



Proceeding Paper Synephrine Analogues as Glucocorticoid Receptor Agonists *

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Abstract: The work carried out the synthesis of a number of new synephrine analogues by universal method. Some of synthetized compounds showed cytotoxicity on myeloid leukemia cells K562 and lymphoma cell line Granta-519. Molecular docking using glucocorticoid receptor (GR) model (PDB identifier 1P93) was performed in order to understand possible under-lying mechanism of compounds action. The simulation showed similarity of synephrine analogues' binding to the binding of dexamethasone in the GR ligand-binding domain. The synthesized analogues exhibited cytotoxicity profiles similar to those of dexamethasone.

Keywords: glucocorticoid receptor; synephrine analogues; chronic myelogenous leukemia; mantle cell lymphoma

1. Introduction

Glucocorticoids (GC) are steroid hormones regulating many cellular and physiological functions and being best known for their anti-inflammatory properties. Recently, more evidence has emerged that glucocorticoid regulation of inflammation affects oncogenesis [1,2]. Steroid GC are being used as immunomodulators during application of main antitumor therapy methods, including chemo- and radiation therapy [3,4]. In addition, GC are widely used in therapy of leukemia and lymphoma as cytostatic drugs [5]. GC implement their biological effect via activation of glucocorticoid receptor which leads to suppression of tumor cells' growth and proliferation, inducing their apoptosis [6–8].

Synthetic GC dexamethasone (Dex) is glucocorticoid receptors' agonist commonly used as a direct chemotherapy agent in case of certain malignant neoplasms' types, however, it has a number of shortcomings. The effect of Dex outside the zone of therapeutic interests may cause wide range of complications, including systemic toxicity, local allergic reactions, changes in heart function etc., which makes the search and development of different less toxic agents especially important [9,10].

Nowadays it is known that the class of non-steroidal Dex analogues shows similar biological effects while being less overall toxic [11,12]. The design of such compounds may consist of replacing Dex sterane backbone with less rigid hydrocarbon skeleton, predominantly preserving spatial arrangement of original functional groups. We have assumed that such analogues could be obtained on the basis of synephrine molecule, which mimics the Dex backbone (Figure 1).

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Figure 1. Structures of Dex, synephrine and its synthetic analogues 1.

These suggestions were examined by molecular docking approach using the glucocorticoid receptor model. Simulation held has shown selective binding of synephrine analogues in the hydrophobic pocket of GR binding domain.

2. Results and Discussion

2.1. Chemistry Section

There are different synthetic approaches to obtaining synephrine analogues [13,14]. We have applied, in our opinion, the most expedient one which consists in the synthesis of intermediate epoxide and its following interaction with aliphatic primary and secondary amines (Figure 2).



Figure 2. Synthesis of synephrine derivatives 1a-o.

The starting compounds **2** were obtained according to known methods [15,16]. 4-Alcoxychloroacetophenones **2** was reduced with the excess of NaBH₄ in methanol followed by the treatment with *KOH* and addition of fivefold excess of amine without isolation of intermediate products. Target compounds **1f–o** were isolated by column chromatography on silica gel after volatile components' evaporation followed by excess amine extraction. The compounds **1a–e** were obtained by hydrogenation of **1k–o** on palladium on carbon (Figure 2).

For the initial study of biological properties compounds were synthesized as a mix of enantiomers. Further investigation suggests synthesis of individual enantiomers only in case of active compounds detection. Individual enantiomers can be obtained by stere-oselective reduction of corresponding ketones **2** [17].

2.2. In Silico Studies

Molecular docking has shown a number of significant non-covalent interactions demonstrated by studied compounds in GR ligand-binding domain. Thus, π -alkyl interactions with Met604, Leu608 were identified, which are also characteristic of steroid

ligands. In addition, important hydrogen interactions which are characteristic of Dex were also found, including interactions with Gln642 μ Thr739 (Figure 3). Dex location determined in the experiment coincides with literature data reported by other authors [12].



Figure 3. Structure of the GR active site with analogue of synephrine **1m** in comparison with Dex (shown in blue and green, respectively).

2.3. Biology Section

In vitro experiments were held to estimate cytotoxicity of new compounds on model of the hematopoietic system malignant neoplasms. Cells proliferation was evaluated using myeloid leukemia cells K562 and lymphoma cell line Granta-519.

		Compound No.				
Cell Line	Time, h	1a	1g	1k	1m	Dex
		(C = 50µM)	$(C = 50 \mu M)$	(C = 100µM)	(C = 100µM)	$(C = 25 \mu M)$
K562	24	0.65 ± 0.08	0.80 ± 0.08	0.75 ± 0.06	0.53 ± 0.05	0.80 ± 0.05
	48	0.52 ± 0.06	0.84 ± 0.07	0.60 ± 0.05	0.28 ± 0.09	0.65 ± 0.04
	72	0.37 ± 0.12	0.53 ± 0.08	0.20 ± 0.05	0.18 ± 0.07	0.44 ± 0.10
Granta-519	24	0.61 ± 0.11	0.93 ± 0.09	0.95 ± 0.04	0.95 ± 0.05	0.90 ± 0.04
	48	0.54 ± 0.08	0.73 ± 0.07	0.48 ± 0.08	0.64 ± 0.08	0.53 ± 0.05
	72	0.84 ± 0.09	1.00-0.07	0.70 ± 0.12	0.85 ± 0.06	0.64 ± 0.07

Table 1. The proportion of live cells compared to the vehicle control.

Dex showed cytostatic on 48 and 72 depending on cell line. Synthesized compounds demonstrated effect similar to that of Dex, which suggests that the mechanism of their action is similar to the mechanism of Dex. In case of the cell line **K**562, studied compounds demonstrated inhibitory effect on cell proliferation in 48 h (**1k**–**m**) and 72 h (**1g**), which is completely similar to the action of reference drug. For the Granta-519 cell line, such pattern could also be traced for **1a**,**g**,**k**,**m**, but this cells did not maintain a long-term effect, unlike Dex.

3. Conclusions

New synephrine analogues modified at the phenolic hydroxyl were synthesized. They showed a comparable to Dex effect on the myeloid leukemia cell line K562 and lymphoma cell line Granta-519. The in silico modeling data is suggested that these analogues may compete with Dex to bind to the GR active site. These results encourage further investigation of synephrine analogues as GR agonists.

4. Materials and Methods

4.1. Materials

All the chemicals were obtained from commercial sources (Merck KGaA, Darmstadt, Germany) and were used without further purification. Deuterated solvents were

purchased from Cambridge Isotope Laboratories, Inc. (Tewksbury, MA, USA). Silica gel 60 (Merck KGaA, Darmstadt, Germany) was used for column chromatography. Analytical TLC was performed on Silufol UV-254 plates.

¹H NMR spectra were recorded at 300 MHz and ¹³C NMR spectra recorded at 75 MHz on Bruker DPX-300 spectrometer. High-resolution mass spectra (HRMS) were recorded on the Agilent 6224 using electron spray ionization (ESI). HPLC measurements were carried out on the Agilent 1200 Series.

4.2. Synthesis

Synephrine analogues 1f-o (general synthesis procedure)

To a solution of 4-alcoxychloroacetophenone **2** (1.5 mmol) in methanol was added 1 eq NaBH₄ by portions while cooling on the ice bath. After compound **2** consumption (controlled by TLC, system petroleum ether/diethyl ether 1:1) KOH (1.2 eq) was added by portions. Subsequently, solution of amine (5 eq) in methanol (1:1 by the volume) was added. Reaction was TLC controlled by conversion of **3** (R_f = 0.65–0.75 system petroleum ether/diethyl ether 1:1) in the reaction mixture. Then the mixture was acidified with an diluted aqueous HCl up to pH = 3, the solvent was removed using a vacuum rotary evaporator, after which the residue was dissolved in 5 mL of water and extracted with methylene chloride (2 times, 10 mL). The organic layer was dried with anhydrous calcium chloride followed by filtering off the drying agent and evaporation. Product was isolated by column chromatography on silica gel using chloroform-methanol eluent.

2-(hexylamino)-1-(4-methoxyphenyl)ethanol (1g)

200 mg (54%) of **1g** were obtained. R_f (10% methanol in chloroform) = 0.44. Purity by HPLC \geq 98%. ¹H NMR (CDCl₃) δ , ppm: 7.35–7.26 (m, 2H, 2×CH); 6.94–6.78 (m, 2H, 2×CH); 5.01–4.71 (m, 1H, CH); 3.90–3.80 (m, 2H, NH and OH); 3.76 (s, 3H, O-CH₃); 3.07–2.60 (m, 4H, 2×CH₂); 1.70–1.47 (m, 2H, CH₂); 1.40–1.17 (m, 6H, 3×CH₂); 0.95–0.80 (m, 3H, CH₃). ¹³C NMR (CDCl₃) δ , ppm: 159.13; 133.70; 127.06; 113.80; 70.24; 56.30; 55.24; 49.11; 31.47; 28.39; 26.67; 22.51;13.99. HRMS: for C₁₅H₂₆NO₂ [M+H]⁺ calculated: 252.1963; found: 252.1967.

1-[4-(benzyloxy)phenyl]-2-piperidin-1-ylethanol (1k)

360 mg (77%) of **1k** were obtained. R_f (5% methanol in chloroform) = 0.46. Purity by HPLC \geq 97% ¹H NMR (CDCl₃) δ , ppm: 7.48–7.20 (m, 7H, 7×CH); 7.00–6.87 (m, 2H, 2×CH); 5.04 (s, 2H, CH₂-O); 4.95–4.82 (m, 1H, C<u>H</u>-OH); 2.98–2.38 (m, 6H, 3×CH₂); 1.87–1.37 (m, 6H, 3×CH₂). ¹³C NMR (CDCl₃) δ , ppm: 158.31; 136.89; 133.81; 128.54; 127.93; 127.43; 127.13; 114.77; 69.96; 67.97; 66.56; 54.62; 24.93; 23.42. HRMS: for C₂₀H₂₆NO₂ [M+H]⁺ calculated: 312.1963; found: 312.1970.

1-[4-(benzyloxy)phenyl]-2-[(2-hydroxyethyl)amino]ethanol (1m)

95 mg (22%) of **1m** were obtained. R_f (20% methanol in chloroform) = 0.33. Purity by HPLC \geq 98% ¹H NMR (DMSO-d₆) δ , ppm: 7.50–7.25 (m, 7H, 7×CH); 7.08–6.95 (m, 2H, 2×CH); 5.09 (s, 2H, CH₂-O); 5.27 (br.s, 1H, C<u>H</u>-OH); 4.89 (br.s, 1H, NH); 4.13–3.95 (m, 1H, CH); 3.74–3.45 (m, 4H, 2×CH₂); 2.85–2.52 (m, 2H, CH₂). ¹³C NMR (DMSO-d₆) δ , ppm: 158.29; 136.96; 129.43; 128.38; 127.78; 127.60; 122.08; 114.74; 69.18; 63.46; 63.00; 57.65; 48.01. HRMS: for C₁₇H₂₂NO₃ [M+H]⁺ calculated: 288.1599; found: 288.1604.

Synephrine analogues 1 a-e (general synthesis procedure)

To 0.5 mmol of **1k–o** dissolved in 5 mL of EtOH, an 10% mass excess of Pd on C was added. The suspension was mixed at room temperature in a hydrogen atmosphere. After compound **1k–o** consumption (controlled by TLC, system 5% methanol in chloroform) the reaction mixture was filtered through a layer of celite and evaporated.

4-(1-hydroxy-2-piperidin-1-ylethyl)phenol (1a)

91 mg (82%) of **1a** were obtained. R_f (25% methanol in chloroform) = 0.30. Purity by HPLC \ge 98% ¹H NMR (DMSO-d₆) δ , ppm: 7.19–7.05 (m, 2H, 2×CH); 6.73–6.63 (m, 2H, 2×CH); 4.60–4.52 (m, 1H, C<u>H</u>-OH); 2.46–2.22 (m, 6H, 3×CH₂); 1.57–1.30 (m, 6H, 3×CH₂). ¹³C NMR

(DMSO-d₆) δ, ppm: 158.19; 134.74; 127.07; 114.64; 69.08; 67.11; 54.32; 25.52; 23.94. HRMS: for C₁₇H₂₈NO₂ [M+H]⁺ calculated: 222.1494; found: 222.1501.

4.3. In Silico Studies

3D-geometry of compounds was optimized using MM2 force field in Chem3D software (Perkin Elmer Informatics, Inc., Waltham, MA, USA).

The crystal structure of GR was obtained from the Protein Data Bank (PDB ID: 1P93). The selected structure of the complex has a resolution of 2.7 Å and does not contain gaps in the main protein chain near the ligand-binding domain. Removal of solvent molecules, adding hydrogen atoms, assigning atom types and combining non-polar hydrogen atoms, calculating partial Gasteiger charges, Kollmann charges were done using AutoDockTools 1.5.7 software (The Scripps Research Institute, La Jolla, CA, USA).

During the docking process, all the torsion bonds of the ligands were free to rotate, while the protein remained rigid. A 40 × 40 grid was created with 1 Å spacing centered on the GR active site. Docking calculations were performed in Autodock Vina software (The Scripps Research Institute, La Jolla, CA, USA) using the Lamarckian genetic algorithm (LGA). Visualization and graphical representation of the results of ligand interaction were done in Discovery Studio Visualizer software (version 21.1.0.20298, Dassault Systems Biovia Corp., San-Diego, CA, USA).

4.4. Biology

Cell viability (cell proliferation). Cells were cultured in 24-well plates (50,000 cells/well) and treated with solvent (DMSO), dexamethasone (25 uM), 1a (50 μ M), 1g (50 μ M), 1k (100 μ M), 1m (100 μ M) for 24, 48 or 72 h for observe cytostatic action. After the incubation cells were mixed 1:1 with 0.4% trypan blue in PBS solution. Viable cells were immediately counted using TC20 automatic cell counter ("Bio-Rad", USA).

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Conflicts of Interest:

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