³ clearly indicates a need to develop novel antiviral agents against HRV.

The capsids of HRV are composed of four structural viral proteins, namely, VP1, VP2, VP3, and VP4.³ Pleconaril, an antiviral agent, has been shown to have a broad spectrum of activities against rhinovirus by binding to the hydrophobic pocket in VP1, resulting in the inhibition of the virus attachment to the cells and uncoating of viral RNA.^{4,5} Subsequent search, spurred by the encouraging results with pleconaril, vielded additional compounds that bind to VP1, including pirodavir, BTA-188, 13 and 5f (Fig. 1). Pirodavir could inhibit 80% of all HRV strains.² BTA-188 has been shown to inhibits 87 of 100 HRV serotypes, and the activity against HRV-14 (EC₅₀: 1.0 ng/ml) was found to be superior to both pleconaril (EC₅₀: 30 ng/ml) and pirodavir (EC₅₀: 3.2 ng/ml).³ Compound 13 displayed efficient activity against 16 HRV strains and the average EC_{50} is 3.88 ng/ml.⁶ Compound 5f was developed in our lab with the equal excellent anti-virus activity against HRV-2 and 14 (EC₅₀: 32 ng/ml).²

* Corresponding author. E-mail address: xiaojunhai@139.com (J. Xiao). Based on the features of the aforementioned compounds, we built a four-point pharmacophore model using the Common Feature Pharmacophore Generation within Accelrys Discovery Studio 2.5.⁷ The optimal pharmacophore Hypo1 contained an aromatic ring (A), a hydrogen bond acceptor (HBA) and two hydrophobic moieties (HY). All features of Hypo1 model were nicely mapped with BTA-188 (Fig. 2A). Search our in-house chemical database which contains nearly 10,000 compounds using Ligand Pharmacophore Mapping within Accelrys Discovery Studio 2.5 with such a pharmacophore identified one hit (compound 1) with a chloro-pyridazine piperazine skeleton (Fig. 2C), and the mapping picture was shown in Figure 2B.

Compound **1** had significant anti-HRV activity against HRV-3. The EC₅₀ of this lead compound in cell culture cytopathic effect (CPE) assay⁸⁻¹¹ was 25 ng/ml. Using compound **1** as a lead compound, a number of novel compounds were synthesized. Modification included replacing of the methoxy group with other hydrophobic moieties (e.g., ethoxyl, methyl and methoxycarbonyl groups) and varying the number of carbon atoms between the piper-azine and benzene ring. Screening of 30 candidate compounds yielded seven compounds (**8a–g**) with promising profiles.

The synthetic route of these compounds (8a-g) is illustrated in Scheme 1. The common intermediate piperazin-1-yl-alkylalcohol 4a-b was synthesized in a two-step reaction by alkylating ethyl piperazine-1-carboxylate 2 with 3a-b in the presence of K_2CO_3 in acetonitrile and deprotecting the ethoxycarbonyl group in the presence of aq NaOH in ethanol. The 3-chloro group of 3,6dichloropyridazine 5 was substituted with 4a-b in the presence



Figure 1. Structure of training set and their biological activity data.



Figure 2. Pharmacophore model of HRV capsid-binding inhibitors generated by Hiphop. (A) Hypo1 mapping with BTA-188. (B) Hypo1 mapping with compound **1**. Pharmacophore features are color-coded with light-blue for hydrophobic feature, orange for ring aromatic feature and green for hydrogen-bond acceptor. (C) The chemical structure of compound **1**.

of Na₂CO₃ in DMA to yield **6a–b**. Finally, **6a–b** were coupled with 4-substituted phenol **7a–g** to produce compounds **8a–g** by Mitsunobu reaction.¹²

The anti-HRV activity (EC₅₀ in CPE assay) of these compounds is presented in Table 1. Relative to compound **5f** (EC₅₀: 50 ng/ml), these compounds were 2–15 times more potent against HRV-3 (EC₅₀: 3.2–25 ng/ml). Among these, **8a** was the most potent, with an EC₅₀ at <3.2 ng/ml. These compounds also had much higher ratio of antiviral potency versus cytotoxicity (CC₅₀/EC₅₀: 4875-624) than **5f** (CC₅₀/EC₅₀: 156).

A docking analysis with LigandFit modular of Discovery Studio 2.5 against crystal structure of HRV-3 VP1 (PDB code: 1RHI) indicated that **8a** could fit into the active site of VP1 in a fashion similar to **5f** (Fig. 3).

In **5f**, the oxygen atom in the carbonyl group is 3.10 Å from the carbamate NH of Val176, indicating H-bond interaction. The N2 of the pyridazine ring and Cl atom are 2.16 and 1.60 Å away from the



Scheme 1. Synthesis of compound 8a–g. Reagents and conditions: (i) K₂CO₃, MeCN, reflux; (ii) 10% NaOH(aq), EtOH, reflux; (iii) Na₂CO₃, DMA, rt; (iv) Ph₃P, DEAD, THF.

 Table 1

 The anti-HRV activity and cytotoxicity of compounds 1, 5f and 8a-g on HRV-3

| Compound | EC ₅₀ (ng/ml) | CC ₅₀ (µg/ml) | SI |
|----------|--------------------------|--------------------------|-------|
| 1 | <25 | 15.6 | 624 |
| 5f | 50 | 7.8 | 156 |
| 8a | <3.2 | 15.6 | >4875 |
| 8b | 25 | 15.6 | 624 |
| 8c | 25 | 15.6 | 624 |
| 8d | <12.5 | 15.6 | >1248 |
| 8e | 6.25 | 15.6 | 2496 |
| 8f | 12.5 | 7.8 | 624 |
| 8g | 6.25 | 15.6 | >2496 |
| | | | |

SI (selectivity index) = CC₅₀ (toxicity)/EC₅₀ (antiviral activity).

phenolic hydroxyl group of Tyr197, respectively, also indicating formation of H-bonds. The benzene ring is 3.77 Å from the methylene group of Tyr152, suggesting potential σ - π effect.

In compound **8a**, the benzene ring performs a similar σ – π effect with the methylene group of Tyr152 to **5f** at a distance of 3.64 Å. The ethoxyl group is 3.03 Å from the backbone NH of Ser175, indicating similar H-bond interaction to **5f** (H-bond between oxygen atom and NH of Val176). N1 and N2 of the 3-chloropyridazine



Figure 3. Compounds **5f** (blue) and **8a** (pink) docked in the active site with similar fashion in the structure of HRV-3 VP1.



Figure 4. Compounds **5f** (blue) and **8a** (pink) docked in the active site: some important amino acid residues in hydrophobic pocket, H-bonds (blue) and σ - π effect (yellow) are present.

group are 2.25 and 2.03 Å from the phenolic hydroxyl group of Tyr197, respectively, also indicating similar H-bonds interaction to **5f**. The Cl atom is also located in hydrophobic pocket by forming a hydrogen-bond with Asp125 in the distance of 2.99 Å, this additional H-bond interaction may result in the higher activity of **8a** than **5f** (Fig. 4).

Similar types of interactions with the active site of HRV-3 VP1 are noted for compounds **8b–g**. The hydrophobic pocket has sufficient space to accommodate a chain of 3–5 carbon atoms between the piperazine and benzene.

In conclusion, the chloro-pyridazine piperazine derivatives developed in this study interacted with the active site of HRV VP1 in a manner similar to **5f**, a compound with reported activity against HRV. Among these, compounds **8a** and **8g** had excellent anti-HRV activity and low cytotoxicity, and represent promising candidates as anti-HRV agents.

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Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.bmcl.2010.12.001.

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- Selected data for compound 8a: ¹H NMR (400 MHz, CD₃Cl) δ = 7.21 (d, 1H, J = 9.6 Hz); 6.90 (d, 1H, J = 9.6 Hz); 6.83 (s, 4H); 3.98 (m, 4H); 3.67 (br, 4H); 2.61 (br, 6H); 2.00 (m, 2H); 1.39 (t, 3H, J = 7.2 Hz). MS (EI) [M+1]⁺: m/z = 376.2. Mp 122–124 °C.