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ORIGINAL RESEARCH

MEDICINAL CHEMISTRY RESEARCH

Design, synthesis, and biological activity of certain quinazolinedione derivatives as potent phosphodiestrase4 inhibitors

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Abstract In this study, a series of 3-butylquinazolinedione linked with different substituent to N1 of quinazoline nucleus have been synthesized. Some of the new final compounds tested in vitro for their inhibitory activity against phosphodiestrase 4B which is the enzyme responsible for the hydrolysis of cyclic adenosine mono phosphate, the second messenger involved in the regulation of important cell functions. Compound 7f (100%) showed inhibition better than rolipram (90%), while the other tested compounds showed moderate activity. Docking study has been done to rationalize the obtained biological results.

Keywords Synthesis -

Phosphodiestase4B (PDE4b) inhibitor · Quinazolindiones · Docking study

Introduction

Phosphodiestrases (PDEs) are enzymes responsible for the hydrolysis of cyclic adenosine mono phosphate (c-AMP) and cyclic guanosine mono phosphate (c-GMP) which are second messengers involved in the regulation of important cell functions such as secretion, contraction, metabolism, and growth (Potter, [1990\)](#page-12-0). The inhibition of PDEs activity increases cellular levels of the key second messengers c-AMP and c-GMP, thereby activating specific protein phosphorylation cascade that elicit a variety of functional response (Palacios et al., [1995\)](#page-12-0). Strong evidence suggests

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that c-AMP play a central role in regulating the function of airway smooth muscle (Torphy, [1998](#page-12-0)), inflammatory cells (Souness et al., [2000\)](#page-12-0), and immune cells and the c-AMP specific PDE4 is the predominant isoenzyme found in proinflammatory cells associated with a number of airways disorders (Barnes, [1999\)](#page-12-0).

There are at least two main reasons for the basis of the rapid development of the chemical, pharmacological and biochemical research in the therapeutic utility of selective PDE4 inhibitors. First, there is a general conviction that the mixed anti-inflammatory and bronchodilator profile of PDE4 inhibitors could allow, through the optimization of first generation prototypes, the discovery of new agents able to compete and, perhaps, to replace corticosteroids which represent the basis of the therapeutic management of asthma. Moreover, PDE4 inhibitors may be beneficial in the treatment of chronic obstructive pulmonary disease (COPD), a major respiratory disease for which pharmacological treatment is still inadequate (Norman, [1999](#page-12-0)).

Second, new and promising therapeutic applications of PDE4 inhibitors in certain unmet autoimmune diseases, e.g. rheumatoid arthritis, multiple sclerosis, and type 2 diabetes have emerged in recent years (Burnouf et al., [1998](#page-12-0)).

The PDE4 family is comprised of four primary gene products (PDE4A, PDE4B, PDE4C, and PDE4D) and is highly expressed in neutrophils and monocytes, CNS tissue, and smooth muscles of the lung (Bender and Beavo, [2006](#page-12-0); McKenna and Muller, [2006](#page-12-0); Zhang et al., [2005](#page-12-0)). Knockout studies have revealed that PDE4B ablation suppresses $TNF-\alpha$ production, and PDE4D may be responsible for the occurrence of nausea and emesis (Robichaud et al., [2002](#page-12-0); Zhang et al., [2005](#page-12-0)), heart failure, and the risk of arrhythmias (Lehnart et al., [2005](#page-12-0)).

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From a structural point of view, selective PDE4 inhibitors in the public domain can be divided into three classes: structural analogues of rolipram, structural analogues of nitraquazone, and structures related to xanthines (Fig. 1).

In fact rolipram, since its discovery as a potent and selective PDE 4 inhibitor (Schneider et al., [1986\)](#page-12-0), has represented a useful pharmacological tool for the characterization of this isoenzyme in different tissues, as well as the main template for the synthesis of novel inhibitors. However, severe limiting side effects (nausea, vomiting, headache) precluded the development of rolipram and many promising candidates have been discontinued. Although a number of studies claiming different chemical classes of PDE 4 inhibitors are increasing in recent years, only few detailed studies evaluated the PDE4 inhibition of structural analogues of nitraquazone. These compounds could be devoid of the central side effects of the archetypal rolipram which hampered its development as a drug (Piaz and Giovannoni, [2000\)](#page-12-0).

On this basis, this work was directed to synthesize a hybrid structure containing the quinazoline-2,4-dione nucleus of nitraquazone along with the *n*-butyl side chain of denbufylline. This scaffold is linked with different substituents at N1, which were chosen by selecting the ones with highest scores in a virtual screening study. Moreover, this paper describes the synthesis, PDE4B inhibition evaluation and docking studies for series of quinazolinones structures. Docking results were compared to biological data with the aim of obtaining useful information for the rational design of new PDE4B antagonist.

Methods and materials

Chemistry

All chemicals and reagents were obtained from Aldrich (Sigma-Aldrich, St. Louis, MO, USA), Lancaster (Alfa Aesar, Johnson Company, Ward Hill, MA, USA) and were used without further purification. Reactions were

monitored by TLC, performed on silica gel glass plates 3558 Med Chem Res (2012) 21:3557–3567

containing 60 GF-254, and visualization on TLC was achieved by UV light or iodine indicator. IR spectra were determined on Shimadzu IR 435 spectrophotometer (KBr, cm^{-1}). ¹H-NMR, C^{13} -NMR spectra were recorded on Gemini Varian-VXR-unity (200 MHz), Gemini Varian 500 MHz (Germany) or Bruker UXNMR/XWIN-NMR (300 MHz) instruments. Chemical shifts (δ) are reported in ppm downfield from internal TMS standard. EI-MS Hewlett Packard 5988 spectrometer, Micro analytical Center, Cairo University, Egypt. ESI-MS Quadrupole VG Quattro Institute of Pharmacy & Molecular Biotechnology in Neuenheimer Field 364 69120 Heidelberg Germany. Elemental analyses were carried out in the Micro analytical Center, Cairo University, Egypt. Melting points were determined with an electro thermal melting point apparatus, and were uncorrected. On the other hand, 2-amino-Nbutylbenzamide (1) (Clark and Wagner, [1944](#page-12-0)) was synthesized according to reported procedures. While 3-butylquinazoline-2,4(1H, 3H)-dione (3) was synthesized by a new procedure rather than the reported one (Staiger and Wagner, [1953](#page-12-0)).

2-Ethoxycarbonylamino-N-butylbenzamide (2)

A mixture containing 2-amino-N-butylbenzamide (1) (1.92 g, 0.01 mol) and ethyl chloroformate (28.5 g, 25 ml, 0.26 mol) was heated over steam for 3 h. The reaction mixture was evaporated under reduced pressure. The solid formed crystallized from ethanol/water mixture.

Yield: 80% mp.: 60°C. IR v_{max} (cm⁻¹) (KBr): 3323 (2 NH), 2958, 2933 (CH aliphatic), 1737 (carbamate C=O), 1662 (C=O). ¹HNMR (500 MHz, CDCl₃₋) δppm: 0.90(t, 3H, CH₃), 1.31(t, 3H, $J = 7.5$ Hz, OCH₂CH₃), 1.38–1.46(m, 2H, CH_2CH_3), 1.58–1.64(m, 2H, $CH_2CH_2CH_3$), 3.42(q, 2H, N₃CH₂), 4.20(q, 2H, $J = 7.5$ Hz, OCH₂CH₃), 6.24(s, 1H, NH, D₂O exchangeable), 7.01(dd, 1H, Ar–C₅H), 7.40–7.49 $(m, 2H, Ar-C₃H + Ar-C₄H), 8.38(d, 1H, Ar-C₆H), 10.40(s,$ 1H, NH). ¹³C NMR (CDCl₃) δ ppm: 13.7 (CH₃), 14.5 (CH₃), 20.2 (CH₂), 31.5 (CH₂), 39.7 (CH₂–NH), 61.0 (OCH₂),

Fig. 1 Compounds representative of the three chemical classes of PDE 4 inhibitors: rolipram, nitraquazone, and xanthine derivatives (denbufylline)

Rolipram Nitraquazone Denbufylline

N

O

114.7–139.9 (Ar–C), 153.9 (C=O), 168.8 (C=O). ESIMS m/z (% rel. abundance): $265.21(M + 1, 100\%)$. Anal. calcd. for $C_{14}H_{20}N_2O_3$: C, 63.62; H, 7.63; N, 10.60; Found C, 63.92; H, 7.34; N, 10.90.

3-Butylquinazoline-2,4(1H,3H)-dione (3)

A mixture of 2-ethoxycarbonylamino-N-butylbenzamide (2) (7.92 g, 0.03 mol) and KOH (3.36 g, 0.06 mol) in absolute ethanol (150 ml) was refluxed over steam for 4 h. The reaction mixture was evaporated under reduced pressure. The residue obtained was dissolved in a minimum amount of water, which was adjusted to pH 7–8 with acetic acid. The precipitated product was crystallized from ethanol/water mixture. Yield: 5.5 g (84%) mp.: 156–157°C (as reported).

3-Butyl-1-(2-chloroethyl) quinazoline-2,4(1H,3H) dione (4)

A ternary mixture of 3-butylquinazoline-2,4(1H,3H)-dione (3) (2.18 g, 0.01 mol), 1-bromo-2-chloroethane(7.17 g, 4.16 ml, 0.05 mol) and anhydrous K_2CO_3 (6.90 g, 0.05 mol) in dry DMF (30 ml) was stirred at room temperature over night. The mixture was poured onto water and the formed precipitate was filtered, dried, and crystallized from ethanol/water mixture.

Yield: 64% mp.: 83°C. IR v_{max} (cm⁻¹) (KBr): 2954, 2931, 2870 (CH aliphatic), 1701 (C=O), 1662 (C=O). ¹HNMR (500 MHz, CDCl₃₋) δ ppm: 0.95(t, 3H, CH₃), 1.37–1.45(m, 2H, CH_2CH_3), 1.64–1.70(m, 2H, $CH_2CH_2CH_3$), 3.80(t, 2H, $J = 7.0$ Hz, CH₂Cl), 4.08(t, 2H, N_3CH_2), 4.45(t, 2H, $J = 7.0$ Hz, N_1CH_2), 7.23–7.29(m, 2H, $C_6H \& C_8H$ of quinazoline), 7.58(dd, 1H, C_7H of quinazoline), 8.24(d, 1H, C_5H of quinazoline). ¹³C NMR (CDCl₃) δ ppm: 13.8 (CH₃), 20.2 (CH₂), 29.9 (CH₂), 39.6 (CH_2Cl) , 41.8 (CH_2-N_3) , 44.9 (CH_2-N_1) , 113.2–139.6 (Ar–C), 150.7 (C=O), 161.4 (C=O). Anal. calcd. for $C_{14}H_{17}CIN_2O_2$: C, 59.89; H, 6.10; N, 9.98; Found C, 60.19; H, 6.12; N, 9.93.

General procedure for the synthesis of compounds 5a–e

To the solution of 3-butyl-1-(2-chloroethyl) quinazoline-2,4(1H,3H)-dione (4) (0.84 g, 0.003 mol) in dry acetonitrile (20 ml), anhydrous K_2CO_3 (2.07 g, 0.015 mol) and few specs of KI were added and the mixture was heated under reflux for 30 min. Appropriate amine (0.009 mol) was then added slowly into the reaction mixture. The resulting mixture was heated under reflux for 15 h, cooled and poured onto ice-cold water. The separated solid was filtered, dried, and crystallized from a suitable solvent.

3-Butyl-1-[2-(pyrrolidin-1-yl)ethyl]quinazoline-2,4(1H,3H)-dione (5a)

Yield: 75% mp.: 75°C (ethanol). IR v_{max} (cm⁻¹) (KBr): 2958, 2931, 2872 (CH aliphatic), 1699 (C=O), 1654 (C=O). ¹HNMR (300 MHz, CDCl₃₋) δ ppm: 0.96(t, 3H, CH₃), 1.35-1.47(m, 2H, CH_2CH_3), $1.62-1.72$ (m, 2H, $CH_2CH_2CH_3$), 1.80–1.84(m, 4H, C_3 & C_4 of pyrrolidine), 2.64–2.68(m, 4H, C_2 & C_5 of pyrrolidine), 2.79(t, 2H, $J = 7.5$ Hz, $N_1CH_2CH_2N$, 4.08(t, 2H, N_3CH_2), 4.29(t, 2H, $J = 7.5$ Hz, N_1CH_2), 7.21–7.29(m, 2H, C₆H & C₈H of quinazoline), 7.65(dd, 1H, C_7H of quinazoline), 8.28(d, 1H, C_5H of quinazoline). ESIMS m/z (% rel. abundance): 316.30 (M + 1, 100%). Anal. calcd for $C_{18}H_{25}N_3O_2$: C, 68.54; H, 7.99; N, 13.32; Found C, 68.60; H, 7.92; N, 12.96.

3-Butyl-1-[2-(morpholin-4-yl)ethyl]quinazoline-2,4(1H,3H)-dione (5b)

Yield: 70% mp.: 102–104 °C (ethanol). IR v_{max} (cm⁻¹) (KBr): 2962, 2931 (CH aliphatic), 1697 (C=O), 1651 (C=O). ¹HNMR $(500 \text{ MHz}, \text{CDCl}_{3-})$ δ ppm: 0.95(t, 3H, CH₃), 1.37–1.44(m, 2H, CH_2CH_3), 1.64–1.70(m, 2H, $CH_2CH_2CH_3$), 2.47–2.53(m, 4H, C_3 & C_5 of morpholine), 2.75(t, 2H, $J = 7.5$ Hz, N₁CH₂CH₂N), 3.65–3.82(m, 4H, C₂ & C₆ of morpholine), 4.08(t, 2H, N₃CH₂), 4.29(t, 2H, $J = 7.5$ Hz, N_1CH_2), 7.22–7.27(m, 2H, C₆H & C₈H of quinazoline), 7.62(dd, 1H, C_7H of quinazoline), 8.25(d, 1H, C_5H of quinazoline). ESIMS m/z (% rel. abundance): 332.27 (M + 1, 100%). Anal. calcd for $C_{18}H_{25}N_3O_3$: C, 65.23; H, 7.60; N, 12.68; Found C, 65.19; H, 7.56; N, 12.49.

3-Butyl-1-[2-(piperidin-1-yl)ethyl]quinazoline-2,4(1H,3H)-dione (5c)

Yield: 78% mp.: 98–100°C (ethanol). IR v_{max} (cm⁻¹) (KBr): 2931, 2862 (CH aliphatic), 1697 (C=O), 1654 (C=O). ¹HNMR (300 MHz, DMSO) dppm: 0.89(t, 3H, CH3), 1.26–1.58(m, 10H, 2CH₂ +3CH₂ of C³, C⁴, C⁵ piperidine), 2.39–2.52(m, 6H, CH₂ + 2CH₂ of C², C⁶ piperidine), 3.94 (t, 2H, N₃C<u>H₂</u>), 4.20(t, 2H, N₁CH₂), 7.27(dd, 1H, C₆H of quinazoline), 7.45 (d, 1H, C_8H of quinazoline), 7.75(dd, 1H, C_7H of quinazoline), 8.04(d, 1H, C₅H of quinazoline), Anal. calcd for $C_{19}H_{27}N_3O_2$: C, 69.27; H, 8.26; N, 12.76; Found C, 69.49; H, 8.25; N, 12.77.

3-Butyl-1-[2-(4-phenylpiperazin-1-yl) ethyl]quinazoline-2,4(1H,3H)-dione (5d)

Yield: 69% mp.: 78–84 °C (hexane/ethanol). IR v_{max} (cm^{-1}) (KBr): 2954, 2927, 2831 (CH aliphatic), 1697(C=O), 1647 (C=O). ¹HNMR (300 MHz, CDCl₃₋) δ ppm: 0.95(t, 3H, CH₃), 1.35–1.47(m, 2H, CH₂CH₃),

 $1.63-1.73(m, 2H, CH_2CH_2CH_3), 2.75-2.81(m, 6H,$ $N_1CH_2CH_2N + 2CH_2$ piperazine), 3.22–3.25(m, 4H, 2CH₂ piperazine), $4.09(t, 2H, N_3CH_2)$, $4.36(t, 2H, N_1CH_2)$, 6.85–8.25(m, 9H, ArHs). EIMS m/z (% rel. abundance): 406.10 $(M^+, 22.62\%)$, 407.00 $(M + 1, 7.31\%)$, 175.05(100%). Anal. calcd for $C_{24}H_{30}N_4O_2$: C, 70.91; H, 7.44; N, 13.78. Found C, 70.86; H, 7.35; N, 13.66.

3-Butyl-1-[2-(diethylamino)ethyl]quinazoline-2,4(1H,3H)-dione (5e)

Yield: 60% mp.: 46–48°C (ethanol). IR v_{max} (cm⁻¹) (KBr): 2966, 2931 (CH aliphatic), 1701(C=O), 1654 (C=O). ¹HNMR (300 MHz, CDCl₃) δ ppm: 0.96(t, 3H, CH₃), 1.05(t, 6H, $J = 7$ Hz, NCH₂CH₃) 1.35–1.47(m, 2H, CH_2CH_3), 1.63–1.73(m, 2H, $CH_2CH_2CH_3$), 2.64(q, 4H, $J = 7$ Hz, NCH₂CH₃), 2.73(t, 2H, $J = 7.5$ Hz, $N_1CH_2CH_2N$, 4.09(t, 2H, N_3CH_2), 4.22(t, 2H, $J = 7.5$ Hz, N_1CH_2), 7.23–7.27(m, 2H, C₆H & C₈H of quinazoline), 7.65(dd, 1H, C_7H of quinazoline), 8.24(d, 1H, C_5H of quinazoline). Anal. calcd for $C_{18}H_{27}N_3O_2$: C, 68.11; H, 8.57; N, 13.24; Found C, 68.23; H, 8.38; N, 13.02.

3-Butyl-1-(3-chloropropyl) quinazoline-2,4(1H,3H) dione (6)

A mixture of 3-butylquinazoline-2,4(1H,3H)-dione (3) (2.18 g, 0.01 mol), 1-bromo-3-chloropropane (4.72 g, 2.968 ml, 0.03 mol) and anhydrous K_2CO_3 (6.90 g, 0.05 mol) in dry DMF (30 ml) was stirred over night at room temperature. The mixture was poured onto cold water and the formed precipitate was filtered, dried, and crystallized from ethanol/water mixture.

Yield: 68% mp.: 90°C. IR v_{max} (cm⁻¹) (KBr): 2960, 2933, 2873, 2862 (CH aliphatic), 1699 (C=O), 1658 (C=O). ¹HNMR (200 MHz, CDCl₃₋) δ ppm: 0.92(t, 3H, CH₃), 1.31–1.46(m, 2H, CH₂CH₃), 1.45–1.75(m, 2H, $CH_2CH_2CH_3$), 2.16–2.29(m, 2H, CH_2CH_2Cl), 3.69(t, 2H, CH₂Cl), 4.08(t, 2H, N₃CH₂), 4.26(t, 2H, N₁CH₂), 7.17–8.26(m, 4H, ArHs). EIMS m/z (% rel. abundance): 294 (M^+ , 22.94%), 296 ($M + 2$, 9.64%), 132 (100%). Anal. calcd for $C_{15}H_{19}CIN_2O_2$: C, 61.12; H, 6.50; N, 9.50; Found: C, 61.20; H, 6.40; N, 9.30.

General procedure for the synthesis of compounds 7a–f

To a solution of 3-butyl-1-(3-chloropropyl) quinazoline-2,4(1H, 3H)-dione (6) (0.88 g, 0.003 mol) in dry acetonitrile (20 ml), few specs of KI and anhydrous K_2CO_3 (2.07 g, 0.015 mol) were added. The resulted mixture was refluxed for 30 min. Appropriate amine (0.009 mol) was then added slowly into the reaction mixture and refluxed for 15 h. The mixture was cooled, diluted with water, and extracted with chloroform. The chloroform layer was washed with water, dried over anhydrous sodium sulfate, and evaporated. The oily product was dissolved in acetone and treated with ethereal hydrochloride. The separated solid was refrigerated for 48 h, filtered and dried.

3-Butyl-1-[3-(piperidin-1-yl)propyl]quinazoline-2,4(1H,3H)-dione hydrochloride (7a)

Yield 40% mp.: 210°C. IR v_{max} (cm⁻¹) (KBr): 3421(NH), 2951, 2808 (CH aliphatic), 1701(C=O), 1654 (C=O). ¹HNMR (300 MHz, DMSO₋) δ ppm: 0.90(t, 3H, CH₃), $1.27-1.34$ (m, 2H, CH₂CH₃), $1.54-1.59$ (m, 2H, $CH_2CH_2CH_3$), 1.63–1.74(m, 6H, CH₂ of C₃,C₄,C₅ of piperidine), 2.05–2.10(m, 2H, $N_1CH_2CH_2CH_2N$), 2.82(t, 2H, N₁CH₂CH₂CH₂N), 3.02-3.12(m, 4H, C₂,C₆ of piperidine), 3.94(t, 2H, N₃CH₂), 4.17(t, 2H, N₁CH₂), 7.30(dd, 1H, C_6 H of quinazoline), 7.55 (d, 1H, C_8 H of quinazoline), 7.77(dd, 1H, C_7H of quinazoline), 8.07(d, 1H, C_5H of quinazoline), 9.94(s, 1H, NH of HCl salt). Anal. calcd for $C_{20}H_{29}N_{3}O_{2}$.HCl. C, 63.22; H, 7.95; N, 11.06; Found C, 63.12; H, 7.87; N, 11.10.

3-Butyl-1-[3-(4-phenylpiperazin-1-yl)propyl] quinazoline-2,4(1H,3H)-dione hydrochloride (7b)

Yield 55% mp.: 180°C. IR v_{max} (cm⁻¹) (KBr): 3487(NH), 2981, 2866 (CH aliphatic), 1697(C=O), 1654 (C=O). ¹HNMR (200 MHz, DMSO₋) δppm:0.94(t, 3H, CH₃), 1.24-1.44(m, 2H, CH₂CH₃), 1.54–1.70(m, 2H, CH₂CH₂CH₃), 2.00–2.32(m, 2H, $N_1CH_2CH_2CH_2N$), 3.10–3.34(m, 4H, $2CH_2$ of piperazine) 3.40(t, 2H, N₁CH₂CH₂CH₂N), 3.70–3.92(m, 4H, 2CH₂ of piperazine), 3.98(t, 2H, N₃CH₂), 4.24(t, 2H, N1CH2), 6.88–8.09(m, 4H, ArHs), 11.38(s, 1H, NH of HCl salt, D_2O exchangeable). EIMS m/z (% rel. abundance): $420 (M^+, 30.36\%)$, $421 (M + 1, 10.19\%)$, 175 (100%). Anal. calcd for $C_{25}H_{32}N_4O_2$.HCl. C, 65.70; H, 7.27; N, 12.25; Found C, 65.67; H, 7.24; N, 12.22.

3-Butyl-1-{3-[4-(4-methoxyphenyl)piperazin-1-yl] propyl}quinazoline-2,4(1H,3H)-dione hydrochloride (7c)

Yield (50%) mp.: 152°C. IR v_{max} (cm⁻¹) (KBr): 3485(NH), 2980, 2858 (CH aliphatic), 1701 (C=O), 1654 (C=O). ¹HNMR $(300 \text{ MHz}, \text{DMSO})$ δ ppm: 0.89(t, 3H, CH₃), 1.26–1.35(m, 2H, CH_2CH_3), 1.52–1.62(m, 2H, $CH_2CH_2CH_3$), 2.10–2.19(m, 2H, N₁CH₂CH₂CH₂N), 2.90-3.15(m, 6H, 2CH₂ of piperazine + N₁CH₂CH₂CH₂N), 3.49–3.57(m, 4H, 2CH₂ of piperazine), 3.68(s, 3H, OCH₃), 3.94(t, 2H, N₃CH₂), 4.19(t, 2H, N_1CH_2), 6.9–6.82 (dd, 4H, ArHs), 7.30(dd, 1H, C₆H of quinazoline), 7.56(d, 1H, C_8H of quinazoline), 7.77(dd, 1H, C_7H of quinazoline), $8.08(d, 1H, C₅H)$ of quinazoline), $10.72(s, 1H,$ NH of HCl salt, D_2O exchangeable). EIMS m/z (% rel. abundance):450 (M^+ , 100%), 451 ($M + 1$, 29.68%). Anal. calcd for C26H34N4O3.HCl C, 64.11; H, 7.24; N, 11.50; Found C, 64.13; H, 7.13; N, 11.46.

3-Butyl-1-[3-(diethylamino)propyl]quinazoline-2,4(1H,3H)-dione hydrochloride (7d)

Yield (42%) mp.: 127°C. IR v_{max} (cm⁻¹) (KBr): 3417(NH), 2954, 2870 (CH aliphatic), 1701 (C=O), 1654 (C=O). ¹HNMR (300 MHz, DMSO) δ ppm: 0.90(t, 3H, CH₃), 1.20(t, 6H, $J = 7$ Hz, NCH₂CH₃), 1.24–1.37(m, 2H, $CH_2CH_2CH_3$), 1.49–1.61(m, 2H, $CH_2CH_2CH_3$), 1.99– 2.09(m, 2H, N₁CH₂CH₂CH₂N), 3.05(q, 4H, $J = 7$ Hz, NCH₂CH₃), 3.15(t, 2H, N₁CH₂CH₂CH₂N), 3.94(t, 2H, N_3CH_2), 4.18(t, 2H, N_1CH_2), 7.30(dd, 1H, C₆H of quinazoline), 7.61(d, 1H, C_8H of quinazoline), 7.76(dd, 1H, C_7H of quinazoline), 8.07(d, 1H, C_5H of quinazoline), 10.76(s, 1H, NH of HCl salt). ESIMS m/z (% rel. abundance): $332.39(M + 1, 100\%)$. Anal. calcd for $C_{19}H_{29}N_3O_2$.HCl C, 62.02; H, 8.21; N, 11.42; Found C, 62.12; H, 8.43; N, 11.41.

3-Butyl-1-[3-(pyrrolidin-1-yl)propyl]quinazoline-2,4(1H,3H)-dione hydrochloride (7e)

Yield (39%) mp.: 142°C. IR v_{max} (cm⁻¹) (KBr): 3412(NH), 2956, 2872 (CH aliphatic), 1701 (C=O), 1654 (C=O). ¹HNMR (500 MHz, CDCl₃₋) δ ppm: 0.91(t, 3H, CH₃), 1.30–1.38(m, 2H, $CH_2CH_2CH_3$), 1.56–1.63(m, 2H, $CH_2CH_2CH_3$), 1.99–2.07(m, 2H, C₃H of pyrrolidine), 2.13–2.22(m, 2H, C4H of pyrrolidine), 2.32–2.38(m, 2H, $N_1CH_2CH_2CH_2N$, 2.80(t, 2H, $N_1CH_2CH_2CH_2N$), 3.20–3.24(m, 2H, C2H of pyrrolidine), 3.74–3.77(m, 2H, C_5H of pyrrolidine), 4.00(t, 2H, N₃CH₂), 4.22(t, 2H, N_1CH_2), 7.20(dd, 1H, C_6H of quinazoline), 7.32 (d, 1H, C_8H of quinazoline), 7.64 (dd, 1H, C_7H of quinazoline), 8.18(d, 1H, C_5H of quinazoline), 12.42(s, 1H, NH of HCl salt). EIMS m/z (% rel. abundance): 329 (M⁺, 8.05%), 330 $(M + 1, 1.97\%)$, 84 (100%) . Anal. calcd for $C_{19}H_{27}N_3O_2$.HCl C, 62.36; H, 7.71; N, 11.48; Found C, 62.18; H, 7.49; N, 11.46.

3-Butyl-1-[3-(morpholin-4-yl)propyl]quinazoline-2,4(1H,3H)-dione hydrochloride (7f)

Yield (45%) mp.: 130°C. IR v_{max} (cm⁻¹) (KBr): 3425(NH), 2970, 2870 (CH aliphatic), 1697 (C=O), 1654 (C=O). ¹HNMR $(300 \text{ MHz}, \text{CDCl}_{3-})$ δ ppm: 0.93(t, 3H, CH₃), 1.31–1.43(m, 2H, $CH_2CH_2CH_3$), 1.57-1.67(m, 2H, $CH_2CH_2CH_3$), 2.34–2.39(m, 2H, N₁CH₂CH₂CH₂N), 3.14–3.20(m, 6H, C₂, C_6 of morpholine and N₁CH₂CH₂CH₂N), 3.94–4.06(m, 6H, $CH₂$ of C₃, C₅ of morpholine and N₃CH₂), 4.25(t, 2H, N₁CH₂), 5.39(s, 1H, NH of HCl salt, D_2O exchangeable), 7.23(dd, 1H, C_6H of quinazoline), 7.36 (d, 1H, C_8H of quinazoline), 7.68(dd, 1H, C_7H of quinazoline), 8.18(d, 1H, C_5H of quinazoline), Anal. calcd for $C_{19}H_{27}N_3O_3$.HCl C, 59.75; H, 7.39; N, 11.00; Found C, 59.63; H, 7.42; N, 11.10.

1-Benzyl-3-butylquinazoline-2,4(1H,3H)-dione (8)

A mixture of 3-butylquinazoline-2,4(1H,3H)-dione (3) (0.218 g, 0.001 mol), benzyl chloride (0.25 g, 0.002 mol), anhydrous K_2CO_3 (0.69 g, 0.005 mol) and few specs of KI in dry acetone (15 ml) was stirred and refluxed for 7 h. The reaction mixture was cooled and poured onto cold water. The formed precipitate was filtered, dried and crystallized from ethanol.

Yield: 0.25 g (81%) mp.: 109–111°C. IR v_{max} (cm⁻¹) (KBr): 2958 (CH aliphatic), 1701(C=O), 1654(C=O). ¹HNMR (300 MHz, CDCl₃₋) δ ppm: 0.99(t, 3H, CH₃), 1.38–1.51(m, 2H, CH2CH3), 1.66–1.79(m, 2H, $CH_2CH_2CH_3$), 4.16 (t, 2H, N₃CH₂), 5.38(s, 2H, N₁CH₂), 7.10–8.25(m, 9H, ArHs). Anal. calcd for $C_{19}H_{20}N_2O_2$ C, 74.00; H, 6.54; N, 9.08; Found C, 74.21; H, 6.43; N, 9.11.

General procedure for the synthesis of compounds 9a–c

A mixture of 3-butylquinazoline-2,4(1H,3H)-dione (3) (0.218 g, 0.001 mol), appropriate phenacyl bromide (0.001 mol) and anhydrous K_2CO_3 (0.69 g, 0.005 mol) in dry DMF (15 ml) was stirred and refluxed for 3 h The reaction mixture was cooled, poured onto cold water and the solid formed was filtered, dried, and crystallized from ethanol.

3-Butyl-1-(2-oxo-2-phenylethyl)quinazoline-2,4(1H,3H)-dione (9a)

Yield: (65%) mp.: 110°C. IR v_{max} (cm⁻¹) (KBr): 2956, 2931(CH aliphatic), 1695(C=O), 1625–1665(C=O). ¹HNMR (200 MHz, CDCl₃₋) δ ppm: 0.96(t, 3H, CH₃), 1.36–1.47(m, 2H, CH₂CH₃), 1.63–1.72(m, 2H, $CH_2CH_2CH_3$), 4.11(t, 2H, N₃CH₂), 5.62(s, 2H, N₁CH₂), 6.79–8.28(m, 9H, ArHs). EIMS m/z (% rel. abundance): 336.20 $(M^+, 12.88\%), 337.20 (M + 1, 3.13\%),$ 105.05(100%). Anal. calcd for $C_{20}H_{20}N_2O_3$: C, 71.41; H, 5.99; N, 8.33; Found C, 71.71; H, 5.79; N, 8.23.

3-Butyl-1-[2-(4-chlorophenyl)-2-oxoethyl]quinazoline-2,4(1H,3H)-dione (9b)

Yield: (68%) mp.: 212°C. IR v_{max} (cm⁻¹) (KBr): 2958, 2935(CH aliphatic), 1701(C=O), 1650-1675(C=O). ¹HNMR

 $(200 \text{ MHz}, \text{CDC1}_{3-})$ δ ppm: 0.96(t, 3H, CH₃), 1.36–1.43(m, 2H, CH₂CH₃), 1.63–1.73(m, 2H, CH₂CH₂CH₃), 4.10(t, 2H, N3CH2), 5.57(s, 2H, N1CH2), 6.79–8.28(m, 8H, ArHs). EIMS m/z (% rel. abundance): 370.15 (M⁺, 7.64%), 371.20 (M + 1, 2.18%), 372.20 ($M + 2$, 2.86%), 132.10(100%). Anal. calcd for $C_{20}H_{19}CIN_2O_3 C$, 64.78; H, 5.16; N, 7.55; Found C, 63.78 H, 5.00; N, 7.25.

1-[2-(4-Bromophenyl)-2-oxoethyl]-3-butylquinazoline-2,4(1H,3H)-dione (9c)

Yield: (71%) mp.: 223°C. IR v_{max} (cm⁻¹) (KBr): 2956, 2935 (CH aliphatic), 1703 (C=O), 1635–1670 (C=O). ¹HNMR (500 MHz, CDCl₃₋) δ ppm: 0.95(t, 3H, CH_3), 1.38–1.45(m, 2H, CH_2CH_3), 1.66–1.72(m, 2H, $CH_2CH_2CH_3$), 4.12(t, 2H, N₃CH₂), 5.59(s, 2H, N₁CH₂), 6.82(d, 1H, C_8H of quinazoline), 7.26 (dd, 1H, C_6H of quinazoline), 7.57(dd, 1H, C7H of quinazoline), 7.65(dd, $J = 8$ Hz, 2H, C₃,C₅ of 4-Br-ph), 7.95(dd, 2H, $J = 8$ Hz, C_2 , C_6 of 4-Br-ph), 8.35(d, 1H, C_5 H of quinazoline). ¹³C NMR (CDCl₃) δppm: 13.79 (CH₃), 20.21 (CH₂), 29.88 (CH_2) , 41.96 (CH_2-N_3) , 49.57 (CH_2-N_1) , 113.08–139.81 (Ar–C), 151.11(C=O), 161.54(C=O), 191.20(Ph–C=O). Anal. calcd for $C_{20}H_{19}BrN_2O_3 C$, 57.84; H, 4.61; N, 6.75; Found C, 58.14; H, 4.36; N, 6.68.

Biological activity

Evaluation of PDE4B inhibitory activity

With several new analogs now in hand, we evaluated their inhibitory potency against PDE4B via a purified enzyme fluorescence polarization assay. PDE activity assays were performed in duplicate at 10μ M. Fluorescence intensity is converted to fluorescence polarization using the Magellan6 software. The fluorescence polarization data were analyzed using the computer software, Graphpad Prism. $100 \mu M$ solutions of the test compounds were prepared with 10% DMSO in assay buffer and 5μ of the solution was added to a 50 ll reaction so that the final concentration of DMSO is 1% in all of the reactions. The enzymatic reactions were conducted at room temperature for 60 min in a 50 μ l mixture containing PDE assay buffer, 100 nM FAMcAMP, PDE4B2, and the test compound. After the enzymatic reaction, 100 μ l of a binding solution (1:100 dilution of the binding agent with the binding agent diluents) was added to each reaction and the reaction was performed at room temperature for 60 min. Fluorescence intensity was measured at an excitation of 470 nm and an emission of 528 nm using a Tecan Infinite M1000 microplate reader.

The percent activity in the presence of the compound was calculated according to the following equation: % activity = $(FP - FP_b)/(FP_t - FP_b) \times 100\%$, where FP is the fluorescence polarization in the presence of the compound. The fluorescence polarizations of PDE4B were then measured in the presence of the synthesized compounds and consequently their % inhibition were calculated.

Molecular docking

All the molecular modeling studies were carried out on an Intel Pentium 1.6 GHz processor, 512 MB memory with Windows XP operating system using Molecular Operating Environment (MOE [2008](#page-12-0).10; Chemical Computing Group, Canada) (MOE [2008.](#page-12-0)10) as the computational software.

All the minimizations were performed with MOE until a RMSD gradient of 0.05 kcal mol⁻¹ \AA^{-1} with MMFF94x force-field and the partial charges were automatically calculated.

The X-ray crystallographic structure of phosphodiesterase 4B complexed with rolipram (PDB ID: 1RO6) was obtained from the protein data bank available at the RCSB Protein Data Bank, http://[www.pdb.org\)](http://www.pdb.org) with a 2.00 Å resolution

- 1. Enzyme structures were checked for missing atoms, bonds and contacts.
- 2. Water molecules were manually deleted.
- 3. Hydrogens and partial charges were added to the system using Protonate3D application.
- 4. The active site was generated using the residues within 5 Å near to the rolipram atoms.
- 5. The ligand molecules were constructed using the builder module and were energy minimized using the MMFF94x force field.
- 6. All antagonist structures were docked into the active site by using the MOE Dock tool. This method is divided into a number of stages:
	- (a) Conformational analysis of ligands: the algorithm generated conformations from a single 3D conformation by conducting a systematic search. In this way, all combinations of angles were created for each ligand.
	- (b) Placement: a collection of poses was generated from the pool of ligand conformations using Triangle Matcher placement method. Poses were generated by superposition of ligand atom triplets and triplets of points in the receptor binding site in a systematic way
	- (c) Scoring: poses generated by the placement methodology were scored using London dG scoring function implemented in MOE, which

estimates the free energy of binding of the ligand from a given pose. The top 30 poses for each ligand were output in a MOE database. Each resulting ligand pose was then subjected to MMFF94x energy minimization until the RMS gradient of the potential energy was less than 0.05 kJ mol mol^{-1} $\rm \AA^{-1}$. The minimized docking conformations were then re-scored using London dG scoring methods.

Result and discussion

The starting compound 2-amino-N-butylbenzamide 1 was prepared as the reported procedure (Clark and Wagner, [1944\)](#page-12-0). Formylation of 1 with ethyl chloroformate afforded 2-ethoxycarbonylamino-N-butylbenzamide 2 which was cyclized to the desired key compound 3. We report here a new application of the method described by Gadekar et al. (Gadekar et al., [1964\)](#page-12-0) for the preparation of 3-butylquinazoline-2,4(1H,

Scheme 1 Synthetic protocol for title compounds 5a–e and 7a–f. Reagents and conditions: (a) butyl amine (b) ethyl chloroformate, heated over steam, 3 h (c) KOH, ethanol, heated over steam,

4 h (d) 1-bromo-2-chloroethane, anhydrous K_2CO_3 , dry DMF, rt, overnight (e) HNR1R2 (f) 1-bromo-3-chloropropane, anhydrous K_2CO_3 , dry DMF, rt, overnight (g) (1) HNR_1R_2 (2) ethereal HCl

3H)-dione 3 by heating the intermediate compound 2 with ethanolic potassium hydroxide. Treatment of quinazolinedione 3 with either 1-bromo-2-chloro ethane or 1-bromo-3 chloropropane using standard reaction conditions (Blizzard et al., [1989\)](#page-12-0) afforded the intermediate compounds 4 and 6, respectively. Nucleophilic displacement of the chlorine atom on the substituted quinazoline ring with different secondary amines afforded compounds 5a–e and 7a–f. On the other hand, Scheme 2 describes alkylation of the key compound 3 with either benzyl chloride or substituted phenacyl chloride to give the desired compounds 8 and 9a–c. Structures of the new compounds 2, 4, 5a–e, 7a–f, 8, and 9a–c were confirmed by elemental analysis and spectral data. The synthetic routes for the preparation of the new compounds are outlined in Schemes [1](#page-8-0) and 2.

Results of PDE4B inhibition activity assessement are very promising as most of the compounds in the present series had PDE4B inhibition activity (Table 1). Compound 7f is the most active one, it demonstrated inhibitory activity (100%) better than rolipram (90%) , while 5d (25%) , 8 (56%), and 9a (22%) showed moderate activity. The rest of the compounds showed mild inhibitory activity (8–13%). The structural feature of the highly active compounds was found to be significantly different as compound 7f has a propyl spacer linked to the morpholine nucleus, while compound 5d has an ethyl spacer linked to phenyl piperazine nucleus and compound 8 has a methylene spacer so a docking study was very important to find an explanation to these biological results.

Scheme 2 Synthetic protocol for title compounds. Reagents and conditions: (a) benzylchloride, dry acetone, reflux, 7 h (b) p-substituted phenacyl bromide, anhydrous $K₂CO₃$, dry DMF, reflux, 3 h

Table 1 Inhibition data for derivatives investigated in the present paper and standard rolipram against PDE4B

Molecular docking studies of the synthesized compounds were performed in order to rationalize the obtained biological results as well as to help us in understanding the various interactions between the ligands and enzyme active site in details.

The X-ray crystallographic structure of PDE4B complexed with rolipram (PDB: 1RO6) was used in our docking studies. All water molecules in the experimental structure were removed. Hydrogen atoms were added and the protonation states of the amino acid residues were assigned using the Protonate3D algorithm. Ligand molecules were modeled

using MOE builder, and the structures were energy minimized using the MMFF94x force field. Validation of the function implemented in MOE was done by docking of the native ligand into its binding site. The docked results were compared to the crystal structure of the bound ligand–protein complex. The RMSD of the docked ligand was 0.32 Å as it seems exactly superimposed on the native bound one (Fig. 2a). These results indicated the high accuracy of the MOE simulation in comparison with the biological methods. Although PDE4 enzyme crystal structure with nitraquazone co-crystallized was absent, a prediction of the binding model for nitraquazone was done by docking nitraquazone in the active site gorge of PDE4B (Fig. 2b). This binding model was useful in our interpretation to the activities of our synthesized compounds.

Then, we performed docking studies to our synthesized compound and the final docked complexes of ligand– enzyme were selected according to the criteria of interaction energy combined with geometrical matching quality.

The saved pose for the ligand–enzyme complex of the most active compound 7f (Fig. 3) revealed that several molecular interactions were considered to be responsible

Fig. 2 a The docked rolipram ligand into PDE4B seems superimposed on the native rolipram ligand, RMSD: 0.32 Å b Predicted binding model of nitraquazone

Fig. 3 a Docked conformation alignment of 7f and its original co-crystallized ligand in PDE4B binding site generated by MOE docking. b Simplified structure of 7f docked at PDE4B active site showing hydrogen bonds and metal coordination

for the observed affinity: (i) The quinazoline nucleus was sandwiched between the side chains of Phe446 and Ile410 showing great overlapping of benzo of quinazoline with the phenyl ring of rolipram. (ii) Quinazolinone's 4-oxo forms hydrogen bond with the side-chain $NH₂$ of Gln443 (distance $= 2.71$ Å). (iii) Unlike nitraquazone *N*-ethyl group, the N-butyl group of 7f was too bulky to be embedded to the rolipram's methoxy group small pocket made up of Tyr403, Tyr233, Thr407, Pro396, Gln443, Asn395, Ile410, and Trp406, instead quinazoline ring of 7f adopted a flipped position so that its n -butyl occupies the rolipram's cyclopentoxy group hydrophobic pocket surrounded by Phe414, Phe446, Met411, Met431, Ser442, and Gln443 (Fig. 4). (iv) Moreover, the morpholine oxygen was weakly hydrogen bond to imidazole's NH of His234 (distance = 3.27 Å) and metal coordinated with the Zn^{2+}

bounded within the active site (distance $= 2.37 \text{ Å}$). This metal coordination seemed to be crucial for the high potency of 7f.

Comparing the active 7f, with a propyl spacer, to its less active congener 5b, with an ethyl spacer, shows similar binding interactions except of Zn^{2+} binding and His234 hydrogen bond, which were lost in 5b as the ethyl spacer was not long enough to allow morpholine's oxygen to reach the Zn^{2+} and His234 in the active site. Although compounds 5d, 8, and 9a showed less inhibitory action to PDE4B than 7f which was rationalized by the fact that they were unable to bind to Zn^{2+} , these compounds still binds to His234 by π -cation interaction. This explained why compounds 5d, 8, and 9a achieved better inhibitory activity to PDE4B (Fig. 5) than the rest of our compounds which lost both Zn^{2+} and His234 bindings.

Fig. 5 Schematic view of a compound 5d, b compound 8 and c compound 9a docking conformations within PDE4B active site showing π -cation interaction with His234

Conclusion

We observed that the bulkiness of N_3 substituent is important in the orientation of quinazoline nucleus in the active site. Metal coordination with the Zn^{2+} bound within the active site greatly increases activity and may lead to potent PDE4 inhibition. Hydrogen bonds to aminoacids residues (Asp392 and His234) or π -cation interaction with His234 increases activity. Moreover quinazolinone's 2-oxo seems to be unessential for PDE4 binding. These preliminary encouraging results of biological screening of the tested compounds could offer an excellent framework in this field that may lead to discovery of potent PDE4B inhibitors which can be used for treatment of several diseases.

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References

- Barnes PJ (1999) Therapeutic strategies for allergic diseases. Nature 402:B31–B38
- Bender AT, Beavo JA (2006) Cyclic nucleotide phosphodiesterases: molecular regulation to clinical use. Pharmacol Rev 58:488–520
- Blizzard TA, Marino G, Mrozik H, Fisher MH, Hoogsteen K, Springer JP (1989) Chemical modification of paraherquamide. 1. Unusual reactions and absolute stereochemistry. J Org Chem 54:2657–2663
- Burnouf C, Pruniaux MP, Szilagyi CM (1998) Phosphodiesterase 4 inhibitors. In: Bristol JA (ed) Annual reports in medicinal chemistry. Academic Press, Michigan, pp 91–109
- Clark RH, Wagner EC (1944) Isatoic anhydride. I. Reactions with primary and secondary amines and with some amides1. J Org Chem 9:55
- Gadekar SM, Kotsen AM, Cohen E (1964) Anthranilamides as Intermediates for 3-Substituted Quinazoline-2,4-diones. J Chem

Soc 4666–4668. [http://pubs.rsc.org/en/content/articlelanding/1964/](http://pubs.rsc.org/en/content/articlelanding/1964/jr/jr9640004633) [jr/jr9640004633](http://pubs.rsc.org/en/content/articlelanding/1964/jr/jr9640004633)

- Lehnart SE, Wehrens XHT, Reiken S, Warrier S, Belevych AE, Harvey RD, Richter W, Jin SLC, Conti M, Marks AR (2005) Phosphodiesterase 4D deficiency in the ryanodine-receptor complex promotes heart failure and arrhythmias. Cell 123:25–35
- McKenna JM, Muller GW (2006) Cyclic nucleotide phosphodiesterases. In: Beavo JA, Francis SH, Houslay MD (eds) Health and disease. CRC Press, pp 667–670
- Molecular Operating Environment (MOE 2008.10); C.C.G., Inc., 1255 University St., Suite 1600, Montreal, Quebec, Canada H3B 3X3. 2005. <http://www.chemcomp.com>
- Norman P (1999) PDE4 inhibitors. Exp Opin Ther Patents 9:1101–1117
- Palacios JM, Beleta J, Segarra V (1995) Second messengers systems as targets for new therapeutic agents: focus on selective phosphodiesterase inhibitors. Farmaco 50:819–827
- Piaz VD, Giovannoni MP (2000) Phosphodiesterase 4 inhibitors, structurally unrelated to Rolipram, as promising agents for the treatment of asthma and other pathologies. Eur J Med Chem 35:463–480
- Potter BVL (1990) Transmembrane signalling second messenger analogues and inositol phosphates. In: Hansch C, Sammes PG, Taylor JB (eds) Comprehensive medicinal chemistry. Pergamon Press, Oxford, pp 102–128
- Robichaud A, Stamatiou PB, Jin SLC, Lachance N, MacDonald D, Laliberte F, Liu S, Huang Z, Conti M, Chan CC (2002) Deletion of phosphodiesterase 4D in mice shortens a2-adrenoceptormediated anesthesia, a behavioral correlate of emesis. J Clin Invest 110:1045–1052
- Schneider HH, Schmiechen R, Brezinski M, Seidler J (1986) Stereospecific binding of the antidepressant rolipram to brain protein structures. Eur J Pharmacol 127:105–115
- Souness JE, Aldous D, Sargent C (2000) Immunosuppressive and anti-inflammatory effects of cyclic AMP phosphodiesterase (PDE) type 4 inhibitors. Immunopharmacol 47:127–162
- Staiger RP, Wagner EC (1953) Isatoic anhydride. III. Reactions with primary and secondary amines. J Org Chem 18:1427–1439
- Torphy TJ (1998) Action of mediators on airway smooth muscle: functional antagonism as a mechanism for bronchodilator drugs. Agents Actions 23(Suppl):S37–S53
- Zhang KYJ, Ibrahim PN, Gillette S, Bollag G (2005) Phosphodiesterase-4 as a potential drug target. Expert Opin Ther Targets 9:1283–1305