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Structure-based virtual screening leading to discovery of highly selective butyrylcholinesterase inhibitors with solanaceous alkaloid scaffolds

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Abstract

According to recent research advance, it is interesting to identify new, potent and selective inhibitors of human butyrylcholinesterase (BChE) for therapeutic treatment of both the Alzheimer's disease (AD) and heroin abuse. In this study, we carried out a structure-based virtual screening followed by *in vitro* activity assays, with the goal to identify new inhibitors that are selective for BChE over acetylcholinesterase (AChE). As a result, a set of new, selective inhibitors of human BChE were identified from natural products with solanaceous alkaloid scaffolds. The most active one of the natural products (compound **1**) identified has an IC₅₀ of 16.8 nM against BChE. It has been demonstrated that the desirable selectivity of these inhibitors for BChE over AChE is mainly controlled by three key residues in the active site cavity, *i.e.* residues Q119, A277, and A328 in BChE *versus* the respective residues Y124, W286, and Y337 in AChE. Based on this structural insight, future rational design of new, potent and selective BChE inhibitors may focus on these key structural differences in the active site cavity.

Introduction

Cholinesterases, including both acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), are among the well-known targets for treatment of Alzheimer's disease (AD), the most serious neurodegenerative disease that has affected about 30 million people [1]. In fact, the first four drugs that have ever been approved by the FDA for the AD treatment are

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Additional Information

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cholinesterase inhibitors that either inhibit both AChE and BChE (tacrine, donepezil, and rivastigmine) or selectively inhibit AChE (galantamine). However, studies reported in recent years have revealed that BChE might be a better target compared to AChE for the AD treatment [2–4]. In other words, a BChE-selective inhibitor might be more promising than an AChE inhibitor for the AD treatment [2–14].

In addition, in our recently reported study [15], we proposed and validated a new therapeutic strategy for heroin toxicity treatment by using a selective BChE inhibitor to block heroin activation. It has been demonstrated that a selective BChE inhibitor can be used to significantly attenuate the heroin-induced toxicity and physiological effects [15]. Hence, it is interesting to develop potent and selective BChE inhibitors in drug development for therapeutic treatment of both the AD and heroin abuse.

In fact, a variety of cholinesterase inhibitors have been reported in literature, with various scaffolds. Most of reported cholinesterase inhibitors are either not sufficiently potent for BChE [16–27] or almost equally potent for both AChE and BChE [25, 28–41]. For some other BChE inhibitors reported, the selectivity is unknown (not tested at all) [42, 43]. Few types of cholinesterase inhibitors have promising potency and selectivity for BChE over AChE [12, 17, 25, 38, 44–56]. Some BChE inhibitors were also identified through virtual screening methods but either their activity was mediocre [57] or their selectivity over AChE was not reported [58, 59]. It is highly desired to identify new, potent and selective BChE inhibitors as options for further drug development.

Here we report the identification of a set of new, selective BChE inhibitors from natural products with solanaceous alkaloid scaffolds through structure-based virtual screening and *in vitro* activity assays.

Materials and methods

Structure-based virtual screening.

Our virtual screening was performed on the Development Therapeutics Program (DTP) Release 4 compound library including ~265,000 compounds available at the National Cancer Institute (NCI) (<https://cactus.nci.nih.gov/download/nci/>) by using the X-ray crystal structures of human BChE (PDB entry 4BDS) [60] and AChE (PDB entry 4EY5) [61]. During the virtual screening, Autodock Vina 1.1.2 software [62] was used to search for the optimum binding conformation for each compound in the NCI compound library. To minimize the searching area, a 15 Å×15 Å×15 Å box containing the active site of BChE or AChE was chosen as the target binding site. The protein was set rigid and all the water molecules in the original crystal structure were removed prior to molecular docking. The default settings of the Autodock Vina was used and no other parameters were modified. The compounds were then ranked by their binding free energies (docking score) with BChE. Within the top-ranked compounds, only the compounds predicted to have a positive binding free energy with AChE will be selected and ordered from the NIH DTP program. All the binding modes were then investigated and visualized using the PyMol [63].

***In vitro* activity tests.**

The top compounds selected from the virtual screening were first ordered from the NCI DTP program and assayed for their inhibitory activity against BChE. The most compromising compounds (**1** to **3**) were also ordered from Sigma-Aldrich (St Louis, MO) for comparison and verification. Both wild-type AChE and BChE were expressed and purified based on our previous reported protocol [64]. For activity determination, we followed the original Ellman's protocol, as described in detail in our previous report [64]. The concentration of substrate butyrylthiocholine for BChE (or acetylthiocholine for AChE) was at 10 μ M. The tested compounds were first dissolved in DMSO and the final DMSO concentration was at 1%.

Results and discussion

Based on the structure-based virtual screening, we selected a set of 10 compounds (**1** to **10** depicted in Figure 1) that were predicted to bind with BChE only, without binding with AChE. All these compounds are natural products with solanaceous alkaloid scaffolds. The binding free energies calculated for AChE binding with compounds **1** to **10** ranged from +4.5 kcal/mol to +17 kcal/mol; the positive binding free energy means that the free energy of the protein-ligand complex is higher than the total free energy of the separated protein and ligand. This is because BChE has a relatively larger active site cavity than AChE such that these larger molecules can only fit the BChE active site cavity, whereas the AChE active site cavity is not large enough to accommodate these molecules (see below for the detailed binding structures).

Next, the computationally selected compounds **1** to **10** (ordered from the NCI DTP) were assayed for their inhibitory activity against human BChE. They were assayed first for their inhibitory activity at a concentration of 5 μ M. As seen in Table 1, these compounds at 5 μ M inhibited the BChE activity by 8-100%. The top-3 compounds (**1** to **3**) inhibited BChE by at least 95%. The most active compounds (**1** to **3**) were tested further for the dose-dependent inhibition in order to determine their IC_{50} values (see Figure 2 and Table 1) against BChE. As seen in Table 1, we obtained IC_{50} = 16.8 nM, 346 nM, and 391 nM for compounds **1** to **3**, respectively. Similar results were also obtained from the use of compounds **1** to **3** ordered from Sigma-Aldrich (St Louis, MO).

Interestingly, according to our detailed literature search, compounds **1** to **3** were tested for their inhibitory activity against AChE by Roddick *et al.* [65], and they demonstrated that none of these compounds (**1** to **3**) at a high concentration of 100 μ M had significant inhibition against AChE. According to our own assays in this study, at a concentration of 5 μ M, compounds **1** to **3** from Sigma-Aldrich (St Louis, MO) inhibited the AChE activity by only about 10%, 19%, and 2%, respectively (see Table 1). To the best of our knowledge, we have not found any report of testing these compounds against BChE. Taking all of these experimental data together, we can conclude that compounds **1** to **3** are indeed selective inhibitors of BChE, which is consistent with the aforementioned prediction from computational screening.

Depicted in Figure 3 are the docked binding structures of BChE with the most active compounds (**1** to **3**) identified. According to the docked binding structures with BChE, the inhibitor (compound **1** or **2** or **3**) stays in a mainly hydrophobic environment, but having a favorable hydrogen bond (HB) between the hydroxyl group of the inhibitor and the backbone oxygen of amino-acid residue H438. The HB with compound **1** is the strongest (with the shortest O···H distance of 1.956 Å), explaining why compound **1** is the most potent inhibitor of BChE with IC₅₀ = 16.8 nM within these three inhibitors. With these three inhibitors, their order of the HB strengths (see Figure 2) is consistent with their order of the IC₅₀ values.

Panels B, D, and F of Figure 3 also show why the AChE active site cavity cannot accommodate any of these compounds. Specifically, panels A, C, and E show the docked favorable binding structures of BChE with compounds **1**, **2**, and **3**, respectively. The corresponding unfavorable interactions of the compounds with AChE (after BChE is replaced with AChE) are depicted in panels B, D, and F, respectively. For the major differences between BChE and AChE in the protein-ligand interactions, residues Q119, A277, and A328 in BChE are replaced with Y124, W286, and Y337, respectively, in AChE. In the X-ray crystal structures of AChE-inhibitor complexes [66, 67], these residues (Y124, W286, and Y337) also played important roles in AChE binding with the inhibitors through hydrophobic interactions. Possible clash with any of these residues is expected to greatly impair the binding of the compound with AChE. According to our molecular modeling studies (see Figure 3), the compound (**1** or **2** or **3**) has clash with the side chains of Y124, W286, and Y337 in AChE, explaining why these compounds are selective for BChE over AChE for their inhibitory activities.

Conclusion

Through combined structure-based virtual screening and *in vitro* activity assays, we have successfully identified a set of new, selective inhibitors of human BChE from natural products with solanaceous alkaloid scaffolds. The most potent BChE inhibitor (compound **1**) identified has an IC₅₀ of 16.8 nM against BChE. These interesting outcomes suggest that natural products may be used as a promising resource in our future search of potent and selective inhibitors of BChE for BChE-based drug discovery.

Notably, the selectivity of these compounds for BChE over AChE is mainly controlled by three key residues in the active site cavity, *i.e.* residues Q119, A277, and A328 in BChE *versus* the respective residues Y124, W286, and Y337 in AChE (all with relatively larger side chains). In light of this structural insight, it is interesting to focus on these key structural differences in future rational design of new, potent and selective BChE inhibitors.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Research Highlights

- Virtual screening using 3D structures of both BChE and AChE is effective.
- Highly selective BChE inhibitors have been identified from natural products.
- The compounds with a solanaceous alkaloid scaffold can bind with BChE only.
- Three key residues are mainly responsible for the extremely high selectivity.

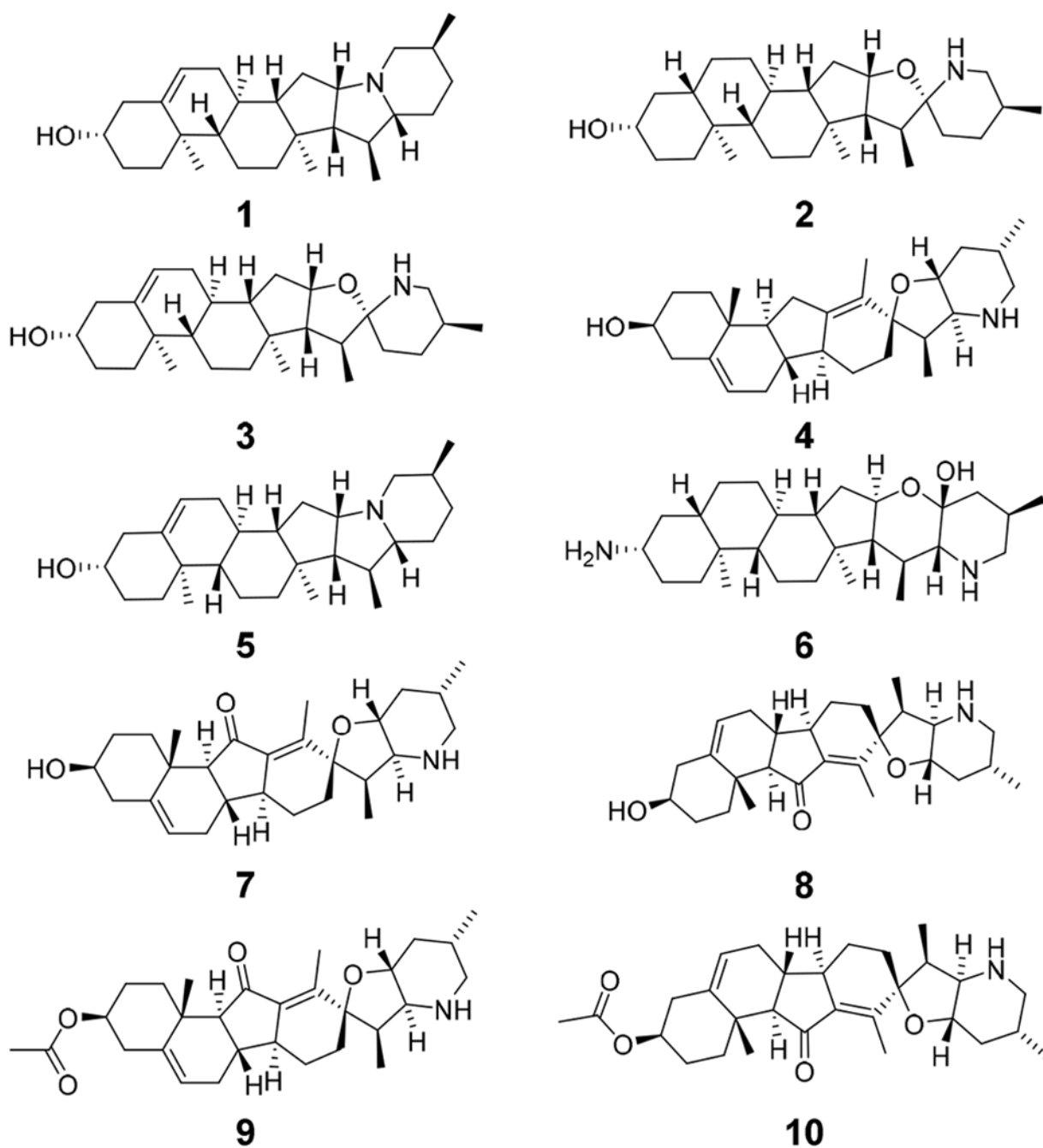


Figure 1.
Molecular structures of the 10 compounds with solanaceous alkaloid scaffolds selected through virtual screening

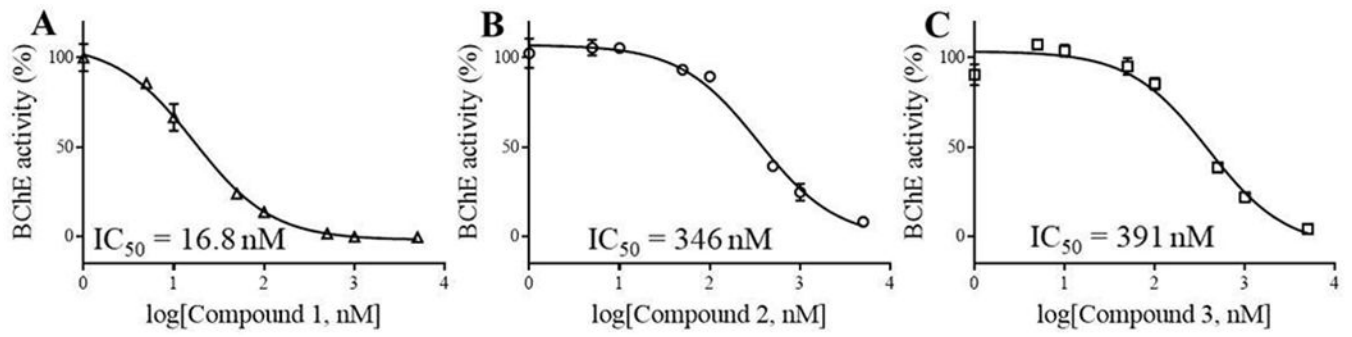


Figure 2.
Dose-dependent inhibition of human BChE by compounds **1** (A), **2** (B), and **3** (C).

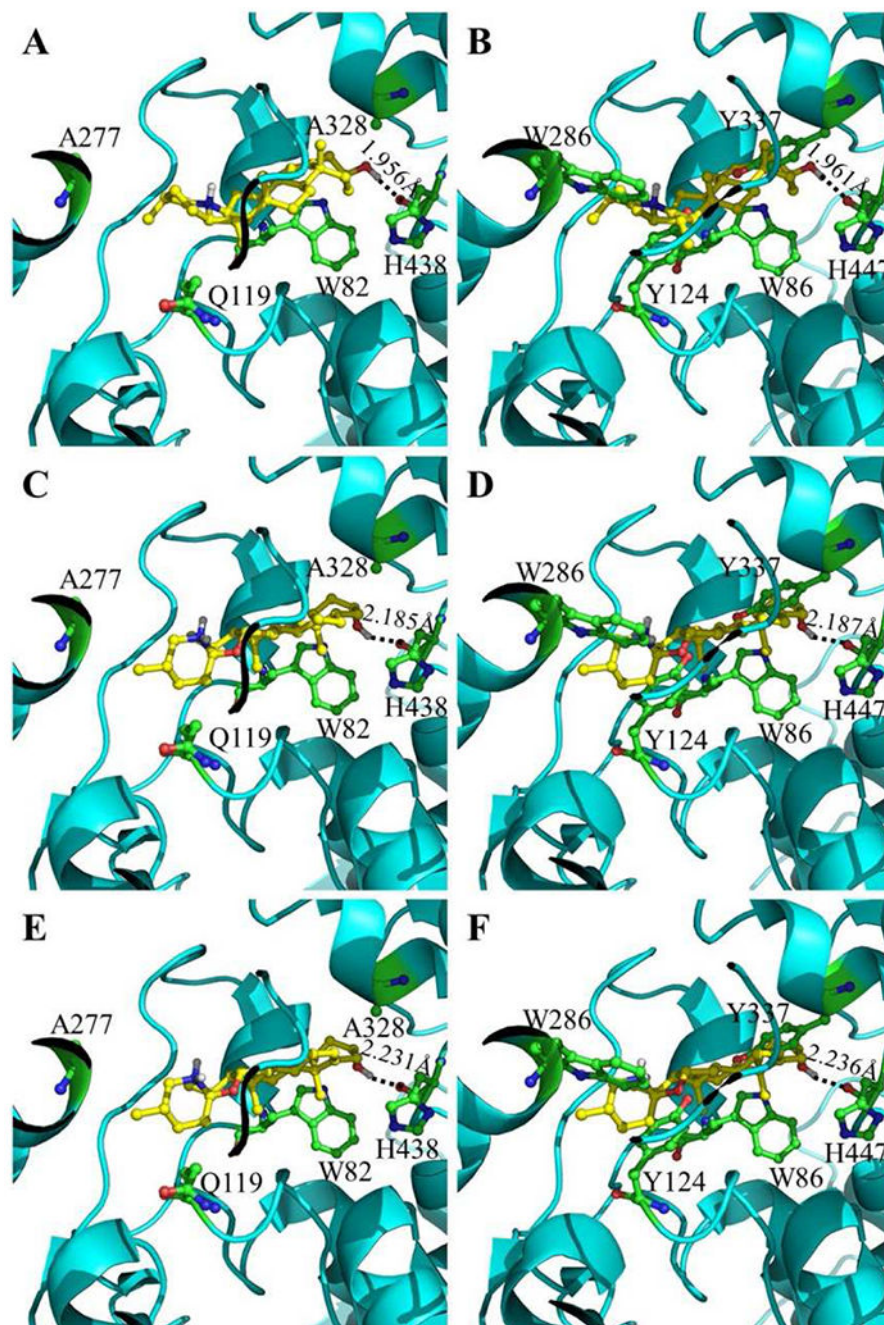


Figure 3. Modeled interactions of BChE and AChE with compounds **1** to **3**. (A) Favorable binding structure of compound **1** with BChE. (B) Unfavorable interaction of compound **1** with AChE after BChE in panel A is replaced with AChE. (C) Favorable binding structure of compound **2** with BChE. (D) Unfavorable interaction of compound **2** with AChE after BChE in panel C is replaced with AChE. (E) Favorable binding structure of compound **3** with BChE. (F)

Unfavorable interaction of compound 3 with AChE after BChE in panel E is replaced with AChE.

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Table 1.Inhibitory activity of computationally selected solanaceous alkaloids (compounds **1** to **3**) against human BChE

Compound ID	NCI ID	Conventional Name	Inhibition (%) of BChE at 5 μ M	Inhibition (%) of AChE at 5 μ M	IC ₅₀ against BChE (nM)
1	76025	Solanidine	100	10	16.8
2	27592	Tomatidine	95	19	346
3	35543	Solasodine	98	2	391
4	734950		44		
5	76026		39		
6	152144		24		
7	23898		22		
8	7520		18		
9	117607		14		
10	117612		8.3		