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Design and Efficient Synthesis of New Stable 1α ,25-Dihydroxy-19-norvitamin D₃ Analogues Containing Amide Bond

Yoshitomo Suhara,^{a,†} Atsushi Kittaka,^a Keiichiro Ono,^a Masaaki Kurihara,^b Toshie Fujishima,^a Akihiro Yoshida^a and Hiroaki Takayama^{a,*}

^aFaculty of Pharmaceutical Sciences, Teikyo University, Sagamiko, Kanagawa 199-0195, Japan ^bNational Institute of Health Sciences, Kamiyoga, Setagaya-ku, Tokyo 158-8501, Japan

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Abstract—The design and synthesis of new 1α ,25-dihydroxy-19-norvitamin D₃ analogues **3a–c**, which have an amide bond in the molecule instead of the diene, are described. The A-ring moiety was constructed by a (3S,5S)-3,5-dihydroxypiperidine derivative (**9**, **11**, or **13**) prepared from D-mannose, and a CD-ring carboxylic acid **16** was synthesized from Grundmann's ketone. Coupling those parts gave desired **3a–c** in good yield. This strategy can be applied in combinatorial chemistry; therefore, those compounds would be applicable as useful tools in the development of new drugs. \bigcirc 2002 Elsevier Science Ltd. All rights reserved.

 1α ,25-Dihydroxyvitamin D₃ (1) is the major active metabolite of vitamin D₃, which exerts hormonal control over important physiological processes, including calcium and phosphorus metabolism, cellular differentiation and immune reactions.¹ A number of vitamin D analogues have been synthesized in order to investigate the biological roles of vitamin D and to develop potential therapeutic agents.² Since effective doses of 1 may cause hypercalcemia, the therapeutic use of 1 in the treatment of certain cancers and skin disorders is limited. Dissociation of the calcemic activity from the other activities of 1 is one of the important issues in searching for novel drugs based on vitamin D analogues. DeLuca et al. synthesized a 19-nor derivative 2, which is a noncalcemic analogue of 1 that still preserves its cell differentiating activities (Fig. 1).³

Previously, we synthesized several 1α ,25-dihydroxyvitamin D₃ derivatives, which systematically introduced a 2α -alkyl, 2α -hydroxyalkyl, or 2α -hydroxyalkoxyl group into the parent hormone 1, in order to investigate the A-ring conformation– and structure–activity relationships.^{4–6} Some of these analogues exhibited interesting biological activities, in particular, 2α -methyl (1a),⁴ 2α -hydroxypropyl (1b),⁵ and 2α -hydroxypropoxyl (1c)⁶ analogues showed higher potency than the natural hormone 1 in terms of bovine thymus vitamin D receptor (VDR) binding affinity, elevation of rat serum calcium concentration, and induction of HL-60 cell differentiation (Fig. 1). For example, compound 1b exhibited 3-fold higher VDR binding affinity and more than double potency in inducing differentiation of HL-60 cells as compared to 1.^{5a}



Figure 1. Structures of the natural hormone 1, and its 2α -substituted analogues 1a-c with higher binding affinity for VDR than that of 1, DeLuca's 19-nor derivative 2, and amide derivatives 3a-c.

^{*}Corresponding author. Tel.: +81-426-85-3713; fax: +81-426-85-3714; e-mail: hi-takay@pharm.teikyo-u.ac.jp

[†]Present address: Department of Hygienic Sciences, Kobe Pharmaceutical University, Kobe 658–8558, Japan.

Based on these results, we then focused on modification of the diene moiety in the 19-nor skeleton of the B-*seco* steroid compound.⁷ We anticipated that if the diene was replaced by an amide bond, the resulting analogues would retain the original biological activities of 19-norvitamin D_3 (2), since they would possibly take on a similar 'flat' conformation.

Our designed analogues are shown in Figure 1. The A-ring moiety was substituted with a piperidine ring having two hydroxyls at C1 α and C3 β (seco-steroidal numbering) with the appropriate stereochemistry, which play a crucial role in VDR binding and biological actions.8 The diene part was converted to an amide bond to connect with the normal CD-ring moiety. We also planned modification at the C2 position with the substituent of the 3-hydroxypropoxyl group, because this motif can strengthen binding affinity to VDR.5,9 The amide structures **3a**-c would allow the N–C6 bond to rotate, whose original structure of the C5–C6 bond is fixed in the natural hormone 1. The relative positions of the two hydroxyls at C1 α and C3 β toward the VDR ligand binding domain (LBD) are retained with the rotation, and the artificial C2 substituent may settle down in an α or a β -orientation in preference when 3b or 3c complexes with LBD. In Figure 2, the X-ray crystal structure of 1 (red) docking in LBD of VDR¹⁰ and the modeled structure of the amide D_3 3a (blue) in the same cavity of the VDR are shown. The latter structure constructed by molecular dynamics calculations (AMBER* force field) using MacroModel ver. 6.5, and 3a could interact with the VDR through six hydrogen bonds (dotted lines) from the $C1\alpha$, $C3\beta$, and C25-hydroxyls as in 1. This modeling also encouraged us to synthesize the amide D_3 analogues.

Scheme 1 shows the synthesis of the A-ring portions 8 (an intermediate) and 9. Treatment of D-mannose with anhydrous $CuSO_4$ and a catalytic amount of concd H_2SO_4 in acetone followed by benzoylation of the anomeric hydroxyl group gave a D-mannofuranose derivative in 86% yield. Selective deprotection of the O4–O6 acetonide using 70% aqueous acetic acid pro-



Figure 2. Crystal structure of VDR bound to 1 (red) by Moras et al.¹⁰ and computer modeling of 3a (blue) in the VDR ligand binding domain.



Scheme 1. Reagents and conditions: (a) (i) anhydrous CuSO₄, acetone, concd H₂SO₄, (ii) BzCl, pyridine (86% in two steps); (b) 70% AcOH aq (quant); (c) (i) NaIO₄, Et₂O, H₂O, (ii) NaBH₄, MeOH (64% in two steps); (d) TsCl, pyridine (75%); (e) NaN₃, DMF (72%); (f) 1 NaOH aq, MeOH (97%); (g) (i) H₂, cat. Pd(OH)₂, MeOH, (ii) CbzCl, Et₂O, sat. NaHCO₃ aq (87% in two steps); (h) 80% AcOH aq, 90 °C (92%); (i) TBSCl, Et₃N, DMF (87%); (j) H₂, cat. Pd/C, MeOH (71%).

duced D-mannofuranoside 4. Oxidative diol cleavage of 4 with sodium periodate, and reduction of the resultant aldehyde afforded the primary alcohol. Azide 5 was prepared from the alcohol through tosylate in good yield. After removal of the benzoyl group of 5, reductive amination with H_2/cat . Pd(OH)₂ in methanol followed by protection of the amino group with Cbz gave the piperidine derivative 6 in 87% yield. Deprotection of the acetonide of 6, then introduction of the TBS group to the C1 and C3 hydroxyl groups afforded 8 in 92 and 87% yields, respectively. Finally, the Cbz group was hydrogenated with cat. Pd/C to give the desired A-ring part 9 for 3b in 71% yield.

We synthesized two additional piperidine derivatives 11 and 13 from 8 as shown in Scheme 2. The A-ring portion 11 was synthesized by Williamson ether synthesis using (3-bromopropoxy)-*tert*-butyldimethylsilane and sodium hydride, followed by hydrogenolysis of the Cbz group. On the other hand, the natural type of A-ring portion 13 was obtained by radical reduction of thiocarbonate 12 with tributyltin hydride and AIBN in good yield.

The CD-ring portion was prepared from Grundmann's ketone 14¹¹ as shown in Scheme 3. After protecting the C25 hydroxyl group with MOM, Horner–Wadsworth– Emmons reaction using triethyl phosphonoacetate and sodium hydride in THF gave the ester 15 in an excellent



Scheme 2. Reagents and conditions: (a) TBSO(CH_2)₃Br, NaH, DMF (20%); (b) H₂, Pd/C, MeOH (quant); (c) PhOC(S)Cl, DMAP, CH₃CN (36%); (d) Bu₃SnH, AIBN, benzene (95%).



Scheme 3. Reagents and conditions: (a) MOMCl, DIEA, CH_2Cl_2 (quant); (b) triethyl phosphonoacetate, NaH, THF (98%); (c) 1 N NaOH, MeOH (86%); (d) 9, 11, or 13, BOP, DIEA, DMF (68–88%); (e) *p*-TsOH, MeOH (40–85%).

yield.¹² The ethyl ester of 15 was subjected to hydrolysis by 1 N aqueous NaOH in a MeOH solution to afford the desired carboxylic acid 16 in 86% yield. Subsequent condensation of 16 with the piperidine derivatives 9, 11, and 13 using a BOP reagent¹³ and DIEA provided the amides 17a-c in good yields, respectively. Finally, deprotection under acidic conditions furnished the target amide analogues $3a-c^{14}$ in considerable yield.

We tested VDR binding affinity of the amide analogues 3a-c using bovine thymus VDR¹⁵ though, unfortunately, we could not recognize the affinity for the VDR $(3 \times 10^{-6}, 2 \times 10^{-6}, \text{ and } 3 \times 10^{-6} \text{ times that of } 1 \text{ for } 3a, 3b, and 3c, respectively).¹⁶$

Two reasons were considered. One would be the electrostatic difference between the amide moiety and the diene part. The polar amide bond in 3a-c could not be well suited for the hydrophobic region surrounded by amino acid residues Phe-150, Leu-233, Tyr-295, and Trp-286 of VDR, which would originally accept the diene part of 2. The other would be the difference in steric energy (9.8 kcal/mol; ab initio MO method, HF/6–31G*) between the active structure in the VDR and the energy minimized structure. Figure 3a shows the energy minimized structure of 3a (green) lacking the side chain, as calculated by Monte Carlo conformational search and



Figure 3. (a) The energy minimized structure of 3a (green) and the modeled structure of 3a (yellow) docking in VDR; (b) the X-ray structure of 1 (yellow) in VDR¹⁰ and the energy minimized structure of 1 (green).

superimposed on the modeled structure of 3a (yellow) binding to the VDR. Conformation of the A-ring is quite different from each other. However, the X-ray structure of 1 (yellow) in the VDR and the energy minimized structure of 1 (green) are shown in Figure 3b, in which the latter modeled structure is very similar to the X-ray structure in VDR. It may be difficult for VDR to recognize the amide analogue 3a as a ligand in a solution.

In summary, we have developed an efficient systematic route for synthesizing new stable amide analogues 3a-c utilizing D-mannose. Takahashi et al. recently reported the synthesis of 1α ,25-dihydroxyvitamin D₃ derivatives by the combinatorial procedure.¹⁷ Our amide analogues can also be applied to this synthetic method and would easily provide many kinds of this class of D₃ analogues. We consider that these syntheses and analogues would contribute to the elucidation of vitamin D₃ action mechanisms with medicinal actions. Further biological studies of the amide analogues are currently in progress in our laboratory.

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14. Data for 3a: ¹H NMR (600 MHz, CD₃OD) δ 0.66 (3H, s), 0.97 (1H, d, J = 6.6 Hz), 1.05 - 1.10 (1H, m), 1.16 - 1.18 (7H, m),1.23-1.29 (2H, m), 1.31-1.48 (9H, m), 1.54-1.59 (2H, m), 1.62–1.67 (2H, m), 1.73–1.80 (2H, m), 1.85–1.89 (1H, m), 1.92–1.98 (1H, m), 2.04 (1H, dt, J=3.0, 12.9 Hz), 2.04–2.10 (1H, m), 2.72 (1H, dt, J=2.9, 13.6 Hz), 3.27 (1H, dd, J=6.9, 12.9 Hz), 3.38 (1H, dd, J=6.0, 13.2 Hz), 3.53 (1H, dd, J=3.0, 13.2 Hz), 3.84 (1H, dd, J = 3.3, 12.9 Hz), 3.95–4.00 (2H, m), 5.61 (1H, s). HRMS (EI) *m*/*z*: calcd for C₂₅H₄₃O₄N 421.3192. Found 421.3181 (M⁺). Data for 3b: ¹H NMR (600 MHz, CD_2Cl_2 , selected) δ 0.61 (3H, s), 0.95 (1H, d, J = 6.6 Hz), 1.07 (1H, t, J=8.1 Hz), 1.92 (1H, m), 2.03–2.06 (2H, m), 2.74–2.83 (2H, m), 2.95–3.02 (1H, m), 3.23 (1H, br d, J=13.2 Hz). 3.50 (1H, br d, J=6.0 Hz), 3.57 (1H, br d, J=6.0 Hz), 3.78 (1H, br s), 3.85 (0.6H, br d, J=13.2 Hz), 3.94-3.97 (1H, m), 4.04 (0.4H, br s), 4.34 (1H, br d, J=10.8 Hz), 5.58 (1H, s). HRMS (EI) m/z: calcd for $C_{25}H_{43}O_5N$ 437.3144. Found 437.3148 (M⁺). Data for 3c: ¹H NMR (600 MHz, CD₂Cl₂, selected) δ 0.61 (3H, s), 0.95 (1H, d, J=6.6 Hz), 3.63-3.67 (4H, m,-OCH₂CH₂CH₂OH), 5.56 (1H, s). HRMS (EI) m/z: calcd for C₂₈H₄₉O₆N 495.3560. Found 495.3558 (M⁺).

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