RSC Advances



PAPER

View Article Online



Cite this: RSC Adv., 2023, 13, 27359

Development of subtype-selective estrogen receptor modulators using the bis(4hydroxyphenyl)silanol core as a stable isostere of bis(4-hydroxyphenyl)methanol†

Yuichiro Matsumoto, a Yuichi Hashimoto and Shinya Fujii b *b

In this study, we synthesized and evaluated silanol-based bisphenol derivatives as stable isosteres of bis(4hydroxyphenyl)methanol. The developed silanols exhibited estrogen receptor (ER)-modulating activity. Among them, bis(4-hydroxyphenyl)(methyl)silanol (5a) showed a characteristic ER subtype selectivity, Accepted 30th August 2023 namely, antagonistic activity toward ERα and agonistic activity toward ERβ. Docking simulation indicated DOI: 10.1039/d3ra04656g that the silanol moiety plays a key role in this selectivity. Our results suggest that silanol-based bisphenols offer a unique scaffold for biologically active compounds.

Received 12th July 2023

rsc li/rsc-advances

Introduction

Silanols are widely used in various fields, including materials chemistry and synthetic chemistry.1 For example, they undergo cross-coupling reactions and are key components of various silicone materials and ceramics.2 In the field of biologically active compounds, silanols have been utilized in place of alcohols,3 since they are more acidic and hydrophobic than the corresponding alcohols, and therefore have distinct profiles of biological activity. We have developed silanol derivatives such as 1 with unique target selectivity.4 In addition, Tacke and coworkers have developed sila-haloperidol (2) and related silicon analogs of dopamine receptor antagonists in order to avoid the formation of neurotoxic metabolites, which are generated by elimination of water during the metabolism of the parent carbon analogs (Fig. 1A).5 We considered that silanols might be more widely applicable, and here we report the development and biological evaluation of silanol-based bisphenol derivatives as candidate estrogen receptor (ER) ligands.

Results and discussion 2

Molecular design

Bis(4-hydroxyphenyl)methanol (3) is a versatile scaffold of functional molecules such as fluorescein.6 However, bis(4hydroxyphenyl)methanols, especially in case of aliphatic substituents (R = alkyl), are readily converted to electrophilic quinone methides (4) by elimination of water, and therefore are not available as biologically active compounds (Fig. 1B). On the other hand, bisphenol is a promising core structure of biologically active compounds,7 particularly modulators of nuclear estrogen receptors (ERs).8 The ERs are members of the nuclear receptor superfamily of ligand-dependent transcription factors.9

There are two subtypes, namely ERα and ERβ, 10 which have distinct target tissue distributions and functional activities, and may have divergent roles. For example, activation of ERα results in the progression of estrogen-dependent breast cancer,

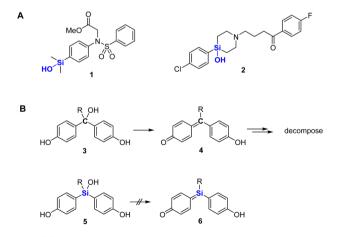


Fig. 1 (A) Structures of some silanol-based biologically active compounds. (B) Structures and properties of bis(4-hydroxyphenyl) methanols (3) and bis(4-hydroxyphenyl)silanols (5). Compounds 3 are easily converted to quinone methides 4, whereas silanols 5 cannot generate the corresponding quinone congeners.

^aInstitute for Quantitative Biosciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-0032, Japan

^bInstitute of Biomaterials and Bioengineering, Tokyo Medical and Dental University (TMDU), 2-3-10 Kanda-Surugadai, Chiyoda-ku, Tokyo 101-0062, Japan. E-mail: fujiis.chem@tmd.ac.jp

[†] Electronic supplementary information (ESI) available. DOI: https://doi.org/10.1039/d3ra04656g

10-72%

Scheme 1 Synthesis of the designed bis(4-hydroxyphenyl)silanols 5a-5h.

Table 1 ER agonistic and antagonistic activity of silanol derivatives determined by means of luciferase reporter gene assay using HEK293 cells transiently transfected with pCX-GAL4-hER-LBD and MH100x4-tk-LUC vectors. Data are presented as mean \pm SD

		ERα		ERβ	
Compd	R	$EC_{50}^{a}(\mu M)$	${\rm IC}_{50}^{b}\left(\mu M\right)$	$EC_{50}^{a}(\mu M)$	$IC_{50}^{b}\left(\mu M\right)$
5a	Me	NA	9.85 ± 1.71	3.35 ± 0.74	NA
5b	Et	$(28 \pm 7\%)^{c}$	$(40 \pm 10\%)^d$	$\textbf{7.87} \pm \textbf{2.36}$	NA
5 c	n-Pr	$(19 \pm 5\%)^{c}$	11.2 ± 2.57	$(30 \pm 4\%)^c$	$(17\% \pm 15)^d$
5d	n-Bu	NA	9.63 ± 2.78	NA	21.5 ± 33
5e	<i>n</i> -Pen	NA	$\textbf{10.0} \pm \textbf{4.93}$	NA	3.62 ± 3.5
5f	n-Hex	NA	6.09 ± 1.86	NA	$\textbf{4.80} \pm \textbf{3.85}$
5g	c-Hex	NA	10.5 ± 5.56	NA	$\textbf{0.59} \pm \textbf{0.31}$
5h	Ph	NA	$(27 \pm 6\%)^d$	NA	22.2 ± 16.1

 a Concentration showing 50% of the maximal activity of E2. b Concentration inhibiting the activity of 0.3 nM E2 by 50%. c Percentage of the maximal activation of E2 at 30 μ M. d Percent inhibition at 30 μ M. NA: no activity.

whereas ERβ inhibits proliferation and invasion of breast cancer cells. Thus, the development of subtype-selective ER modulators is an attractive approach for anticancer drug discovery. Bisphenol derivatives function as modulators of ERs, and the substituents on the central carbon atom of bisphenols greatly influence their ER subtype selectivity. Therefore, introduction of a hydroxyl group on the bisphenol core structure is a reasonable approach to develop novel subtype-selective ER modulators. However, since bis(4-hydroxyphenyl)methanols (3) are insufficiently stable, we aimed to synthesize bis(4-hydroxyphenyl)silanols (5) as more stable isosteres of bis(4-hydroxyphenyl)methanols (3), and to investigate their potency as ER modulators.

2.2 Synthesis

Synthesis of the designed bis(4-hydroxyphenyl)silanols 5a-5h is summarized in Scheme 1. From 4-benzyloxybromobenzene (7) as the starting material, lithiation and arylation with

trimethoxymethylsilane gave methoxysilane **8a**, and removal of the benzyl groups and methyl group afforded the desired silanol **5a**. Silanol derivatives **5b–5h** were synthesized similarly, using alkyltrichlorosilane instead of trimethoxysilane. Namely, lithiation of **7** and arylation with alkyltrichlorosilane gave the corresponding silanols **8b–8h**, and removal of the benzyl groups afforded the desired silanols **5b–5h**, respectively (Scheme 1).

2.3 ER modulating activity

5b-h

The ER-modulating activities of the synthesized bis(4hydroxyphenyl)silanol derivatives were evaluated by means of luciferase reporter gene assay using HEK293 cells, and the results are summarized in Table 1. Agonistic activities toward each ER subtype were assessed in terms of the increase in luciferase activity and are shown as 50% effective concentration (EC₅₀). Antagonistic activities were assessed in terms of the decrease in the luciferase activity induced by 0.3 nM estradiol (E2) and are shown as 50% inhibitory concentration (IC₅₀). All the synthesized compounds exhibited ER-modulating potency, and compounds 5d-5g bearing a large aliphatic substituent at the silicon atom exhibited significant antagonistic activity toward both ERα and ERβ. Compound 5h bearing a phenyl group showed moderate antagonistic activity. Decrease in the bulkiness of the substituent, interestingly, had different effects on the two subtypes. The methyl (5a) and propyl (5c) derivatives exhibited antagonistic activity towards ERα with potency similar to those of 5d-5g. On the other hand, propyl derivative 5c exhibited weak antagonistic activity and partial agonistic activity towards ERβ. Methyl (5a) and ethyl (5b) derivatives did not exhibit ERβ-antagonistic activity, but showed ERβ-agonistic activity. Thus, the methyl derivative 5a serves as a unique ER subtype-selective modulator, i.e., an antagonist toward ERα and a full agonist toward ER β (Fig. 2). Although the activity of 5a was weaker than the developed ER modulators, the unique subtype selectivity profile of 5a is interesting and suggestive for development of novel ER modulators.

2.4 Docking simulation

In order to understand the subtype-selective activity of silanol 5a, docking simulation using the crystal structures of human $ER\alpha$ (PDB ID: 3ERT)¹² and $ER\beta$ (PDB-ID: 3OLS)¹³ was performed (Fig. 3 and 4). The homology of the ligand-binding domains of

Paper

ERα

4.0

3.0

1.0

DMSO

E2

0.3 nM

TAM (nM)

+ E2 0.3 nM

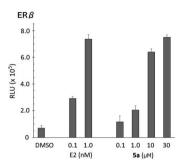


Fig. 2 Dose–response relationship of 5a in reporter gene assay using HEK293 cells. Compound 5a induced transcription of ER β , but suppressed the transcription of ER α induced by E2. Data are presented as mean \pm SD. TAM: tamoxifen.

the two ER subtypes is very high, and only two residues in the ligand-binding pocket are different, namely, Leu (Leu384) and Met (Met421) in ERα are replaced by Met (Met336) and Ile (Ile373) in ERβ, respectively. Therefore, we postulated that the interaction with these residues would be the key to the subtypeselective action of 5a. In the case of ERa, one of the phenolic hydroxyl groups of 5a interacts with Glu353 and Arg394, which form hydrogen-bonds with the 3-OH group of estradiol. The OH group of silanol is located near Met421. Although the hydrogen bonding between His524 and a ligand is important for ERa agonistic activity, 5a did not interact with His524 in the calculated structure (Fig. 3 left). On the other hand, in the docked structure with ERβ, compound 5a forms hydrogen bonds with Glu305 and Arg346, which correspond to Glu353 and Arg394 in ERα, respectively, as well as with His475, which corresponds to His524 in ERa. The OH group of silanol is also located near

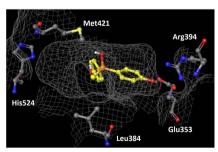
Met336 (Fig. 4 left). Thus, compound 5a can form suitable hydrogen bonds for agonistic activity with ER β . These results suggests that the silanol moiety of 5a plays a key role in recognizing the structural difference between ER α and ER β , and the loss of hydrogen bonding with His524 results in the ER α -antagonistic activity of 5a.

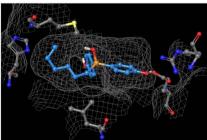
We also performed docking simulation of *n*-hexyl derivative 5f which acted as an antagonist towards both ERα and ERβ. In the docked structure with ERa, the bisphenol core of compound 5f takes a similar conformation to that of 5a, in which the OH group of silanol is located near Met421, and the n-hexyl group occupies the hydrophobic cavity (Fig. 3 center). In the docked structure with ERβ, on the other hand, the conformation of compound 5f is quite different from that of 5a. One phenolic OH group of 5f interacts with Glu305 and Arg346, but there is no interaction with His475, and the n-hexyl group occupies the cavity that is occupied by the phenol group of 5a (Fig. 4 center). This calculated structure of 5f in ER β is similar to that in ER α , which may explain why the silanol derivatives 5d-5h bearing a bulky substituent function as antagonists toward both ERa and ERB. These results suggests that the loss of hydrogen bonding with His524 is responsible for the ERα-antagonistic activity of 5a.

We performed docking simulation of imaginary methyl and hexyl carbinol analogs with hER α LBD. These carbon analogs adopt conformation similar to the corresponding silanols 5a and 5f, respectively (Fig. S1 \dagger). However, these carbon analogs are inherently unstable. Thus, the silanol moiety plays a key role in realization of the characteristic activity.

3 Conclusions

In order to expand the utility of silicon-based molecular construction in medicinal chemistry, we designed and synthesized a series of silanol-based bisphenol derivatives as stable isosteres of bis(4-hydroxyphenyl)methanol derivatives, which readily undergo dehydration to form electrophilic quinone methide species. The synthesized silanol derivatives served as ligands of ER α and ER β , and methyl silanol **5a** exhibited a unique subtype selectivity profile, namely, antagonist activity toward ER α and agonist activity toward ER β . Docking simulation suggested that the interaction of the silanol moiety with methionine (Met421 in ER α or Met336 in ER β) and hydrophobic





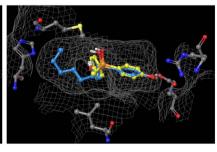


Fig. 3 Docking models of silanol 5a and 5f with hER α LBD (PDB ID: 3ERT) obtained with AutoDock $4.2.^{14}$ The protein surface is indicated as a grey mesh. (Left) Docking model of 5a (yellow) in the hER α LBD. (Center) Docking model of 5f (cyan) in the hER α LBD. (Right) Superimposition of the docking models of 5a and 5f.

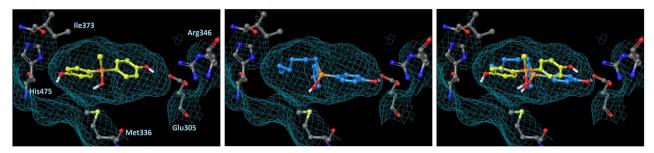


Fig. 4 Docking models of silanol 5a and 5f with hERβ LBD (PDB ID: 3OLS) obtained with AutoDock 4.2. The protein surface is indicated as a blue mesh. (Left) Docking model of 5a (yellow) in the hERβ LBD. (Center) Docking model of 5f (cyan) in the hERβ LBD. (Right) Superimposition of the docking models of 5a and 5f.

interaction of the alkyl substituent are key factors. Since both antagonistic activity toward ER α and agonistic activity toward ER β are desirable for anticancer activity, ¹¹ the compounds developed in this study may be promising lead compounds for cancer drug discovery.

4 Experimental

The detailed procedures for synthesis of compounds, biological evaluation and docking simulation is given in the ESI file.†

Conflicts of interest

There are no conflicts to declare.

Acknowledgements

This work was partially supported by Grants in-Aid for Scientific Research from JSPS (KAKENHI Grant No. 17H03997, 19K22486 and 23K06046 (SF)), Takeda Science Foundation (SF), and Research Support Project for Life Science and Drug Discovery (Basis for Supporting Innovative Drug Discovery and Life Science Research (BINDS)) from AMED under Grant Number JP23ama121043.

Notes and references

- 1 (*a*) V. Chandrasekhar, R. Boomishankar and S. Nagendran, *Chem. Rev.*, 2004, **104**, 5847–5910; (*b*) M. Jeon, J. Han and J. Park, *ACS Catal.*, 2012, **2**, 1539–1549.
- 2 (a) S. E. Denmark and A. Ambrosi, *Org. Process Res. Dev.*, 2015, **19**, 982–994; (b) S. E. Denmark, *J. Org. Chem.*, 2009, **74**, 2915–2927.
- 3 (a) R. Ramesh and D. S. Reddy, J. Med. Chem., 2018, 61, 3779–3798; (b) S. Fujii and Y. Hashimoto, Future Med. Chem., 2017, 9, 485–505; (c) A. K. Franz and S. O. Wilson, J. Med. Chem., 2013, 56, 388–405.
- 4 (a) H. Toyama, S. Sato, H. Shirakawa, M. Komai, Y. Hashimoto and S. Fujii, *Bioorg. Med. Chem. Lett.*, 2016, **26**, 1817–1820; (b) H. Toyama, H. Shirakawa, M. Komai, Y. Hashimoto and S. Fujii, *Bioorg. Med. Chem.*, 2018, **26**, 4493–4501.

- 5 (a) R. Tacke, T. Heinrich, R. Bertermann, C. Burschka,
 A. Hamacher and M. U. Kassack, *Organometallics*, 2004, 23,
 4468–4477; (b) R. Tacke, F. Popp, B. Müller B, B. Theis,
 C. Burschka, A. Hamacher, M. U. Kassack, D. Schepmann,
 B. Wünsch, U. Jurva and E. Wellner, *ChemMedChem*, 2008,
 3, 152–164.
- 6 X. Chen, T. Pradhan, F. Wang, J.-S. Kim and J. Yoon, *Chem. Rev.*, 2012, 112, 1910–1956.
- 7 S. Hosoda, D. Matsuda, H. Tomoda and Y. Hashimoto, *Mini-Rev. Med. Chem.*, 2009, **9**, 572–580.
- 8 K. Maruyama, M. Nakamura, S. Tomoshige, K. Sugita, M. Makishima, Y. Hashimoto and M. Ishikawa, *Bioorg. Med. Chem. Lett.*, 2013, 23, 4031–4036.
- 9 (a) H. Gronemeyer, J.-A. Gustafsson and V. Laudet, *Nat. Rev. Drug Discovery*, 2004, 3, 950–964; (b) D. J. Mangelsdorf, C. Thummel, M. Beato, P. Herrlich, G. Schütz, K. Umesono, B. Blumberg, P. Kastner, M. Mark, P. Chambon and R. M. Evans, *Cell*, 1995, 83, 835–839; (c) R. M. Evans, *Science*, 1988, 240, 889–894.
- 10 (a) N. Heldring, A. Pike, S. Andersson, J. Matthews, G. Cheng, J. Hartman, M. Tujague, A. Ström, E. Treuter, M. Warner and J.-A. Gustafsson, *Physiol. Rev.*, 2007, 87, 905–931; (b) B. J. Deroo and K. S. Korach, *J. Clin. Invest.*, 2006, 116, 561–570; (c) C. Thomas and J.-Å. Gustafsson, *Nat. Rev. Cancer*, 2011, 11, 597–608; (d) B. S. Katzenellenbogen, M. M. Montano, T. R. Ediger, J. Sun, K. Ekena, G. Lazennec, P. G. Martini, E. M. McInerney, R. Delage-Mourroux, K. Weis and J. A. Katzenellenbogen, *Recent Prog. Horm. Res.*, 2000, 55, 163–193.
- 11 (a) I. Paterni, C. Granchi, J. A. Katzenellenbogen and F. Minutolo, *Steroids*, 2014, **90**, 13–29A; (b) K. Shiau, D. Barstad, J. T Radek, M. J. Meyers, K. W. Nettles, B. S. Katzenellenbogen, J. A. Katzenellenbogen, D. A. Agard and G. L. Greene, *Nat. Struct. Biol.*, 2002, **9**, 359–364.
- 12 A. K. Shiau, D. Barstad, P. M. Loria, L. Cheng, P. J. Kushner, D. A. Agard and G. L. Greene, *Cell*, 1998, 95, 927–937.
- 13 S. Mocklinghoff, R. Rose, M. Carraz, A. Visser, C. Ottmann and L. Brunsveld, *ChemBioChem*, 2010, 11, 2251–2254.
- 14 G. M. Morris, R. Huey, W. Lindstrom, M. F. Sanner, R. K. Belew, D. S. Goodsell and A. J. Olson, *J. Comput. Chem.*, 2009, **16**, 2785–2791.